

Supplementary Information

Biogeography of marine giant viruses reveals their interplay with eukaryotes and ecological functions

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Supplementary Table 1 The number of samples representing each biome, oceanic region, depth and size fraction.

	Ecozone	Abbreviation	Pico-size (0.22–1.6/3 μm)				Femto-size (<0.22 μm)			
			SRF	DCM	MES	Total	SRF	DCM	MES	Total
Biome	Coastal Biome	Coastal	18	11	6	35	16	9	1	26
	Trade winds Biome	Trades	27	19	16	62	23	15	6	44
	Westerlies Biome	Westerlies	17	12	8	37	2	3	1	6
	Polar Biome	Polar	21	8	9	38	19	8	8	35
Oceanic region	North Atlantic Ocean	NAO	11	5	7	23	0	1	1	2
	Mediterranean Sea	MS	6	6	0	12	2	2	0	4
	Red Sea	RS	4	2	0	6	5	1	0	6
	Indian Ocean	IO	12	9	6	27	17	11	3	31
	South Atlantic Ocean	SAO	8	6	5	19	7	5	1	13
	Southern Ocean	SO	2	1	1	4	0	1	0	1
	South Pacific Ocean	SPO	15	9	7	31	7	4	2	13
	North Pacific Ocean	NPO	6	5	5	16	3	3	1	7
Arctic Ocean	AO	19	7	8	34	19	7	8	34	
	Total		83	50	39	172	60	35	16	111

Supplementary Data 1: List of the MAGs and the predicted genes exhibited a best hit to the transcripts of chrysoyphytes .

MAG	MAG ID	Overlap with the other MAGs	Contig ID	Query sequence	Best hit (MMETSP transcripts ID)	Identity (%)	Alignment length (AA)	E-value	Bitscore	
MoMAGs	ERX552279_2_dc	-	Moniruzzaman_EP01_ERX552279_2_dc_000000000013	gene_2205[GeneMark.hmm]523_aa j9106 10677	GSChrysoyphyteH2.ASY1.ANO1.872.1	61.4	158	1e-45	192.2	
	ERX552270_73_dc	-	Moniruzzaman_MM01_ERX552270_73_dc_000000000003	gene_47732[GeneMark.hmm]180_aa j6634 7176	GSChrysoyphyteH1.ASY1.ANO1.800.1	56.8	176	6e-52	211.5	
	ERX552270_73_dc	-	Moniruzzaman_MM01_ERX552270_73_dc_000000000005	gene_47766[GeneMark.hmm]363_aa j1661 2752	GSChrysoyphyteH2.ASY1.ANO1.55.1	53.9	323	3e-91	342.8	
	ERX552283_5_dc	-	Moniruzzaman_MM01_ERX552283_5_dc_000000000005	gene_51310[GeneMark.hmm]365_aa j1739 8236	GSChrysoyphyteH2.ASY1.ANO1.55.1	58.4	334	3e-101	376.3	
	ERX552296_8_dc	-	Moniruzzaman_MM01_ERX552296_8_dc_000000000008	gene_56524[GeneMark.hmm]356_aa j24203 25273	GSChrysoyphyteH2.ASY1.ANO1.55.1	53.9	330	2e-91	343.6	
	ERX555943_12_dc	GVMAG-M-3300009497-12	Moniruzzaman_MM01_ERX555943_12_dc_000000000004	gene_61969[GeneMark.hmm]180_aa j9700 10242	GSChrysoyphyteH1.ASY1.ANO1.800.1	57.4	176	8e-52	211.1	
	ERX555943_9_dc	GVMAG-S-ERX555943-30	Moniruzzaman_MM01_ERX555943_9_dc_000000000007	gene_62837[GeneMark.hmm]183_aa j12778 13329	GSChrysoyphyteH1.ASY1.ANO1.800.1	58	174	3e-52	212.6	
	ERX555964_34_dc	-	Moniruzzaman_MM01_ERX555964_34_dc_000000000012	gene_64702[GeneMark.hmm]227_aa j11681	GSChrysoyphyteH1.ASY1.ANO1.1156.1	55.2	210	3e-57	229.6	
	ERX555967_26_dc	-	Moniruzzaman_MM01_ERX555967_26_dc_000000000004	gene_67777[GeneMark.hmm]227_aa j2269 2952	GSChrysoyphyteH2.ASY1.ANO1.800.1	52.7	186	2e-36	160.2	
	ERX555967_26_dc	-	Moniruzzaman_MM01_ERX555967_26_dc_000000000010	gene_68055[GeneMark.hmm]186_aa j30703 31263	GSChrysoyphyteH1.ASY1.ANO1.800.1	58.2	158	3e-47	195.7	
	ERX556019_45_dc	GVMAG-S-ERX555943-30	Moniruzzaman_MM01_ERX556019_45_dc_000000000010	gene_73941[GeneMark.hmm]183_aa j21765 22316	GSChrysoyphyteH1.ASY1.ANO1.800.1	58	174	3e-52	212.6	
	ERX556031_42_dc	-	Moniruzzaman_MM01_ERX556031_42_dc_000000000010	gene_76095[GeneMark.hmm]318_aa j40647 41603	GSChrysoyphyteH2.ASY1.ANO1.89.1	58.9	297	5e-94	352.1	
	ERX556106_20_dc	GVMAG-S-ERX556106-38	Moniruzzaman_MM01_ERX556106_20_dc_000000000001	gene_80949[GeneMark.hmm]341_aa j10456 11481	GSChrysoyphyteH2.ASY1.ANO1.55.1	63.4	298	1e-103	384	
	SRX474032_22_dc	-	Moniruzzaman_MM01_SRX474032_22_dc_000000000006	gene_89402[GeneMark.hmm]147_aa j43546 43989	GSChrysoyphyteH1.ASY1.ANO1.800.1	56.1	148	1e-42	180.3	
	SRX802073_139_dc	GVMAG-M-3300025699-48	Moniruzzaman_MM01_SRX802073_139_dc_000000000006	gene_90612[GeneMark.hmm]182_aa j27256 27804	GSChrysoyphyteH1.ASY1.ANO1.800.1	62.2	156	1e-52	213.8	
	SRX802073_61_dc	-	Moniruzzaman_MM01_SRX802073_61_dc_000000000004	gene_92288[GeneMark.hmm]183_aa j16026 16577	GSChrysoyphyteH1.ASY1.ANO1.800.1	55.2	165	2e-48	199.9	
	SRX802073_68_dc	-	Moniruzzaman_MM01_SRX802073_68_dc_000000000013	gene_92650[GeneMark.hmm]197_aa j31593	GSChrysoyphyteH2.ASY1.ANO1.900.1	53.1	179	7e-33	148.3	
	SRX802073_99_dc	-	Moniruzzaman_MM01_SRX802073_99_dc_000000000002	gene_93416[GeneMark.hmm]1069_aa j17302 20511	GSChrysoyphyteH1.ASY1.ANO1.3101.1	73.1	535	2e-240	840.1	
	SRX802143_8_dc	-	Moniruzzaman_MM01_SRX802143_8_dc_000000000013	gene_99397[GeneMark.hmm]219_aa j9589 10248	GSChrysoyphyteH1.ASY1.ANO1.1156.1	54.3	186	8e-51	208	
	SRX802202_64_dc	GVMAG-S-1016713-123	Moniruzzaman_MM01_SRX802202_64_dc_000000000004	gene_103035[GeneMark.hmm]1088_aa j11357 14623	GSChrysoyphyteH1.ASY1.ANO1.3101.1	74.5	537	8e-245	854.7	
	SRX802202_75_dc	GVMAG-M-3300001348-35	Moniruzzaman_MM01_SRX802202_75_dc_000000000004	gene_103199[GeneMark.hmm]183_aa j7875 8426	GSChrysoyphyteH1.ASY1.ANO1.800.1	62.4	157	7e-53	214.5	
	ERX552270_36_dc	-	Moniruzzaman_MM05_ERX552270_36_dc_000000000004	gene_111021[GeneMark.hmm]413_aa j17418 18659	GSChrysoyphyteH2.ASY1.ANO1.205.1	55.9	186	9e-56	225.3	
	ERX555941_31_dc	-	Moniruzzaman_MM09_ERX555941_31_dc_000000000010	gene_143091[GeneMark.hmm]988_aa j18732 21698	GSChrysoyphyteH1.ASY1.ANO1.1156.1	50.7	221	5e-57	230.7	
	ERX555978_20_dc	-	Moniruzzaman_MM09_ERX555978_20_dc_000000000009	gene_146435[GeneMark.hmm]987_aa j18830 21781	GSChrysoyphyteH1.ASY1.ANO1.1156.1	50.7	221	1e-56	229.6	
	ERX556015_14_dc	-	Moniruzzaman_MM09_ERX556015_14_dc_000000000022	gene_149160[GeneMark.hmm]983_aa j18830 21781	GSChrysoyphyteH1.ASY1.ANO1.1156.1	50.7	221	8e-58	233.4	
	ERX556103_23_dc	-	Moniruzzaman_MM09_ERX556103_23_dc_000000000003g_1275	gene_151554[GeneMark.hmm]285_aa j14612 15469	GSChrysoyphyteH1.ASY1.ANO1.1156.1	57.1	233	3e-68	266.2	
	GVMAGs high quality	GVMAG-M-3300001348-35	SRX802202_75_dc	GVMAG-M-3300001348-35JG2015414316_10002040	gene_2663[GeneMark.hmm]183_aa j897 1448	GSChrysoyphyteH1.ASY1.ANO1.800.1	62.4	157	7e-53	214.5
		GVMAG-M-3300009159-4	-	gene_21921[GeneMark.hmm]147_aa j4204 4647	GSChrysoyphyteH1.ASY1.ANO1.800.1	57.4	148	8e-44	184.1	
		GVMAG-M-3300009436-33	-	GVMAG-M-3300009436-33[Ga0115008_10001449	gene_37351[GeneMark.hmm]374_aa j17944 19068	GSChrysoyphyteH2.ASY1.ANO1.55.1	54.2	332	4e-95	355.9
		GVMAG-M-3300009436-33	-	GVMAG-M-3300009436-33[Ga0115008_10002902	gene_37360[GeneMark.hmm]186_aa j1743 7703	GSChrysoyphyteH1.ASY1.ANO1.800.1	55	171	1e-52	213.8
GVMAG-M-3300009497-12		ERX555943_12_dc	GVMAG-M-3300009497-12[Ga0115569_10001015	gene_38282[GeneMark.hmm]183_aa j4325 4876	GSChrysoyphyteH1.ASY1.ANO1.800.1	55.2	165	2e-48	199.9	
GVMAG-M-3300010368-24		-	GVMAG-M-3300010368-24[Ga0128924_10000109	gene_46584[GeneMark.hmm]170_aa j25786 26298	GSChrysoyphyteH1.ASY1.ANO1.800.1	57.6	165	5e-50	204.9	
GVMAG-M-3300017724-7		-	GVMAG-M-3300017724-7[Ga0181388_1000057	gene_58161[GeneMark.hmm]187_aa j21400 21963	GSChrysoyphyteH1.ASY1.ANO1.800.1	55.9	152	1e-46	193.7	
GVMAG-M-3300018428-16		-	GVMAG-M-3300018428-16[Ga0181568_10000144	gene_68595[GeneMark.hmm]182_aa j1254 1802	GSChrysoyphyteH1.ASY1.ANO1.800.1	55.9	161	1e-49	203.8	
GVMAG-M-3300020185-39		-	GVMAG-M-3300020185-39[Ga0206131_10007858	gene_79797[GeneMark.hmm]741_aa j312228	GSChrysoyphyteH2.ASY1.ANO1.205.1	53.5	579	8e-156	558.5	
GVMAG-M-3300021340-15		-	GVMAG-M-3300021340-15[Ga0194041_10002413	gene_92713[GeneMark.hmm]731_aa j2889 5084	GSChrysoyphyteH2.ASY1.ANO1.205.1	55.1	227	6e-68	266.5	
GVMAG-M-3300021389-31		-	GVMAG-M-3300021389-31[Ga0213868_10000432	gene_95481[GeneMark.hmm]2934_aa j3038 39185	GSChrysoyphyteH2.ASY1.ANO1.358.1	52.7	300	4e-59	239.2	
GVMAG-M-3300021425-21		-	GVMAG-M-3300021425-21[Ga0213866_10001650	gene_96884[GeneMark.hmm]149_aa j1563 2912	GSChrysoyphyteH1.ASY1.ANO1.1156.1	51.8	218	1e-50	208.4	
GVMAG-M-3300021962-46		-	GVMAG-M-3300021962-46[Ga0222713_10000006	gene_101370[GeneMark.hmm]562_aa j186550 188238	GSChrysoyphyteH2.ASY1.ANO1.464.1	58.4	541	7e-181	641.3	
GVMAG-M-3300022173-22		-	GVMAG-M-3300022173-22[Ga0255776_10001064	gene_109378[GeneMark.hmm]628_aa j371 2257	GSChrysoyphyteH1.ASY1.ANO1.205.1	57.3	567	7e-182	644.8	
GVMAG-M-3300023174-92		-	GVMAG-M-3300023174-92[Ga0214921_10004619	gene_129283[GeneMark.hmm]331_aa j14900 15895	GSChrysoyphyteH2.ASY1.ANO1.55.1	55	300	3e-90	339.3	
GVMAG-M-3300023184-105		-	GVMAG-M-3300023184-105[Ga0214919_10000301	gene_149022[GeneMark.hmm]310_aa j4581 46746	GSChrysoyphyteH2.ASY1.ANO1.55.1	60.8	296	6e-99	368.2	
GVMAG-M-3300023184-81		-	GVMAG-M-3300023184-81[Ga0214919_10000640	gene_166539[GeneMark.hmm]147_aa j51203 51646	GSChrysoyphyteH1.ASY1.ANO1.800.1	60.1	148	7e-46	191	
GVMAG-M-3300024261-61		-	GVMAG-M-3300024261-61[Ga02233439_10000557	gene_176096[GeneMark.hmm]373_aa j2238 23359	GSChrysoyphyteH1.ASY1.ANO1.55.1	59.3	334	1e-102	380.9	
GVMAG-M-3300024299-4		-	GVMAG-M-3300024299-4[Ga0233448_1000541	gene_178322[GeneMark.hmm]351_aa j38004 39059	GSChrysoyphyteH1.ASY1.ANO1.2156.1	52	348	2e-90	340.5	
GVMAG-M-3300024314-16		-	GVMAG-M-3300024314-16[Ga0228657_1000014	gene_180240[GeneMark.hmm]370_aa j993 2105	GSChrysoyphyteH2.ASY1.ANO1.55.1	54.8	334	2e-93	350.1	
GVMAG-M-3300025699-48		SRX802073_139_dc	GVMAG-M-3300025699-48[Ga0209715_10001123	gene_184856[GeneMark.hmm]182_aa j19751 20299	GSChrysoyphyteH1.ASY1.ANO1.800.1	62.2	156	1e-52	213.8	
GVMAG-M-3300027833-11		-	GVMAG-M-3300027833-11[Ga0209092_10000013	gene_204138[GeneMark.hmm]347_aa j8593 90436	GSChrysoyphyteH1.ASY1.ANO1.2156.1	54.3	346	3e-93	349.4	
GVMAG-M-3300027983-55		-	GVMAG-M-3300027983-55[Ga0209264_10003575	gene_209916[GeneMark.hmm]184_aa j7077 7631	GSChrysoyphyteH1.ASY1.ANO1.800.1	63.1	157	6e-52	211.5	
GVMAG-S-1016713-123		SRX802202_64_dc	GVMAG-S-1016713-123 1016713_contig_19	gene_212534[GeneMark.hmm]1088_aa j86684 89950	GSChrysoyphyteH1.ASY1.ANO1.3101.1	74.5	537	8e-245	854.7	
GVMAG-S-1016713-165		-	GVMAG-S-1016713-165 1016713_contig_1407	gene_213900[GeneMark.hmm]1642_aa j15115 10043	GSChrysoyphyteH2.ASY1.ANO1.205.1	54.1	1110	0e+00	1119.8	
GVMAG-S-1017745-107		-	GVMAG-S-1017745-107 1017745_contig_2596	gene_217304[GeneMark.hmm]289_aa j4274 5143	GSChrysoyphyteH1.ASY1.ANO1.2156.1	55.4	294	2e-86	327	
GVMAG-S-1039734-46		-	GVMAG-S-1039734-46 1039734_contig_292	gene_228578[GeneMark.hmm]356_aa j12930 14000	GSChrysoyphyteH2.ASY1.ANO1.1416.1	50.2	231	1e-59	238	
GVMAG-S-1039734-46		-	GVMAG-S-1039734-46 1039734_contig_1703	gene_228773[GeneMark.hmm]319_aa j6506 7465	GSChrysoyphyteH2.ASY1.ANO1.89.1	63.2	302	9e-101	374.4	
GVMAG-S-1093511-40		-	GVMAG-S-1093511-40 1093511_contig_2160	gene_236839[GeneMark.hmm]327_aa j7503 8486	GSChrysoyphyteH2.ASY1.ANO1.900.1	50.2	213	5e-41	176	
GVMAG-S-1096102-67		-	GVMAG-S-1096102-67 1096102_contig_275	gene_237037[GeneMark.hmm]667_aa j2745 129454	GSChrysoyphyteH2.ASY1.ANO1.690.1	69.1	524	5e-212	745	
GVMAG-S-1096102-67	-	GVMAG-S-1096102-67 1096102_contig_7880	gene_237217[GeneMark.hmm]351_aa j1394 2449	GSChrysoyphyteH1.ASY1.ANO1.2156.1	52.6	346	3e-91	343.2		
GVMAG-S-3300005662-156	-	GVMAG-S-3300005662-156 3300005662.a.Ga0078894_10002790	gene_262305[GeneMark.hmm]147_aa j15458	GSChrysoyphyteH1.ASY1.ANO1.800.1	61.5	148	8e-47	194.1		
GVMAG-S-ERX555943-30	ERX555943_9_dc; ERX556019_45_dc	GVMAG-S-ERX555943-30 ERX555943_contig_1662	gene_286838[GeneMark.hmm]145_aa j6075 6512	GSChrysoyphyteH1.ASY1.ANO1.800.1	59.2	147	1e-43	183.3		
GVMAG-S-ERX555965-56	-	GVMAG-S-ERX555965-56 ERX555965_contig_449	gene_288636[GeneMark.hmm]185_aa j30384 30941	GSChrysoyphyteH1.ASY1.ANO1.800.1	50.9	163	2e-39	169.9		
GVMAG-S-ERX555967-113	-	GVMAG-S-ERX555967-113 ERX555967_contig_1541	gene_289243[GeneMark.hmm]137_aa j9068 9481	GSChrysoyphyteH1.ASY1.ANO1.800.1	62.7	126	8e-38	164.1		
GVMAG-S-ERX555967-93	-	GVMAG-S-ERX555967-93 ERX555967_contig_66	gene_290496[GeneMark.hmm]1072_aa j7981 11199	GSChrysoyphyteH2.ASY1.ANO1.205.1	51.7	379	6e-94	353.6		
GVMAG-S-ERX556054-45	-	GVMAG-S-ERX556054-45 ERX556054_contig_588	gene_296205[GeneMark.hmm]386_aa j16545 17705	GSChrysoyphyteH2.ASY1.ANO1.872.1	62	234	5e-79	302.4		
GVMAG-S-ERX556106-38	ERX556106_20_dc	GVMAG-S-ERX556106-38 ERX556106_contig_19	gene_298754[GeneMark.hmm]341_aa j79882 80907	GSChrysoyphyteH2.ASY1.ANO1.55.1	63.4	298	1e-103	384		
GVMAGs medium quality	GVMAG-M-3300001349-29	-	GVMAG-M-3300001349-29JG2016014292_10001917	gene_4990[GeneMark.hmm]1068_aa j1803 15009	GSChrysoyphyteH1.ASY1.ANO1.3101.1	73.1	535	4e-240	839	
	GVMAG-M-3300001589-11	-	GVMAG-M-3300001589-11JG20400515628_10004999	gene_8853[GeneMark.hmm]416_aa j1929 3179	GSChrysoyphyteH2.ASY1.ANO1.205.1	61.8	356	1e-125	457.2	
	GVMAG-M-3300001589-11	-	GVMAG-M-3300001589-11JG20400515628_10004999	gene_8855[GeneMark.hmm]196_aa j3863 4453	GSChrysoyphyteH1.ASY1.ANO1.1156.1	51.6	128	8e-29	134.8	
	GVMAG-M-3300002242-2	-	GVMAG-M-3300002242-2 KVVW_GV2_10289253	gene_10574[GeneMark.hmm]407_aa j38172 39395	GSChrysoyphyteH2.ASY1.ANO1.205.1	63.1	244	6e-84	318.9	
	GVMAG-M-3300002242-2</									

Supplementary Data 2: Result of BLASTP search of the chrysophyte-related genes (CRGs) associated with NCLDV MAGs against RefSeq database. Only the best hit results are shown.

Non-redundant CDSs in MMETSP	Accession ID	Description [Organism]	Identity (%)	Alignment length (AA)	E-value	Bitscore
GSChrysophyteH1.ASY1.ANO1.800.1	WP_052110684	hypothetical protein [Porphyromonadaceae bacterium COT-184 OH4590]	40.6	128	7e-12	80.9
GSChrysophyteH1.ASY1.ANO1.869.1	WP_119496874	DUF285 domain-containing protein [Bisgaard Taxon 44]	59.6	401	3e-134	488
GSChrysophyteH1.ASY1.ANO1.1001.1	WP_130024373	DUF285 domain-containing protein, partial [Emticicia sp. 17J42-9]	53	634	8e-190	673.3
GSChrysophyteH1.ASY1.ANO1.1138.1	XP_005849281	hypothetical protein CHLNCDRAFT_143577 [Chlorella variabilis]	45.7	208	1e-43	187.6
GSChrysophyteH1.ASY1.ANO1.1156.1	WP_086234886	MULTISPECIES: DUF285 domain-containing protein [unclassified Campylobacter]	61.5	234	3e-74	289.3
GSChrysophyteH1.ASY1.ANO1.1410.1	WP_017663439	alpha/beta hydrolase [Geitlerinema sp. PCC 7105]	31.1	627	5e-58	235.7
GSChrysophyteH1.ASY1.ANO1.1570.1	NP_601438	bifunctional RNase H/acid phosphatase [Corynebacterium glutamicum ATCC 13032]	42.7	150	7e-20	106.7
GSChrysophyteH1.ASY1.ANO1.2156.1	XP_005649489	WD40 repeat-like protein [Coccomyxa subellipsoidea C-169]	39.4	274	2e-53	219.5
GSChrysophyteH1.ASY1.ANO1.3101.1	XP_019644030	PREDICTED: autocrine proliferation repressor protein A-like [Branchiostoma belcheri]	37	522	2e-83	319.7
GSChrysophyteH2.ASY1.ANO1.55.1	XP_008869517	hypothetical protein H310_06290 [Aphanomyces invadans]	48.5	293	3e-69	271.6
GSChrysophyteH2.ASY1.ANO1.89.1	WP_028878535	hydroxymethylglutaryl-CoA lyase [Terasakiella pusilla]	62.8	301	1e-99	372.9
GSChrysophyteH2.ASY1.ANO1.205.1	WP_086247819	BspA family leucine-rich repeat surface protein [Campylobacter sp. S0112]	49.5	1115	5e-307	1063.5
GSChrysophyteH2.ASY1.ANO1.358.1	XP_005756181	hypothetical protein EMIHUDDRAFT_221916 [Emiliana huxleyi CCMP1516]	34.7	591	3e-51	214.5
GSChrysophyteH2.ASY1.ANO1.464.1	YP_008052532	hypothetical protein PGCG_00214 [Phaeocystis globosa virus]	43	603	5e-129	471.5
GSChrysophyteH2.ASY1.ANO1.690.1	XP_001746043	hypothetical protein [Monosiga brevicollis MX1]	35	509	2e-61	246.9
GSChrysophyteH2.ASY1.ANO1.872.1	WP_051605661	BspA family leucine-rich repeat surface protein [Polaribacter sp. Hel_I_88]	56.6	348	6e-103	384.4
GSChrysophyteH2.ASY1.ANO1.900.1	WP_157151613	hypothetical protein [Brachyspira sp. SAP_772]	46.7	332	3e-65	258.8
GSChrysophyteH2.ASY1.ANO1.1416.1	WP_079977971	WD40 repeat domain-containing protein [Criblamydia sequanensis]	40.2	189	6e-37	164.1
GSChrysophyteH2.ASY1.ANO1.1537.1	WP_130021580	DUF285 domain-containing protein, partial [Emticicia sp. 17J42-9]	53.6	707	1e-221	779.6

Supplementary Data 3: List of the MAGs and the PoIB genes exhibited a best hit to NCLDV PoIB sequences detected in OM-RGC.v2.

MAG	MAG ID	Contig ID	Query sequence	Best hit (PoIB in OM-RGC.v2)	Identity (%)	Alignment length (AA)	E-value	Bitscore
MoMAGs	ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_4095 GeneMark.hmm 1311_aa- 129970 133905	TARA_138_SRF_0.22-3_G_scaffold44499_1_gene27938	100	1265	0e+00	2617
	SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_7269 GeneMark.hmm 1248_aa+ 105957 109703	TARA_191_SRF_0.22-3_G_scaffold95013_2_gene108442	99.878	823	0e+00	1718
	ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_2671 GeneMark.hmm 1305_aa- 9066 12983	TARA_133_SRF_0.22-3_G_scaffold185108_2_gene177877	100	1305	0e+00	2682
	ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_2403 GeneMark.hmm 1294_aa- 17462 21346	TARA_004_SRF_0.22-1.6_G_scaffold50931_3_gene36782	100	1294	0e+00	2674
	ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_3445 GeneMark.hmm 1317_aa+ 19742 23695	TARA_137_SRF_0.22-3_G_scaffold253183_1_gene235673	100	1317	0e+00	2719
	ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_9215 GeneMark.hmm 1214_aa+ 18167 21811	TARA_034_SRF_0.22-1.6_G_scaffold83689_1_gene74996	99.918	1214	0e+00	2503
	ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_9215 GeneMark.hmm 1214_aa+ 18167 21811	TARA_078_DCM_0.22-0.45_G_scaffold399115_1_gene367841	96.205	1212	0e+00	2421
	ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_8693 GeneMark.hmm 1214_aa- 2124 5768	TARA_034_SRF_0.22-1.6_G_scaffold83689_1_gene74996	100	1214	0e+00	2503
	ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_8693 GeneMark.hmm 1214_aa- 2124 5768	TARA_078_DCM_0.22-0.45_G_scaffold399115_1_gene367841	96.287	1212	0e+00	2426
	ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_590 GeneMark.hmm 1319_aa- 45 4004	TARA_065_DCM_0.1-0.22_G_scaffold21735_1_gene16919	100	1319	0e+00	2719
	SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_6656 GeneMark.hmm 1151_aa- 3 3455	TARA_194_DCM_0.22-3_G_C18885779_1_gene563899	99.438	1067	0e+00	2187
	ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_1933 GeneMark.hmm 1391_aa+ 63688 67863	TARA_032_SRF_0.22-1.6_G_scaffold30260_1_gene20320	99.856	1391	0e+00	2864
	ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_2875 GeneMark.hmm 1391_aa- 26511 30686	TARA_032_SRF_0.22-1.6_G_scaffold30260_1_gene20320	99.856	1391	0e+00	2864
	ERX556103_23_dc	Moniruzzaman_MM09_ERX556103_23_dc_000000000006	gene_9605 GeneMark.hmm 1562_aa- 675 5363	TARA_142_DCM_0.22-3_G_C15876979_1_gene597453	100	1038	0e+00	2125
	ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_286 GeneMark.hmm 1068_aa- 22402 25608	TARA_109_SRF_0.22-3_G_scaffold291921_1_gene282506	96.816	1068	0e+00	2144
	SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_5000 GeneMark.hmm 1043_aa- 12284 15415	TARA_205_SRF_0.22-3_G_C11176073_1_gene516020	91.583	796	0e+00	1519
	ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_7927 GeneMark.hmm 1199_aa+ 28218 31817	TARA_067_SRF_0.22-0.45_G_scaffold109150_1_gene106231	100	1199	0e+00	2413
	ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_152 GeneMark.hmm 1045_aa- 15146 18283	TARA_122_DCM_0.1-0.22_G_scaffold106627_1_gene185933	100	885	0e+00	1845
GVMAGs high quality	GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_10724 GeneMark.hmm 1248_aa+ 13917 17663	TARA_206_SRF_0.22-3_G_scaffold91556_1_gene113005	96.179	1230	0e+00	2434
	GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_13627 GeneMark.hmm 1311_aa+ 57803 61738	TARA_138_SRF_0.22-3_G_scaffold44499_1_gene27938	100	1265	0e+00	2617
	GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_8765 GeneMark.hmm 1248_aa+ 106166 109912	TARA_191_SRF_0.22-3_G_scaffold95013_2_gene108442	99.878	823	0e+00	1718
	GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_12385 GeneMark.hmm 1525_aa- 12482 17059	TARA_078_SRF_0.22-0.45_G_scaffold100252_1_gene64986	98.885	1076	0e+00	2218
	GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_12385 GeneMark.hmm 1525_aa- 12482 17059	TARA_133_SRF_0.22-3_G_scaffold511774_1_gene580411	100	1002	0e+00	2086
	GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_7155 GeneMark.hmm 1318_aa+ 127763 131719	TARA_076_SRF_0.22-3_G_scaffold195419_1_gene126012	96.245	799	0e+00	1584
	GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_6223 GeneMark.hmm 1317_aa- 19926 23879	TARA_205_SRF_0.22-3_G_scaffold149975_1_gene194354	96.128	1317	0e+00	2622
	GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_6223 GeneMark.hmm 1317_aa- 19926 23879	TARA_191_SRF_0.22-3_G_scaffold181124_1_gene204366	93.524	1297	0e+00	2524
	GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_6223 GeneMark.hmm 1317_aa- 19926 23879	TARA_191_SRF_0.22-3_G_scaffold198149_1_gene230360	90.122	1316	0e+00	2461
	GVMAG-S-ERX555967-93	GVMAG-S-ERX555967-93 ERX555967_contig_3023	gene_12953 GeneMark.hmm 1177_aa- 8225 11758	TARA_133_SRF_0.22-3_G_scaffold88330_2_gene80336	100	975	0e+00	1983
	GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_6656 GeneMark.hmm 1669_aa- 12032 17041	TARA_191_SRF_0.22-3_G_scaffold157411_1_gene175609	92.326	1668	0e+00	3237
	GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_11376 GeneMark.hmm 1391_aa+ 41330 45505	TARA_032_SRF_0.22-1.6_G_scaffold30260_1_gene20320	99.856	1391	0e+00	2864
	GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_8940 GeneMark.hmm 1310_aa- 11641 15573	TARA_173_SRF_0.22-3_G_scaffold203285_1_gene247632	97.801	1319	0e+00	2687
GVMAGs medium quality	GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_10199 GeneMark.hmm 1248_aa+ 47236 50982	TARA_191_SRF_0.22-3_G_scaffold95013_2_gene108442	98.299	823	0e+00	1691
	GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_5218 GeneMark.hmm 1296_aa- 9649 13539	TARA_102_DCM_0.22-3_G_scaffold398860_1_gene467233	96.756	863	0e+00	1738
	GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_8247 GeneMark.hmm 1323_aa- 12003 15974	TARA_152_SRF_0.22-3_G_scaffold220752_1_gene191097	94.182	825	0e+00	1613
	GVMAG-S-3300000226-21	GVMAG-S-3300000226-21 3300000226.a:SI34jun09_135mDRAF	gene_11016 GeneMark.hmm 1091_aa+ 1 3276	TARA_032_SRF_0.22-1.6_G_scaffold30260_1_gene20320	92.942	1091	0e+00	2063

Supplementary Data 4: Result of BLASTP search of the genes on the contigs that contained the chrysophyte homologs against RefSeq database. Only the best hit results are shown. Taxonomic compositions of each contig are shown in Extended Data Fig. 6.

MAG	MAG ID	Contig ID	Query sequence	Best hit (Accession ID)	Description [Organism]	Identity (%)	Alignment length (AA)	E-value	Bitscore
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_1 GeneMark.hmm 76_aa -91 321	no hit	-	-	-	-	-
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_2 GeneMark.hmm 292_aa -622 1500	no hit	-	-	-	-	-
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_3 GeneMark.hmm 233_aa -1745 2446	XP_032237593	uncharacterized protein LOC116618225 [Nematostella vectensis]	29.2	216	2.8E-13	85.5
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_4 GeneMark.hmm 3726_aa -2513 13693	no hit	-	-	-	-	-
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_5 GeneMark.hmm 221_aa -13807 14472	no hit	-	-	-	-	-
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_6 GeneMark.hmm 212_aa -14478 15116	XP_005781197	hypothetical protein EMIHUDDRAFT_424111 [Emiliania huxleyi CCMP1516]	37	208	2E-26	129
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_7 GeneMark.hmm 1045_aa -15146 18283	YP_004061614	hypothetical protein BpV1_184 [Bathycoccus sp. RCC1105 virus BpV1]	28.3	974	2.1E-92	350.5
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_8 GeneMark.hmm 55_aa -18324 18491	no hit	-	-	-	-	-
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_9 GeneMark.hmm 227_aa -18521 19204	no hit	-	-	-	-	-
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_10 GeneMark.hmm 202_aa -19201 19809	no hit	-	-	-	-	-
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_11 GeneMark.hmm 1326_aa -19909 23889	no hit	-	-	-	-	-
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_12 GeneMark.hmm 57_aa -23920 24093	no hit	-	-	-	-	-
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_13 GeneMark.hmm 100_aa -24130 24432	no hit	-	-	-	-	-
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_14 GeneMark.hmm 229_aa -24904 25593	XP_002293378	predicted protein [Thalassiosira pseudonana CCMP1335]	48.6	222	1.4E-44	189.5
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_15 GeneMark.hmm 217_aa -25633 26286	no hit	-	-	-	-	-
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_16 GeneMark.hmm 551_aa -26322 27977	WP_163350692	hypothetical protein [Desulfovibrio sp. JC010]	26	227	2.9E-08	70.1
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_17 GeneMark.hmm 81_aa -27988 28233	no hit	-	-	-	-	-
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_18 GeneMark.hmm 335_aa -28343 29350	XP_013345457	hypothetical protein AUEXF2481DRAFT_46539 [Aureobasidium subglaciale EXF-2481]	27	256	1.5E-10	77
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_19 GeneMark.hmm 319_aa -29795 30754	no hit	-	-	-	-	-
	EP01_ERX552279_2_dc	Moniruzzaman_EP01_ERX552279_2_dc_000000000011	gene_20 GeneMark.hmm 28_aa -30766 30852	no hit	-	-	-	-	-
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_21 GeneMark.hmm 715_aa -2 2146	YP_003969992	hypothetical protein crov359 [Cafeteria roenbergensis virus BV-PW1]	35.2	253	2.2E-32	150.6
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_22 GeneMark.hmm 321_aa -2171 3136	no hit	-	-	-	-	-
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_23 GeneMark.hmm 1848_aa -3235 8781	YP_008052505	hypothetical protein PGCG_00187 [Phaeocystis globosa virus]	26	431	6.3E-15	94
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_24 GeneMark.hmm 1140_aa -8866 12288	no hit	-	-	-	-	-
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_25 GeneMark.hmm 125_aa -12349 12726	no hit	-	-	-	-	-
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_26 GeneMark.hmm 119_aa -12692 13051	no hit	-	-	-	-	-
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_27 GeneMark.hmm 114_aa -13076 13420	no hit	-	-	-	-	-
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_28 GeneMark.hmm 60_aa -13547 13729	no hit	-	-	-	-	-
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_29 GeneMark.hmm 237_aa -13762 14475	no hit	-	-	-	-	-
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_30 GeneMark.hmm 191_aa -14519 15094	YP_009174082	hypothetical protein [Yellowstone lake mimivirus]	36.3	190	5.5E-23	117.5
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_31 GeneMark.hmm 264_aa -15164 15958	YP_009173366	hypothetical protein ceV_111 [Chrysochromulina ericina virus]	36.3	226	5.1E-27	131.3
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_32 GeneMark.hmm 189_aa -16018 16587	YP_008052438	Erv family thiol oxidoreductase [Phaeocystis globosa virus]	53.8	182	5.1E-53	217.2
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_33 GeneMark.hmm 158_aa -16654 17130	no hit	-	-	-	-	-
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_34 GeneMark.hmm 286_aa -17119 17979	YP_008052436	patatin-like phospholipase [Phaeocystis globosa virus]	30	307	4.8E-39	171.4
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_35 GeneMark.hmm 194_aa -18029 18613	YP_008052435	hypothetical protein PGCG_00116 [Phaeocystis globosa virus]	42.1	190	1.9E-31	145.6
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_36 GeneMark.hmm 377_aa -18637 19770	YP_008052570	extracellular link domain-containing protein [Phaeocystis globosa virus]	31.9	282	6.4E-39	171.4
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_37 GeneMark.hmm 119_aa -19783 20142	YP_009173615	ubiquitin specific peptidase C19 [Chrysochromulina ericina virus]	42.4	118	1.7E-22	115.2
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_38 GeneMark.hmm 212_aa -20541 21176	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	45.5	213	4.7E-47	197.6
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_39 GeneMark.hmm 384_aa -21216 22370	no hit	-	-	-	-	-
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_40 GeneMark.hmm 1068_aa -22402 25608	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	47.2	1077	4E-257	897.9
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_41 GeneMark.hmm 262_aa -25926 26711	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	41.9	258	2.5E-42	182.2
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_42 GeneMark.hmm 167_aa -26819 27322	XP_007487834	PREDICTED: protein disulfide-isomerase TMX3 isoform X1 [Monodelphis domestica]	32.7	107	2.4E-06	62
	MM01_ERX552270_73_dc	Moniruzzaman_MM01_ERX552270_73_dc_000000000004	gene_43 GeneMark.hmm 31_aa -27782 27874	no hit	-	-	-	-	-
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_44 GeneMark.hmm 1319_aa -45 4004	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	45.9	1311	0	1098.6
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_45 GeneMark.hmm 83_aa -4096 4347	no hit	-	-	-	-	-
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_46 GeneMark.hmm 160_aa -4384 4866	no hit	-	-	-	-	-
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_47 GeneMark.hmm 240_aa -4929 5651	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	38.9	211	5.3E-31	144.4
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_49 GeneMark.hmm 74_aa -6587 6811	no hit	-	-	-	-	-
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_50 GeneMark.hmm 335_aa -6919 7926	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	63.3	316	1E-114	422.5
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_51 GeneMark.hmm 1170_aa -7990 11502	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	42.8	1017	1E-213	753.4
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_52 GeneMark.hmm 671_aa -11534 13549	no hit	-	-	-	-	-
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_53 GeneMark.hmm 116_aa -13607 13957	no hit	-	-	-	-	-
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_55 GeneMark.hmm 143_aa -15000 15431	no hit	-	-	-	-	-
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_56 GeneMark.hmm 309_aa -15522 16451	WP_052784148	SDR family oxidoreductase [Campylobacter coli]	65.4	309	3E-114	421.4
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_57 GeneMark.hmm 711_aa -16482 18617	WP_082901326	glycosyltransferase [Leptolyngbya valderiana]	28.6	370	4.3E-36	162.9
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_58 GeneMark.hmm 309_aa -18655 19584	WP_152589204	DUF2974 domain-containing protein [Nostoc sphaeroides]	33.5	200	1.6E-16	96.7
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_60 GeneMark.hmm 170_aa -20016 20528	YP_009173322	eukaryotic initiation factor 4E [Chrysochromulina ericina virus]	58.7	150	7.3E-43	183.3
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_61 GeneMark.hmm 286_aa -20579 21439	no hit	-	-	-	-	-
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_62 GeneMark.hmm 76_aa -21492 21722	no hit	-	-	-	-	-
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_63 GeneMark.hmm 477_aa -21763 23196	YP_009173584	hypothetical protein ceV_329 [Chrysochromulina ericina virus]	36.2	461	3.1E-59	239.2
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_64 GeneMark.hmm 311_aa -23210 24145	YP_009173585	hypothetical protein ceV_330 [Chrysochromulina ericina virus]	39	308	3.2E-36	162.2
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_65 GeneMark.hmm 29_aa -24204 24293	no hit	-	-	-	-	-
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_66 GeneMark.hmm 165_aa -24294 24791	no hit	-	-	-	-	-
	MM01_ERX552283_5_dc	Moniruzzaman_MM01_ERX552283_5_dc_000000000008	gene_67 GeneMark.hmm 155_aa -24829 25296	no hit	-	-	-	-	-
	MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_68 GeneMark.hmm 215_aa -1 1645	YP_009173460	VV A18-like helicase [Chrysochromulina ericina virus]	42.9	196	5.8E-37	164.1
	MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_69 GeneMark.hmm 149_aa -1746 1195	no hit	-	-	-	-	-
	MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_70 GeneMark.hmm 469_aa -1234 2643	no hit	-	-	-	-	-
	MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_71 GeneMark.hmm 211_aa -2690 3325	YP_009173333	hypothetical protein ceV_078 [Chrysochromulina ericina virus]	34.9	209	5.2E-30	141
	MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_72 GeneMark.hmm 210_aa -3387 4019	no hit	-	-	-	-	-
	MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_73 GeneMark.hmm 176_aa -4051 4581	no hit	-	-	-	-	-
	MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_74 GeneMark.hmm 336_aa -4605 5615	YP_004062114	hypothetical protein Mpv1_231c [Micromonas sp. RCC1109 virus Mpv1]	55.1	207	1.4E-58	236.5
	MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_75 GeneMark.hmm 42_aa -5689 5817	no hit	-	-	-	-	-
	MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_76 GeneMark.hmm 330_aa -5810 6802	YP_009173500	ribonucleoside-diphosphate reductase small subunit [Chrysochromulina ericina virus]	65.6	320	4E-117	431
	MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_77 GeneMark.hmm 186_aa -6803 7363	no hit	-	-	-	-	-
	MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_78 GeneMark.hmm 649_aa -7406 9355	XP_005827322	hypothetical protein GUIHDDRAFT_113578 [Guillardia theta CCMP2712]	44.4	565	8E-111	411
	MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_79 GeneMark.hmm 609_aa -9382 11211	YP_009173631	asparagine synthetase B [Chrysochromulina ericina virus]	45.9	614	3E-135	492.3
	MM01_ERX5								

MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_81 GeneMark.hmm 97_aa - 11591 11884	WP_146342711	aquaporin [Lactobacillus algidus]	42.2	90	1.4E-06	62
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_82 GeneMark.hmm 117_aa - 12042 12395	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_83 GeneMark.hmm 147_aa - 12443 12886	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_84 GeneMark.hmm 162_aa - 12935 13423	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_85 GeneMark.hmm 335_aa - 13478 14485	YP_009173634	C-terminal catalytic domain of Ulp1 protease [Chrysochromulina ericina virus]	37.8	275	5.8E-44	188
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_86 GeneMark.hmm 205_aa - 14493 15110	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_87 GeneMark.hmm 248_aa - 15136 15882	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_88 GeneMark.hmm 196_aa - 15950 16540	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_89 GeneMark.hmm 235_aa - 16578 17285	WP_137385183	CDP-glycerol glycerophosphotransferase family protein [Pantoea sp. SO10]	33.7	202	4.3E-25	124.8
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_90 GeneMark.hmm 298_aa - 17290 18186	YP_008052350	hypothetical protein PGCG_00031 [Phaeocystis globosa virus]	30.5	269	2.9E-18	102.4
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_91 GeneMark.hmm 121_aa - 18282 18647	YP_009173301	putative thioredoxin family protein [Chrysochromulina ericina virus]	35.1	97	1.9E-08	68.6
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_92 GeneMark.hmm 264_aa - 18651 19445	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_93 GeneMark.hmm 107_aa - 19538 19861	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_94 GeneMark.hmm 104_aa - 20198 20509	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_95 GeneMark.hmm 147_aa - 20604 21044	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_96 GeneMark.hmm 232_aa - 21367 22065	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_97 GeneMark.hmm 357_aa - 22112 23185	YP_009173415	hypothetical protein ceV_160 [Chrysochromulina ericina virus]	42.6	197	2.9E-33	152.5
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_98 GeneMark.hmm 328_aa - 23272 24258	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_99 GeneMark.hmm 434_aa - 24621 25925	YP_008052499	hypothetical protein PGCG_00181 [Phaeocystis globosa virus]	29.9	365	1.1E-26	131
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_100 GeneMark.hmm 49_aa - 25943 26089	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_101 GeneMark.hmm 31_aa - 26401 26496	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_102 GeneMark.hmm 83_aa - 26493 26744	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_103 GeneMark.hmm 49_aa - 26812 26958	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_104 GeneMark.hmm 64_aa - 27367 27561	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_105 GeneMark.hmm 77_aa - 27587 27820	YP_009173355	hypothetical protein ceV_100 [Chrysochromulina ericina virus]	42.1	76	1.3E-10	75.1
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_106 GeneMark.hmm 102_aa - 27846 28154	YP_008052487	hypothetical protein PGCG_00169 [Phaeocystis globosa virus]	36.7	79	2.1E-08	68.2
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_107 GeneMark.hmm 226_aa - 28193 28873	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_108 GeneMark.hmm 504_aa - 28905 30419	YP_009173345	putative polyA polymerase catalytic subunit [Chrysochromulina ericina virus]	50.5	424	7E-116	427.6
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_109 GeneMark.hmm 353_aa - 30450 31511	YP_009173344	putative phosphoinositide-specific phospholipase C-beta2 [Chrysochromulina ericina virus]	24.7	360	3.6E-20	109
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_110 GeneMark.hmm 549_aa - 31582 33231	YP_009174114	putative major capsid protein MCP2 [Yellowstone lake mimivirus]	51	563	5E-162	580.9
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_111 GeneMark.hmm 563_aa - 33289 34980	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_112 GeneMark.hmm 424_aa - 35015 36289	YP_009173339	putative glycosyltransferase [Chrysochromulina ericina virus]	49.9	399	3E-100	375.6
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_113 GeneMark.hmm 206_aa - 36338 36958	WP_101762060	glycosyltransferase family 25 protein [Pantoea endophytica]	32.4	207	5.2E-19	104.4
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_114 GeneMark.hmm 453_aa - 37011 38372	YP_009174125	putative replication factor C large subunit [Yellowstone lake mimivirus]	50	450	2E-117	432.6
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_115 GeneMark.hmm 647_aa - 38445 40388	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_116 GeneMark.hmm 236_aa - 40551 41261	YP_008052440	ribonuclease HIII [Phaeocystis globosa virus]	47.6	210	6.8E-47	197.2
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_117 GeneMark.hmm 676_aa - 41210 43240	YP_009174077	putative glycosyl transferase [Yellowstone lake mimivirus]	39.3	682	5E-114	421.8
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_118 GeneMark.hmm 194_aa - 43332 43916	YP_009174076	hypothetical protein [Yellowstone lake mimivirus]	41.3	155	2.7E-25	125.2
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_119 GeneMark.hmm 600_aa - 43986 45788	YP_009174075	hypothetical protein [Yellowstone lake mimivirus]	36.7	602	6.5E-86	328.2
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_120 GeneMark.hmm 272_aa - 45839 46657	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_121 GeneMark.hmm 56_aa - 46722 46889	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_122 GeneMark.hmm 310_aa - 47312 48244	YP_008052591	hypothetical protein PGCG_00273 [Phaeocystis globosa virus]	38.2	283	9.2E-36	160.6
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_123 GeneMark.hmm 37_aa - 49054 49167	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_124 GeneMark.hmm 431_aa - 49460 50755	WP_105939792	ankyrin repeat domain-containing protein [Arcobacter cryaerophilus]	36.2	312	1.2E-44	190.7
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_125 GeneMark.hmm 190_aa - 50752 51324	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_126 GeneMark.hmm 226_aa - 51393 52073	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_127 GeneMark.hmm 129_aa - 52164 52553	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_128 GeneMark.hmm 389_aa - 52610 53779	XP_002305073	senescence-specific cysteine protease SAG12 [Populus trichocarpa]	33.9	322	1.3E-42	183.7
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_129 GeneMark.hmm 160_aa - 53835 54317	XP_011400216	Structure-specific endonuclease subunit SLX1-like protein [Auxenochlorella protothecoides]	38.9	131	1.5E-10	75.9
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_130 GeneMark.hmm 101_aa - 54314 54619	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_131 GeneMark.hmm 1269_aa - 54664 58473	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	38.7	1025	2E-185	659.8
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_132 GeneMark.hmm 352_aa - 58588 59646	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	61.7	334	3E-116	428.3
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_133 GeneMark.hmm 93_aa - 59661 59942	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_134 GeneMark.hmm 275_aa - 60013 60840	YP_009173624	ERCC4-type nuclease [Chrysochromulina ericina virus]	31.5	276	3.2E-24	122.1
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_135 GeneMark.hmm 390_aa - 60842 62014	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_136 GeneMark.hmm 234_aa - 62320 63024	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	38.5	205	5.7E-30	141
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_137 GeneMark.hmm 173_aa - 63074 63595	XP_022183857	protein disulfide-isomerase [Nilaparvata lugens]	36.2	94	5.9E-08	67.4
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_138 GeneMark.hmm 1391_aa - 63688 67863	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	45.9	1327	4E-284	988
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_139 GeneMark.hmm 150_aa - 67914 68366	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_140 GeneMark.hmm 270_aa - 68355 69167	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_141 GeneMark.hmm 84_aa - 69668 69919	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_142 GeneMark.hmm 352_aa - 70008 71066	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	38.9	350	2.6E-66	262.3
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_143 GeneMark.hmm 367_aa - 71078 72181	YP_008052570	extracellular link domain-containing protein [Phaeocystis globosa virus]	33	282	6.8E-38	167.9
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_144 GeneMark.hmm 103_aa - 72238 72549	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_145 GeneMark.hmm 126_aa - 72574 72954	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_146 GeneMark.hmm 392_aa - 73362 74540	YP_009173609	hypothetical protein ceV_354 [Chrysochromulina ericina virus]	35.9	195	7.1E-25	124.8
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_147 GeneMark.hmm 155_aa - 74615 75082	YP_009173608	hypothetical protein ceV_353 [Chrysochromulina ericina virus]	50.5	107	5.3E-16	94
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_148 GeneMark.hmm 200_aa - 75203 75805	YP_009173607	hypothetical protein ceV_352 [Chrysochromulina ericina virus]	63.8	199	1.8E-64	255.4
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_149 GeneMark.hmm 87_aa - 75900 76163	YP_009174055	hypothetical protein [Yellowstone lake mimivirus]	60.3	78	6E-17	96.3
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_150 GeneMark.hmm 292_aa - 76228 77106	YP_009173458	hypothetical protein ceV_203 [Chrysochromulina ericina virus]	50	272	5.8E-72	280.8
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_151 GeneMark.hmm 622_aa - 77201 79066	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_152 GeneMark.hmm 54_aa - 79387 79551	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_153 GeneMark.hmm 278_aa - 79573 80409	YP_009173380	putative VV A32-like packaging ATPase [Chrysochromulina ericina virus]	79.1	278	5E-131	476.9
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_154 GeneMark.hmm 574_aa - 80526 82250	YP_009173379	putative phosphotransferase [Chrysochromulina ericina virus]	46.6	558	3E-101	379
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_155 GeneMark.hmm 135_aa - 82242 82649	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_156 GeneMark.hmm 979_aa - 82705 85644	YP_009173744	DNA polymerase X/NAD-dependent DNA ligase fusion protein [Chrysochromulina ericina vi	43.6	1040	6E-225	790.8
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_157 GeneMark.hmm 87_aa - 85752 86015	no hit	-	-	-	-	-
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_158 GeneMark.hmm 360_aa - 86049 87131	YP_009174071	hypothetical protein [Yellowstone lake mimivirus]	68.5	178	2.2E-65	259.2
MM01_ERX55								

MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_163 GeneMark.hmm 1155_aa + 90656 94123	YP_009173474	Ribonucleotide reductase large subunit [Chrysochromulina ericina virus]	40.4	1685	0	1198
MM01_ERX555943_9_dc	Moniruzzaman_MM01_ERX555943_9_dc_000000000009	gene_164 GeneMark.hmm 97_aa + 94198 94488	no hit	-	-	-	-	-
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_165 GeneMark.hmm 389_aa + 11170	no hit	-	-	-	-	-
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_166 GeneMark.hmm 130_aa + 1240 1632	no hit	-	-	-	-	-
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_167 GeneMark.hmm 118_aa + 1629 1985	YP_009174078	hypothetical protein [Yellowstone lake mimivirus]	43.6	117	3.4E-15	90.9
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_168 GeneMark.hmm 140_aa + 2029 2451	no hit	-	-	-	-	-
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_169 GeneMark.hmm 145_aa + 2498 2935	no hit	-	-	-	-	-
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_170 GeneMark.hmm 750_aa + 3079 5331	no hit	-	-	-	-	-
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_171 GeneMark.hmm 644_aa + 5442 7376	no hit	-	-	-	-	-
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_172 GeneMark.hmm 212_aa + 7732 8367	no hit	-	-	-	-	-
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_173 GeneMark.hmm 197_aa + 8407 9000	YP_009174082	hypothetical protein [Yellowstone lake mimivirus]	38.5	187	9.4E-26	126.7
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_174 GeneMark.hmm 278_aa + 9068 9904	YP_009174085	hypothetical protein [Yellowstone lake mimivirus]	37.8	222	1.7E-28	136.3
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_175 GeneMark.hmm 197_aa + 9992 10585	YP_009173469	Erv1 / Alr family [Chrysochromulina ericina virus]	51.6	184	2.2E-46	195.3
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_176 GeneMark.hmm 156_aa + 10663 11133	YP_009173468	Protein Disulfide Isomerase (PDla) [Chrysochromulina ericina virus]	34.4	96	8.8E-11	76.6
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_177 GeneMark.hmm 296_aa + 11312 12202	YP_009173467	patatin-like phospholipase [Chrysochromulina ericina virus]	30.8	279	4.7E-37	164.9
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_178 GeneMark.hmm 190_aa + 12253 12825	YP_008052435	hypothetical protein PGCG_00116 [Phaeocystis globosa virus]	46.5	185	2.7E-38	168.3
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_179 GeneMark.hmm 423_aa + 12907 14178	YP_008052570	extracellular link domain-containing protein [Phaeocystis globosa virus]	34.7	288	3.9E-37	165.6
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_180 GeneMark.hmm 350_aa + 14202 15254	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	46.4	347	1.3E-91	346.3
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_181 GeneMark.hmm 337_aa + 15302 16315	no hit	-	-	-	-	-
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_182 GeneMark.hmm 344_aa + 16433 17467	XP_024455022	senescence-specific cysteine protease SAG12-like [Populus trichocarpa]	41.3	213	1.8E-40	176.4
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_183 GeneMark.hmm 1294_aa + 17462 21346	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	46	1299	0	1075.1
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_184 GeneMark.hmm 184_aa + 21395 21949	no hit	-	-	-	-	-
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_185 GeneMark.hmm 179_aa + 21969 22508	no hit	-	-	-	-	-
MM01_ERX555964_34_dc	Moniruzzaman_MM01_ERX555964_34_dc_000000000011	gene_186 GeneMark.hmm 69_aa + 22772 22978	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	55.8	52	1.7E-06	61.2
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_187 GeneMark.hmm 128_aa + 3 389	YP_009173466	hypothetical protein ceV_211 [Chrysochromulina ericina virus]	42.2	128	4.1E-22	114
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_188 GeneMark.hmm 195_aa + 430 1017	XP_021966128	tRNA 2'-phosphotransferase 1-like [Folsomia candida]	45.9	183	1.5E-36	162.5
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_189 GeneMark.hmm 101_aa + 1071 1376	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_190 GeneMark.hmm 142_aa + 1526 1954	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_191 GeneMark.hmm 409_aa + 1967 3196	WP_147714641	3-phosphoserine/phosphohydroxythreonine transaminase [Reinekea sp. SSH23]	36.5	392	1E-58	237.3
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_192 GeneMark.hmm 407_aa + 3254 4477	YP_008052570	extracellular link domain-containing protein [Phaeocystis globosa virus]	34.8	299	2.2E-37	166.4
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_193 GeneMark.hmm 352_aa + 4498 5556	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	47.6	347	7.1E-93	350.5
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_194 GeneMark.hmm 416_aa + 5612 6862	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_195 GeneMark.hmm 236_aa + 6896 7606	WP_017663504	diguanylate cyclase [Francisella frigiditurris]	39.2	240	8.3E-37	163.7
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_196 GeneMark.hmm 158_aa + 7598 8074	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_197 GeneMark.hmm 68_aa + 8201 8407	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_198 GeneMark.hmm 194_aa + 8479 9063	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_199 GeneMark.hmm 1305_aa + 9066 12983	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	46	1313	0	1080.9
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_200 GeneMark.hmm 176_aa + 13033 13563	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_201 GeneMark.hmm 102_aa + 13620 13928	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_202 GeneMark.hmm 180_aa + 13971 14513	XP_016916233	thioredoxin domain-containing protein 5 [Apis cerana]	30.1	133	2E-06	62.4
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_203 GeneMark.hmm 240_aa + 14581 15303	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	39.9	208	2.6E-30	142.1
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_204 GeneMark.hmm 274_aa + 15306 16130	YP_009173624	ERCC4-type nuclease [Chrysochromulina ericina virus]	34.1	273	4.3E-29	138.3
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_205 GeneMark.hmm 76_aa + 16179 16409	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_206 GeneMark.hmm 343_aa + 16498 17529	YP_008052638	ribonuclease III [Phaeocystis globosa virus]	56.5	338	3E-109	404.8
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_207 GeneMark.hmm 118_aa + 17534 17890	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_208 GeneMark.hmm 246_aa + 17992 18732	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_209 GeneMark.hmm 375_aa + 18828 19955	XP_020385274	cathepsin L1-like [Rhinocodon typus]	41	222	2.8E-39	172.6
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_210 GeneMark.hmm 57_aa + 20021 20194	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_211 GeneMark.hmm 325_aa + 20475 21452	YP_008052591	hypothetical protein PGCG_00273 [Phaeocystis globosa virus]	32.4	336	6.3E-35	157.9
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_212 GeneMark.hmm 1214_aa + 21461 25105	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	40.6	1062	7E-201	711.1
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_213 GeneMark.hmm 112_aa + 25132 25470	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_214 GeneMark.hmm 168_aa + 25502 26008	YP_008052395	hypothetical protein PGCG_00076 [Phaeocystis globosa virus]	50.7	148	8.6E-28	133.3
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_215 GeneMark.hmm 267_aa + 26077 26883	YP_009173324	proliferating cell nuclear antigen [Chrysochromulina ericina virus]	61.9	265	2.1E-92	348.6
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_216 GeneMark.hmm 120_aa + 26946 27308	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_217 GeneMark.hmm 77_aa + 27325 27558	XP_033505814	ubiquitin-like [Epinephelus lanceolatus]	93.5	77	9E-33	148.7
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_218 GeneMark.hmm 121_aa + 27589 27954	WP_084230203	fibronectin/fibrinogen-binding protein [Peptoniphilus asaccharolyticus]	37.1	105	6.6E-06	60.1
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_219 GeneMark.hmm 170_aa + 28001 28513	YP_009173322	eukaryotic initiation factor 4E [Chrysochromulina ericina virus]	57.1	154	4.6E-45	190.7
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_220 GeneMark.hmm 251_aa + 28551 29306	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_221 GeneMark.hmm 171_aa + 29356 29871	WP_152891049	dihydrofolate reductase [Clostridium tarantellae]	44.1	170	3.3E-27	131.3
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_222 GeneMark.hmm 369_aa + 29890 30999	XP_005855718	rieske (2Fe-2S) domain protein [Nannochloropsis gaditana CCMP526]	37.6	322	1.4E-46	196.8
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_223 GeneMark.hmm 182_aa + 31044 31592	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_224 GeneMark.hmm 479_aa + 31624 33063	YP_009173584	hypothetical protein ceV_329 [Chrysochromulina ericina virus]	37.7	499	2.1E-71	279.6
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_225 GeneMark.hmm 290_aa + 33072 33944	YP_009173585	hypothetical protein ceV_330 [Chrysochromulina ericina virus]	36.8	288	6.6E-28	134.4
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_226 GeneMark.hmm 168_aa + 34024 34530	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_227 GeneMark.hmm 221_aa + 34562 35227	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_228 GeneMark.hmm 220_aa + 35400 36062	no hit	-	-	-	-	-
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_229 GeneMark.hmm 237_aa + 36111 36824	YP_009173402	hypothetical protein ceV_147 [Chrysochromulina ericina virus]	51.1	227	1.1E-57	233
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_230 GeneMark.hmm 185_aa + 36867 37424	XP_011435243	PREDICTED: uncharacterized protein LOC105333776 [Crassostrea gigas]	56.9	181	2E-54	221.9
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_231 GeneMark.hmm 184_aa + 37436 37990	YP_009173560	hypothetical protein ceV_305 [Chrysochromulina ericina virus]	42.2	180	9.1E-31	143.3
MM01_ERX555967_26_dc	Moniruzzaman_MM01_ERX555967_26_dc_000000000006	gene_232 GeneMark.hmm 1284_aa + 38034 41888	YP_009173561	putative helicase [Chrysochromulina ericina virus]	39.8	1238	3E-232	815.5
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_233 GeneMark.hmm 71_aa + 1 213	no hit	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_234 GeneMark.hmm 1155_aa + 252 3719	YP_009173474	Ribonucleotide reductase large subunit [Chrysochromulina ericina virus]	40.4	1685	0	1198
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_235 GeneMark.hmm 493_aa + 3806 5287	YP_009173475	YqaJ-like viral recombinate [Chrysochromulina ericina virus]	36.3	402	1.6E-69	273.5
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_236 GeneMark.hmm 138_aa + 5367 5783	YP_008052450	hypothetical protein PGCG_00131 [Phaeocystis globosa virus]	41.6	113	8.3E-13	83.2
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_237 GeneMark.hmm 174_aa + 5851 6375	YP_009173478	hypothetical protein ceV_223 [Chrysochromulina ericina virus]	39.2	153	5.8E-19	104
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000							

MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_245 GeneMark.hmm 54_aa - 14824 14988	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_246 GeneMark.hmm 606_aa - 15359 17176	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_247 GeneMark.hmm 292_aa - 17271 18149	YP_009173458	hypothetical protein ceV_203 [Chrysochromulina ericina virus]	50	272	5.8E-72	280.8	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_248 GeneMark.hmm 87_aa - 18214 18477	YP_009174055	hypothetical protein [Yellowstone lake mimivirus]	60.3	78	6E-17	96.3	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_249 GeneMark.hmm 200_aa - 18572 19174	YP_009173607	hypothetical protein ceV_352 [Chrysochromulina ericina virus]	63.8	199	1.8E-64	255.4	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_250 GeneMark.hmm 169_aa - 19295 19804	YP_009173608	hypothetical protein ceV_353 [Chrysochromulina ericina virus]	50.5	107	5.8E-16	94	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_251 GeneMark.hmm 392_aa - 19837 21015	YP_009173609	hypothetical protein ceV_354 [Chrysochromulina ericina virus]	35.9	195	7.1E-25	124.8	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_252 GeneMark.hmm 126_aa+ 21423 21803	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_253 GeneMark.hmm 103_aa+ 21828 22139	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_254 GeneMark.hmm 367_aa+ 22196 23299	YP_008052570	extracellular link domain-containing protein [Phaeocystis globosa virus]	33	282	6.8E-38	167.9	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_255 GeneMark.hmm 352_aa+ 23311 24369	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	38.9	350	2.6E-66	262.3	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_256 GeneMark.hmm 84_aa+ 24458 24709	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_257 GeneMark.hmm 277_aa+ 25186 26019	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_258 GeneMark.hmm 125_aa+ 26008 26385	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_259 GeneMark.hmm 1391_aa+ 26511 30686	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	45.9	1327	4E-284	988	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_260 GeneMark.hmm 173_aa+ 30779 31300	XP_022183857	protein disulfide-isomerase [Nilaparvata lugens]	36.2	94	5.9E-08	67.4	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_261 GeneMark.hmm 234_aa+ 31350 32054	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	38.5	205	5.7E-30	141	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_262 GeneMark.hmm 390_aa+ 32360 33532	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_263 GeneMark.hmm 275_aa+ 33534 34361	YP_009173624	ERCC4-type nuclease [Chrysochromulina ericina virus]	31.5	276	3.2E-24	122.1	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_264 GeneMark.hmm 93_aa+ 34432 34713	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_265 GeneMark.hmm 352_aa+ 34728 35786	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	61.7	334	3E-116	428.3	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_266 GeneMark.hmm 1269_aa+ 35901 39710	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	38.7	1025	2E-185	659.8	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_267 GeneMark.hmm 101_aa+ 39755 40060	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_268 GeneMark.hmm 160_aa+ 40057 40539	XP_011400216	Structure-specific endonuclease subunit SLX1-like protein [Auxenochlorella protothecoides]	38.9	131	1.5E-10	75.9	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_269 GeneMark.hmm 389_aa+ 40595 41764	XP_002305073	senescence-specific cysteine protease SAG12 [Populus trichocarpa]	33.9	322	1.3E-42	183.7	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_270 GeneMark.hmm 129_aa+ 41821 42210	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_271 GeneMark.hmm 226_aa+ 42301 42981	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_272 GeneMark.hmm 190_aa+ 43050 43622	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_273 GeneMark.hmm 431_aa+ 43619 44914	WP_105939792	ankyrin repeat domain-containing protein [Arcobacter cryaerophilus]	36.2	312	1.2E-44	190.7	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_274 GeneMark.hmm 37_aa+ 45207 45320	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_275 GeneMark.hmm 310_aa+ 46130 47062	YP_008052591	hypothetical protein PGCG_00273 [Phaeocystis globosa virus]	38.2	283	9.2E-36	160.6	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_276 GeneMark.hmm 64_aa+ 47127 47321	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_277 GeneMark.hmm 272_aa+ 47386 48204	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_278 GeneMark.hmm 600_aa+ 48255 50057	YP_009174075	hypothetical protein [Yellowstone lake mimivirus]	36.7	602	6.5E-86	328.2	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_279 GeneMark.hmm 194_aa+ 50127 50711	YP_009174076	hypothetical protein [Yellowstone lake mimivirus]	41.3	155	2.7E-25	125.2	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_280 GeneMark.hmm 676_aa+ 50803 52833	YP_009174077	putative glycosyl transferase [Yellowstone lake mimivirus]	39.3	682	4E-114	422.2	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_281 GeneMark.hmm 236_aa+ 52782 53492	YP_008052440	ribonuclease HII [Phaeocystis globosa virus]	47.6	210	6.8E-47	197.2	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_282 GeneMark.hmm 647_aa+ 53655 55598	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_283 GeneMark.hmm 453_aa+ 55671 57032	YP_009174125	putative replication factor C large subunit [Yellowstone lake mimivirus]	50	450	2E-117	432.6	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_284 GeneMark.hmm 206_aa+ 57085 57705	WP_101762060	glycosyltransferase family 25 protein [Pantoea endophytica]	32.4	207	5.2E-19	104.4	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_285 GeneMark.hmm 424_aa+ 57754 59028	YP_009173339	putative glycosyltransferase [Chrysochromulina ericina virus]	49.9	399	3E-100	375.6	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_286 GeneMark.hmm 563_aa+ 59063 60754	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_287 GeneMark.hmm 549_aa+ 60812 62461	YP_009174114	putative major capsid protein MCP2 [Yellowstone lake mimivirus]	51	563	5E-162	580.9	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_288 GeneMark.hmm 353_aa+ 62532 63593	YP_009173344	putative phosphoinositide-specific phospholipase C-beta2 [Chrysochromulina ericina virus]	24.7	360	3.6E-20	109	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_289 GeneMark.hmm 504_aa+ 63624 65138	YP_009173345	putative polyA polymerase catalytic subunit [Chrysochromulina ericina virus]	50.5	424	7E-116	427.6	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_290 GeneMark.hmm 226_aa+ 65170 65850	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_291 GeneMark.hmm 102_aa+ 65889 66197	YP_008052487	hypothetical protein PGCG_00169 [Phaeocystis globosa virus]	36.7	79	2.1E-08	68.2	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_292 GeneMark.hmm 77_aa+ 66223 66456	YP_009173355	hypothetical protein ceV_100 [Chrysochromulina ericina virus]	42.1	76	1.3E-10	75.1	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_293 GeneMark.hmm 138_aa+ 66482 66898	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_294 GeneMark.hmm 157_aa+ 66966 67439	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_295 GeneMark.hmm 434_aa+ 67457 68761	YP_008052499	hypothetical protein PGCG_00181 [Phaeocystis globosa virus]	29.9	365	1.1E-26	131	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_296 GeneMark.hmm 328_aa+ 69124 70110	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_297 GeneMark.hmm 357_aa+ 70197 71270	YP_009173415	hypothetical protein ceV_160 [Chrysochromulina ericina virus]	42.6	197	2.9E-33	152.5	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_298 GeneMark.hmm 232_aa+ 71317 72015	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_299 GeneMark.hmm 147_aa+ 72337 72777	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_300 GeneMark.hmm 210_aa+ 72872 73501	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_301 GeneMark.hmm 264_aa+ 73941 74735	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_302 GeneMark.hmm 121_aa+ 74739 75104	YP_009173301	putative thioredoxin family protein [Chrysochromulina ericina virus]	35.1	97	1.9E-08	68.6	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_303 GeneMark.hmm 298_aa+ 75200 76096	YP_008052350	hypothetical protein PGCG_00031 [Phaeocystis globosa virus]	30.5	269	2.9E-18	102.4	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_304 GeneMark.hmm 235_aa+ 76101 76808	WP_137385183	CDP-glycerol glycerophosphotransferase family protein [Pantoea sp. SO10]	33.7	202	4.3E-25	124.8	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_305 GeneMark.hmm 196_aa+ 76846 77436	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_306 GeneMark.hmm 248_aa+ 77504 78250	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_307 GeneMark.hmm 205_aa+ 78276 78893	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_308 GeneMark.hmm 335_aa+ 78901 79908	YP_009173634	C-terminal catalytic domain of Ulp1 protease [Chrysochromulina ericina virus]	37.8	275	5.8E-44	188	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_309 GeneMark.hmm 162_aa+ 79963 80451	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_310 GeneMark.hmm 147_aa+ 80500 80943	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_311 GeneMark.hmm 117_aa+ 80991 81344	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_312 GeneMark.hmm 97_aa+ 81502 81795	WP_146342711	aquaporin [Lactobacillus algidus]	42.2	90	1.4E-06	62	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_313 GeneMark.hmm 92_aa+ 81846 82124	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_314 GeneMark.hmm 609_aa+ 82175 84004	YP_009173631	asparagine synthetase B [Chrysochromulina ericina virus]	45.9	614	3E-135	492.3	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_315 GeneMark.hmm 649_aa+ 84031 85980	XP_005827322	hypothetical protein GUITHDRAFT_113578 [Guillardia theta CCMP2712]	44.4	565	8E-111	411	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_316 GeneMark.hmm 186_aa+ 86023 86583	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_317 GeneMark.hmm 330_aa+ 86584 87576	YP_009173500	ribonucleoside-diphosphate reductase small subunit [Chrysochromulina ericina virus]	65.6	320	4E-117	431	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_318 GeneMark.hmm 42_aa+ 87569 87697	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_319 GeneMark.hmm 336_aa+ 87771 88781	YP_004062114	hypothetical protein MpV1_231c [Micromonas sp. RCC1109 virus MpV1]	55.1	207	1.4E-58	236.5	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_320 GeneMark.hmm 176_aa+ 88805 89335	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_321 GeneMark.hmm 210_aa+ 89367 89999	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_322 GeneMark.hmm 211_aa+ 90061 90696	YP_009173333	hypothetical protein ceV_078 [Chrysochromulina ericina virus]	34.9	209	5.2E-30	141	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_323 GeneMark.hmm 469_aa+ 90743 92152	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_324 GeneMark.hmm 149_aa+ 92191 92640	no hit	-	-	-	-	-	-
MM01_ERX55									

MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_327 GeneMark.hmm 184_aa + 94640 95194	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_328 GeneMark.hmm 240_aa + 95241 95963	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_329 GeneMark.hmm 336_aa + 95958 96968	YP_009173495	hypothetical protein ceV_240 [Chrysochromulina ericina virus]	33.5	331	1.4E-42	183.3	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_330 GeneMark.hmm 72_aa + 97007 97225	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_331 GeneMark.hmm 86_aa + 97344 97604	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_332 GeneMark.hmm 148_aa + 97643 98089	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_333 GeneMark.hmm 284_aa + 98560 99411	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_334 GeneMark.hmm 233_aa + 99566 100267	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_335 GeneMark.hmm 157_aa + 100360 100833	YP_008052514	transcription elongation factor TFIIS_C domain-containing protein [Phaeocystis globosa virus]	45.6	149	1.5E-29	139	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_336 GeneMark.hmm 228_aa + 100923 101609	YP_008052515	DNA-directed RNA polymerase II subunit RPB6 [Phaeocystis globosa virus]	45.2	124	2.7E-24	122.1	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_337 GeneMark.hmm 114_aa + 101668 102012	YP_009173521	DNA-directed RNA polymerase, subunit M/Transcription elongation factor TFIIS/RPB9 [Chr	47.4	116	1.6E-25	125.2	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_338 GeneMark.hmm 969_aa + 102178 105087	YP_009173524	D5 family helicase [Chrysochromulina ericina virus]	35.3	943	8E-150	541.2	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_339 GeneMark.hmm 242_aa + 105137 105865	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_340 GeneMark.hmm 271_aa + 105880 106695	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_341 GeneMark.hmm 254_aa + 106730 107494	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_342 GeneMark.hmm 144_aa + 107516 107950	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_343 GeneMark.hmm 364_aa + 107990 109084	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_344 GeneMark.hmm 158_aa + 109117 109593	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_345 GeneMark.hmm 150_aa + 109621 110073	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_346 GeneMark.hmm 207_aa + 110104 110727	YP_008052525	DNA-directed RNA polymerase II subunit RPB5 [Phaeocystis globosa virus]	43.1	204	7.5E-42	180.3	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_347 GeneMark.hmm 1654_aa + 110792 115756	YP_008052526	DNA-directed RNA polymerase II subunit RPB2 [Phaeocystis globosa virus]	52	1299	0	1389	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_348 GeneMark.hmm 629_aa + 115884 117773	YP_009173498	glucosamine-fructose-6-phosphate aminotransferase [Chrysochromulina ericina virus]	41	636	4E-116	428.7	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_349 GeneMark.hmm 84_aa + 117796 118050	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_350 GeneMark.hmm 199_aa + 118095 118694	YP_009174089	hypothetical protein [Yellowstone lake mimivirus]	40.3	186	1.2E-31	146.4	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_351 GeneMark.hmm 215_aa + 118710 119357	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_352 GeneMark.hmm 132_aa + 119432 119830	YP_009174087	hypothetical protein [Yellowstone lake mimivirus]	41.8	122	2.1E-21	111.7	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_353 GeneMark.hmm 249_aa + 119963 120079	WP_150463643	phosphoribosylaminoimidazolesuccinocarboxamide synthase [Francisella sp. XLW-1]	40.1	252	1.7E-35	159.5	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_354 GeneMark.hmm 609_aa + 121281 123110	XP_006866432	Phosphoribosylaminoimidazole carboxylase [Yamadazyma tenuis ATCC 10573]	39.3	387	4.2E-56	229.2	
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_355 GeneMark.hmm 62_aa + 123111 123299	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_356 GeneMark.hmm 153_aa + 123345 123806	no hit	-	-	-	-	-	-
MM01_ERX556019_45_dc	Moniruzzaman_MM01_ERX556019_45_dc_000000000002	gene_357 GeneMark.hmm 74_aa + 123787 124011	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_358 GeneMark.hmm 322_aa + 11969	XP_031617622	ankyrin repeat domain-containing protein 29-like, partial [Contarinia nasturtii]	42.6	155	3.4E-25	125.6	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_359 GeneMark.hmm 247_aa + 9641 1392	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_360 GeneMark.hmm 267_aa + 2154 2957	XP_005832793	hypothetical protein GUITHDRAFT_86917 [Guillardia theta CCMP2712]	33.2	271	1.4E-37	166.4	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_361 GeneMark.hmm 433_aa + 2975 4276	XP_002287956	predicted protein [Thalassiosira pseudonana CCMP1335]	25	216	9.6E-07	64.7	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_362 GeneMark.hmm 187_aa + 4331 4894	YP_008052401	phosphoesterase PA-phosphatase related protein [Phaeocystis globosa virus]	39.5	152	1.5E-20	109.4	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_363 GeneMark.hmm 316_aa + 5005 5955	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_364 GeneMark.hmm 85_aa + 5999 6256	YP_009173457	hypothetical protein ceV_202 [Chrysochromulina ericina virus]	66.2	80	4.8E-19	103.2	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_365 GeneMark.hmm 307_aa + 6365 7288	YP_009173458	hypothetical protein ceV_203 [Chrysochromulina ericina virus]	53.3	255	1.3E-74	289.7	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_366 GeneMark.hmm 281_aa + 7326 8171	YP_009173380	putative VV A32-like packaging ATPase [Chrysochromulina ericina virus]	76.9	281	2E-126	461.8	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_367 GeneMark.hmm 558_aa + 8271 9947	YP_009173379	putative phosphotransferase [Chrysochromulina ericina virus]	46.2	546	3E-105	392.5	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_368 GeneMark.hmm 47_aa + 10037 10180	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_369 GeneMark.hmm 88_aa + 10170 10436	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_370 GeneMark.hmm 116_aa + 10454 10804	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_371 GeneMark.hmm 331_aa + 10856 11851	WP_054535284	restriction endonuclease [Herpetosiphon geysericola]	30.1	345	9.5E-39	170.6	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_372 GeneMark.hmm 442_aa + 11872 13200	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_373 GeneMark.hmm 273_aa + 13291 14112	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_374 GeneMark.hmm 57_aa + 14241 14414	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_375 GeneMark.hmm 107_aa + 14428 14751	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_376 GeneMark.hmm 336_aa + 14797 15807	YP_009174071	hypothetical protein [Yellowstone lake mimivirus]	62.1	285	8.7E-72	280.4	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_377 GeneMark.hmm 264_aa + 15848 16642	YP_009173374	replication factor C small subunit [Chrysochromulina ericina virus]	48.6	253	3.4E-55	224.9	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_378 GeneMark.hmm 751_aa + 16719 18974	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_379 GeneMark.hmm 212_aa + 19024 19662	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_380 GeneMark.hmm 1317_aa + 19742 23695	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	46	1322	0	1083.9	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_381 GeneMark.hmm 83_aa + 23696 23947	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_382 GeneMark.hmm 111_aa + 23993 24328	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_383 GeneMark.hmm 240_aa + 24386 25108	YP_009173510	Deoxyribonucleoside kinase [Chrysochromulina ericina virus]	42.4	198	9.7E-33	150.2	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_384 GeneMark.hmm 60_aa + 25105 25287	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_385 GeneMark.hmm 95_aa + 25666 25950	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_386 GeneMark.hmm 224_aa + 25996 26670	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_387 GeneMark.hmm 350_aa + 26699 27751	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_388 GeneMark.hmm 307_aa + 27804 28727	YP_009174414	hypothetical protein [Yellowstone lake phycodnavirus 3]	34.6	217	1.4E-12	83.6	
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_389 GeneMark.hmm 158_aa + 28751 29227	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_390 GeneMark.hmm 73_aa + 31597 31818	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_391 GeneMark.hmm 41_aa + 35263 35388	no hit	-	-	-	-	-	-
MM01_ERX556031_42_dc	Moniruzzaman_MM01_ERX556031_42_dc_000000000003	gene_392 GeneMark.hmm 41_aa + 36837 36962	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_393 GeneMark.hmm 111_aa + 36959 37291	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_394 GeneMark.hmm 91_aa + 91 366	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_395 GeneMark.hmm 180_aa + 457 999	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_396 GeneMark.hmm 238_aa + 1059 1775	WP_127033475	phytanoyl-CoA dioxygenase family protein [Legionella sp. km711]	30.9	223	1.3E-18	103.2	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_397 GeneMark.hmm 99_aa + 2215 2511	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_398 GeneMark.hmm 168_aa + 2597 3103	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_399 GeneMark.hmm 250_aa + 3168 3920	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_400 GeneMark.hmm 115_aa + 3977 4324	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_401 GeneMark.hmm 105_aa + 4386 4703	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_402 GeneMark.hmm 89_aa + 4848 5117	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_403 GeneMark.hmm 326_aa + 5174 6154	XP_012940436	PREDICTED: chymotrypsin inhibitor-like [Aplysia californica]	52.9	70	2.5E-07	66.2	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_404 GeneMark.hmm 368_aa + 6209 7315	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_405 GeneMark.hmm 1181_aa + 7387 10932	YP_008052553	mRNA capping enzyme [Phaeocystis globosa virus]	47.3	1056	2E-274	955.3	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_406 GeneMark.hmm 263_aa + 11015 11806	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_407 GeneMark.hmm 127_aa + 11836 12219	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_408 GeneMark.hmm 180_aa + 12341 12883	YP_009173560	hypothetical protein ceV_305 [Chrysochromulina ericina virus]	47.9	165	2.7E-35	158.3	

MoMAGs

MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_409 GeneMark.hmm 97_aa - 12976 13269	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_410 GeneMark.hmm 1269_aa - 13313 17122	YP_009173561	putative helicase [Chrysochromulina ericina virus]	41	1250	1E-242	849.7	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_411 GeneMark.hmm 297_aa - 17137 18030	YP_009173562	Nudix-like hydrolase [Chrysochromulina ericina virus]	52.1	257	2.8E-74	288.5	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_412 GeneMark.hmm 143_aa+ 18089 18520	YP_009173563	Erv1 / Alr family [Chrysochromulina ericina virus]	44.1	143	2.2E-32	148.3	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_413 GeneMark.hmm 448_aa+ 18576 19922	YP_009173564	hypothetical protein ceV_309 [Chrysochromulina ericina virus]	30.7	342	2.3E-35	159.8	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_414 GeneMark.hmm 201_aa+ 19949 20554	YP_009173567	HNH nuclease [Chrysochromulina ericina virus]	48.5	200	8.3E-46	193.4	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_415 GeneMark.hmm 801_aa+ 20606 23011	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_416 GeneMark.hmm 258_aa+ 23107 23883	YP_009173569	hypothetical protein ceV_314 [Chrysochromulina ericina virus]	31.3	262	1.2E-25	126.7	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_417 GeneMark.hmm 297_aa+ 23993 24886	YP_009173570	hypothetical protein ceV_315 [Chrysochromulina ericina virus]	38.4	292	3.5E-48	201.8	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_418 GeneMark.hmm 345_aa+ 24971 26008	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_419 GeneMark.hmm 175_aa - 26082 26609	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_420 GeneMark.hmm 132_aa+ 26608 27006	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_421 GeneMark.hmm 367_aa - 27038 28141	YP_009173573	hypothetical protein ceV_318 [Chrysochromulina ericina virus]	32.3	359	8.1E-55	224.2	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_422 GeneMark.hmm 143_aa+ 28022 29149	YP_009173574	SAM dependent methyltransferase domain containing protein [Chrysochromulina ericina vir	41.9	265	3.1E-47	198.7	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_423 GeneMark.hmm 75_aa - 29116 29343	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_424 GeneMark.hmm 408_aa+ 29449 30675	YP_009173579	N-acyltransferase/N-myristoyltransferase [Chrysochromulina ericina virus]	30.9	405	3E-42	182.6	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_425 GeneMark.hmm 124_aa+ 30723 31097	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_426 GeneMark.hmm 252_aa+ 31171 31929	YP_008052624	hypothetical protein PGCG_00306 [Phaeocystis globosa virus]	53.6	69	9.9E-12	80.5	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_427 GeneMark.hmm 192_aa+ 32072 32650	YP_009173581	hypothetical protein ceV_326 [Chrysochromulina ericina virus]	42.2	116	1.7E-19	105.9	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_428 GeneMark.hmm 91_aa - 32685 32960	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_429 GeneMark.hmm 2197_aa - 33061 39654	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_430 GeneMark.hmm 440_aa+ 39736 41058	YP_008052619	2-polyphenylphenol 6-hydroxylase [Phaeocystis globosa virus]	25.7	377	6.3E-22	115.2	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_431 GeneMark.hmm 193_aa+ 41087 41668	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_432 GeneMark.hmm 495_aa+ 41814 43301	YP_009173584	hypothetical protein ceV_329 [Chrysochromulina ericina virus]	43.6	518	4.2E-91	345.1	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_433 GeneMark.hmm 274_aa+ 43371 44195	YP_008052612	putative Holliday junction resolvase [Phaeocystis globosa virus]	39.4	277	3.1E-43	185.3	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_434 GeneMark.hmm 136_aa+ 44404 44814	YP_008052610	hypothetical protein PGCG_00292 [Phaeocystis globosa virus]	36	139	1E-07	66.2	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_435 GeneMark.hmm 288_aa+ 44848 45714	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_436 GeneMark.hmm 598_aa+ 45799 47595	YP_009173588	MutS8 [Chrysochromulina ericina virus]	36.6	579	4E-100	375.6	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_437 GeneMark.hmm 423_aa+ 47658 48929	YP_009173589	Helicase 45 [Chrysochromulina ericina virus]	57.2	374	3E-124	455.3	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_438 GeneMark.hmm 335_aa+ 49123 50137	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_439 GeneMark.hmm 155_aa+ 50191 50658	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_440 GeneMark.hmm 669_aa+ 50809 52818	YP_008052605	hypothetical protein PGCG_00287 [Phaeocystis globosa virus]	28.5	698	5E-55	225.7	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_441 GeneMark.hmm 59_aa+ 52866 53045	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_442 GeneMark.hmm 181_aa+ 53092 53637	YP_009174655	hypothetical protein [Yellowstone lake phycodnavirus 2]	29.4	160	6.6E-10	73.9	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_443 GeneMark.hmm 75_aa+ 53713 53940	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_444 GeneMark.hmm 459_aa+ 53930 55309	YP_009173595	hypothetical protein ceV_340 [Chrysochromulina ericina virus]	28.2	294	5.6E-29	138.7	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_445 GeneMark.hmm 301_aa+ 55393 56298	YP_009173596	PIN domain of flap Endonuclease 1 [Chrysochromulina ericina virus]	37.2	298	6E-48	201.1	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_446 GeneMark.hmm 305_aa+ 56458 57375	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_447 GeneMark.hmm 239_aa+ 57436 58155	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_448 GeneMark.hmm 207_aa+ 58317 58940	YP_009173598	SWIB-domain containing protein [Chrysochromulina ericina virus]	63.7	135	2.8E-36	161.8	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_449 GeneMark.hmm 403_aa+ 59141 60352	YP_008052602	hypothetical protein PGCG_00284 [Phaeocystis globosa virus]	36.4	346	4.4E-54	221.9	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_450 GeneMark.hmm 311_aa+ 60539 61474	YP_009173648	DUF2738 superfamily protein [Chrysochromulina ericina virus]	37.5	261	1.3E-32	150.2	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_451 GeneMark.hmm 234_aa+ 61729 62433	XP_005794348	hypothetical protein EMIHUDDRAFT_431867 [Emiliania huxleyi CCMP1516]	31.7	208	1.6E-11	79.7	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_452 GeneMark.hmm 317_aa+ 62448 63401	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_453 GeneMark.hmm 321_aa+ 63468 64433	YP_009173646	hypothetical protein ceV_391 [Chrysochromulina ericina virus]	39.4	327	8E-59	237.3	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_454 GeneMark.hmm 162_aa+ 64535 65023	YP_008052597	hypothetical protein PGCG_00279 [Phaeocystis globosa virus]	29.9	164	1.1E-11	79.7	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_455 GeneMark.hmm 56_aa+ 65024 65194	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_456 GeneMark.hmm 204_aa+ 65273 65887	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_457 GeneMark.hmm 584_aa+ 65961 67715	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_458 GeneMark.hmm 827_aa+ 67797 70280	YP_009173643	DNA topoisomerase IA [Chrysochromulina ericina virus]	41.7	803	3E-159	572.4	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_459 GeneMark.hmm 86_aa+ 70374 70634	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_460 GeneMark.hmm 99_aa+ 71258 71557	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_461 GeneMark.hmm 79_aa+ 71615 71854	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_462 GeneMark.hmm 291_aa+ 71967 72842	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_463 GeneMark.hmm 148_aa+ 72973 73419	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_464 GeneMark.hmm 191_aa+ 73463 74038	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_465 GeneMark.hmm 353_aa+ 74090 75151	YP_008052348	hypothetical protein PGCG_00029 [Phaeocystis globosa virus]	33.4	311	1.9E-29	139.8	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_466 GeneMark.hmm 162_aa+ 75849 76337	YP_009173661	hypothetical protein ceV_406 [Chrysochromulina ericina virus]	44.4	160	8.3E-28	133.3	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_467 GeneMark.hmm 174_aa+ 76439 76963	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_468 GeneMark.hmm 296_aa+ 77054 77944	YP_009173639	hypothetical protein ceV_384 [Chrysochromulina ericina virus]	38.2	301	5E-55	224.6	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_469 GeneMark.hmm 560_aa+ 77974 79656	YP_009173639	hypothetical protein ceV_384 [Chrysochromulina ericina virus]	32	147	1E-08	71.6	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_470 GeneMark.hmm 113_aa+ 79895 80236	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_471 GeneMark.hmm 115_aa+ 80308 80655	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_472 GeneMark.hmm 777_aa+ 80785 83118	YP_009173654	ATP-dependent Lon protease [Chrysochromulina ericina virus]	64.5	397	8E-148	534.3	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_473 GeneMark.hmm 284_aa+ 83232 84086	YP_009173576	N-4 cytosine/N-6 adenine -specific DNA methylase [Chrysochromulina ericina virus]	67.5	277	5E-108	400.6	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_474 GeneMark.hmm 229_aa+ 84141 84830	YP_008052647	hypothetical protein PGCG_00329 [Phaeocystis globosa virus]	35.1	222	6.9E-20	107.5	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_475 GeneMark.hmm 950_aa+ 84920 87772	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_476 GeneMark.hmm 172_aa+ 87792 88310	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_477 GeneMark.hmm 1488_aa+ 88446 92912	YP_009173653	DNA-directed RNA polymerase II, subunit RpB1 [Chrysochromulina ericina virus]	62	1507	0	1905.2	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_478 GeneMark.hmm 78_aa+ 92999 93235	YP_009052202	hypothetical protein AaV_126 [Aureococcus anophagefferens virus]	65.6	64	7.5E-19	102.4	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_479 GeneMark.hmm 71_aa+ 93263 93478	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_480 GeneMark.hmm 972_aa+ 93574 96492	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_481 GeneMark.hmm 223_aa+ 96589 97260	WP_108864097	FAD-dependent thymidylate synthase [Rhodobacteraceae bacterium Water-Bin34]	59.6	228	3E-68	268.1	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_482 GeneMark.hmm 108_aa+ 97319 97645	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_483 GeneMark.hmm 1787_aa+ 97686 103049	YP_009173600	repeat containing protein [Chrysochromulina ericina virus]	30.9	957	4E-112	416.8	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_484 GeneMark.hmm 153_aa+ 103201 103662	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_485 GeneMark.hmm 141_aa+ 103698 104123	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_486 GeneMark.hmm 138_aa+ 104262 104678	WP_048089435	ribonuclease HI family protein [Candidatus Methanoperedens nitroreducens]	46	126	7.5E-22	113.2	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_487 GeneMark.hmm 276_aa+ 104720 105550	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000								

MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_491 GeneMark.hmm 284_aa - 107586 108440	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_492 GeneMark.hmm 240_aa+ 108528 109250	YP_008052654	hypothetical protein PGCG_00336 [Phaeocystis globosa virus]	39.1	138	4.8E-24	121.3	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_493 GeneMark.hmm 140_aa+ 109368 109790	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_494 GeneMark.hmm 154_aa+ 111584 112041	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_495 GeneMark.hmm 82_aa+ 110342 110590	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_496 GeneMark.hmm 278_aa+ 110663 111499	YP_008052649	hypothetical protein PGCG_00331 [Phaeocystis globosa virus]	32.3	257	4.9E-28	134.8	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_497 GeneMark.hmm 154_aa+ 111584 112041	XP_026424758	glucosamine 6-phosphate N-acetyltransferase-like [Papaver somniferum]	42.9	154	1.8E-19	105.5	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_498 GeneMark.hmm 365_aa+ 112045 113142	XP_006364102	PREDICTED: uncharacterized protein LOC102586362 [Solanum tuberosum]	39.9	283	3.3E-40	175.6	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_499 GeneMark.hmm 60_aa - 113356 113538	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_500 GeneMark.hmm 215_aa+ 113809 114456	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_501 GeneMark.hmm 304_aa - 114540 115454	XP_001450879	hypothetical protein (macronuclear) [Paramecium tetraurelia strain d4-2]	44.4	279	2.1E-53	219.2	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_502 GeneMark.hmm 643_aa - 115492 117423	XP_024572007	acyl-dehydrogenase [Plasmopara halstedii]	39.7	544	6E-108	401.4	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_503 GeneMark.hmm 107_aa+ 117611 117934	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_504 GeneMark.hmm 118_aa+ 118021 118377	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_505 GeneMark.hmm 176_aa+ 118407 118937	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_506 GeneMark.hmm 108_aa+ 119029 119355	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_507 GeneMark.hmm 628_aa - 119468 121354	YP_009173631	asparagine synthetase B [Chrysochromulina ericina virus]	47.3	636	2E-142	516.2	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_508 GeneMark.hmm 168_aa+ 121477 121983	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_509 GeneMark.hmm 315_aa+ 122035 122982	YP_009173634	C-terminal catalytic domain of Ulp1 protease [Chrysochromulina ericina virus]	49.4	259	7.4E-65	257.3	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_510 GeneMark.hmm 329_aa+ 123097 124086	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_511 GeneMark.hmm 316_aa+ 124196 125146	XP_002178029	predicted protein [Phaeodactylum tricornutum CCAP 1055/1]	32.4	188	3.1E-15	92.4	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_512 GeneMark.hmm 505_aa+ 125303 126820	WP_117784804	ribonuclease R [Clostridium sp. AF15-31]	25.7	354	1.5E-14	90.9	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_513 GeneMark.hmm 377_aa+ 126994 128127	YP_009448291	UV damage endonuclease UvdE [Orpheovirus IHUMI-LCC2]	46.5	316	2E-80	309.3	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_514 GeneMark.hmm 159_aa+ 128160 128639	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_515 GeneMark.hmm 288_aa+ 128641 129507	WP_169975941	NAD-dependent deacetylase [Campylobacter sp. RM16191]	36.6	284	1.7E-44	189.5	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_516 GeneMark.hmm 110_aa+ 129582 129914	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_517 GeneMark.hmm 1311_aa+ 129970 133905	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	50.2	1314	0	1153.3	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_518 GeneMark.hmm 150_aa+ 133967 134419	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_519 GeneMark.hmm 289_aa+ 134452 135321	YP_009173390	hypothetical protein ceV_135 [Chrysochromulina ericina virus]	47.5	101	2.2E-15	92.8	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_520 GeneMark.hmm 269_aa+ 135405 136214	YP_008052632	hypothetical protein PGCG_00314 [Phaeocystis globosa virus]	30.9	256	7E-24	120.9	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_521 GeneMark.hmm 140_aa+ 136314 136736	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_522 GeneMark.hmm 112_aa+ 136804 137142	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_523 GeneMark.hmm 280_aa+ 137288 138130	YP_008052636	ERCC4-type DNA repair nuclease [Phaeocystis globosa virus]	36.8	285	1.7E-28	136.3	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_524 GeneMark.hmm 93_aa+ 138237 138518	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_525 GeneMark.hmm 335_aa+ 138633 139640	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	62.3	324	7E-122	446.8	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_526 GeneMark.hmm 1156_aa+ 139725 143195	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	39.1	1180	6E-208	734.6	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_527 GeneMark.hmm 136_aa+ 143278 143688	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_528 GeneMark.hmm 621_aa+ 143722 145587	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_529 GeneMark.hmm 348_aa+ 145657 146703	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	53.5	340	5E-105	391	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_530 GeneMark.hmm 369_aa+ 146723 147832	YP_009173614	Link (Hyaluronan-binding) domain containing protein [Chrysochromulina ericina virus]	53.3	150	1.3E-44	190.3	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_531 GeneMark.hmm 208_aa+ 147834 148460	WP_035004769	class II aldolase/adducin family protein, partial [Betaproteobacteria bacterium MOLA814]	31.9	216	8.7E-14	87	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_532 GeneMark.hmm 112_aa+ 148536 148874	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_533 GeneMark.hmm 113_aa+ 148913 149254	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_534 GeneMark.hmm 162_aa+ 149375 149863	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_535 GeneMark.hmm 114_aa+ 149893 150237	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_536 GeneMark.hmm 494_aa+ 150230 151714	YP_009173609	hypothetical protein ceV_354 [Chrysochromulina ericina virus]	37.9	203	6.2E-34	155.2	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_537 GeneMark.hmm 245_aa+ 151749 152486	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_538 GeneMark.hmm 376_aa+ 152548 153678	YP_008052657	hypothetical protein PGCG_00339 [Phaeocystis globosa virus]	28.2	291	1.7E-15	93.6	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_539 GeneMark.hmm 599_aa+ 153792 155591	YP_009173669	ribonuclease II family protein [Chrysochromulina ericina virus]	38.3	592	4E-111	411.8	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_540 GeneMark.hmm 181_aa+ 155700 156245	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_541 GeneMark.hmm 846_aa+ 156303 158843	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_542 GeneMark.hmm 286_aa+ 158977 159837	WP_146921314	FkbM family methyltransferase [Algoriphagus aquimarinus]	34.7	167	5.7E-16	94.7	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_543 GeneMark.hmm 299_aa+ 159885 160784	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_544 GeneMark.hmm 241_aa+ 160976 161701	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_545 GeneMark.hmm 256_aa+ 161747 162517	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_546 GeneMark.hmm 239_aa+ 162573 163292	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_547 GeneMark.hmm 160_aa+ 163432 163914	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_548 GeneMark.hmm 250_aa+ 163973 164725	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_549 GeneMark.hmm 208_aa+ 164786 165412	YP_009254762	hypothetical protein [Tokyovirus A1]	35.7	185	9.6E-21	110.2	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_550 GeneMark.hmm 322_aa+ 165409 166377	YP_009174067	putative site-specific DNA methyltransferase [Yellowstone lake mimivirus]	69.3	306	5E-123	450.7	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_551 GeneMark.hmm 318_aa+ 166528 167484	YP_008052744	hypothetical protein PGCG_00433 [Phaeocystis globosa virus]	32.6	304	1.2E-35	160.2	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_552 GeneMark.hmm 177_aa+ 168521 169054	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_553 GeneMark.hmm 83_aa+ 169063 169314	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_554 GeneMark.hmm 908_aa+ 169371 172097	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_555 GeneMark.hmm 725_aa+ 172191 174368	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_556 GeneMark.hmm 273_aa+ 174469 175290	YP_008052380	DNA methylase [Phaeocystis globosa virus]	82.2	258	2E-126	461.8	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_557 GeneMark.hmm 286_aa+ 175396 176256	YP_009174084	putative DNA N6-adenine methyltransferase [Yellowstone lake mimivirus]	49.6	278	4E-70	274.6	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_558 GeneMark.hmm 71_aa+ 176289 176504	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_559 GeneMark.hmm 250_aa+ 176583 177335	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_560 GeneMark.hmm 147_aa+ 177472 177915	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_561 GeneMark.hmm 857_aa+ 178038 180611	YP_009173671	DEAD-like RNA helicase, superfamily II [Chrysochromulina ericina virus]	41.4	816	7E-172	614.4	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_562 GeneMark.hmm 1262_aa+ 180714 184502	XP_022305630	serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C-like [Crassostre	34.2	733	3.5E-97	366.7	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_563 GeneMark.hmm 115_aa+ 184675 185022	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_564 GeneMark.hmm 294_aa+ 185209 186093	XP_006390629	casein kinase 1-like protein 2 [Eutrema salsugineum]	33.3	261	1E-31	147.1	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_565 GeneMark.hmm 152_aa+ 186102 186560	XP_004367486	succinate dehydrogenase, cytochrome b556 subunit protein [Acanthamoeba castellanii str.	40.2	112	2.5E-10	75.1	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_566 GeneMark.hmm 107_aa+ 186644 186967	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_567 GeneMark.hmm 242_aa+ 186960 187688	XP_009826543	succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial [Aphanomyces ast	68	228	2.4E-84	321.6	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_568 GeneMark.hmm 609_aa+ 187790 189619	XP_021874351	FAD binding domain-domain-containing protein [Kockovaella imperatae]	66.7	598	2E-229	804.7	
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_569 GeneMark.hmm 170_aa+ 189774 190286	no hit	-	-	-	-	-	-
MM01_ERX556106_20_dc	Moniruzzaman_MM01_ERX556106_20_dc_000000000003	gene_570 GeneMark.hmm 37_aa+ 190276 190389	no hit	-	-	-	-	-	-
MM01_ERX556106_2									

MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_573 GeneMark.hmm 143_aa +919 1350	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_574 GeneMark.hmm 127_aa +1361 11744	YP_009174078	hypothetical protein [Yellowstone lake mimivirus]	47.4	116	7.9E-18	99.8	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_575 GeneMark.hmm 114_aa +1764 2108	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_576 GeneMark.hmm 366_aa +2268 3368	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_577 GeneMark.hmm 188_aa +3436 4002	YP_009174082	hypothetical protein [Yellowstone lake mimivirus]	38.5	182	3.4E-25	124.8	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_578 GeneMark.hmm 128_aa +4071 4457	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_579 GeneMark.hmm 288_aa +4512 5378	YP_008052501	hypothetical protein PGCG_00183 [Phaeocystis globosa virus]	35.3	224	6E-29	137.9	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_580 GeneMark.hmm 219_aa +5473 6132	YP_009173469	Erv1 / Alr family [Chrysochromulina ericina virus]	53	202	5.5E-51	210.7	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_581 GeneMark.hmm 155_aa +6247 6714	XP_031219633	protein disulfide-isomerase A5 isoform X1 [Mastomys coucha]	34.3	105	2.6E-07	65.1	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_582 GeneMark.hmm 316_aa +6711 7661	WP_083241009	MULTISPECIES: patatin-like phospholipase family protein [Methanobacterium]	29.1	206	4E-18	102.1	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_583 GeneMark.hmm 195_aa +7867 8454	YP_008052435	hypothetical protein PGCG_00116 [Phaeocystis globosa virus]	41.1	192	2.2E-35	158.7	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_584 GeneMark.hmm 414_aa +8486 9730	YP_009173614	Link (Hyaluronan-binding) domain containing protein [Chrysochromulina ericina virus]	36.4	239	5E-37	165.2	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_585 GeneMark.hmm 350_aa +9754 10806	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	52.6	346	2E-103	386	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_586 GeneMark.hmm 419_aa +10869 12128	NP_180361	-box superfamily protein [Arabidopsis thaliana]	35.9	78	1.2E-06	64.3	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_587 GeneMark.hmm 1043_aa +12284 15415	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	46.6	1033	3E-245	858.2	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_588 GeneMark.hmm 258_aa +15495 16271	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	40.9	247	1.1E-42	183.3	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_589 GeneMark.hmm 341_aa +16363 17388	XP_032806963	protein disulfide-isomerase A5 [Petromyzon marinus]	37.3	110	5.8E-07	65.1	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_590 GeneMark.hmm 218_aa +17525 18181	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	37.7	183	1.1E-24	123.2	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_591 GeneMark.hmm 57_aa +18310 18483	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_592 GeneMark.hmm 305_aa +18500 19417	YP_009173624	ERCC4-type nuclease [Chrysochromulina ericina virus]	29.2	291	4E-23	118.6	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_593 GeneMark.hmm 72_aa +19443 19661	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_594 GeneMark.hmm 349_aa +19747 20796	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	62.5	317	5E-115	424.1	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_595 GeneMark.hmm 48_aa +20961 21107	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_596 GeneMark.hmm 335_aa +21150 22157	YP_008052640	multiple copy protein PGM_MIGE [Phaeocystis globosa virus]	32.7	343	1.8E-37	166.4	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_597 GeneMark.hmm 143_aa +22183 22614	YP_009173487	hypothetical protein ceV_232 [Chrysochromulina ericina virus]	52.8	123	2.6E-25	124.8	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_598 GeneMark.hmm 233_aa +22687 23388	YP_008052461	deoxynucleoside kinase [Phaeocystis globosa virus]	42.2	218	5.7E-38	167.5	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_599 GeneMark.hmm 191_aa +23412 23987	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_600 GeneMark.hmm 195_aa +24025 24612	YP_009173485	hypothetical protein ceV_230 [Chrysochromulina ericina virus]	58.5	188	1.2E-52	216.1	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_601 GeneMark.hmm 861_aa +24748 27333	YP_009174052	hypothetical protein [Yellowstone lake mimivirus]	43	642	3E-135	492.7	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_602 GeneMark.hmm 209_aa +27423 28052	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_603 GeneMark.hmm 597_aa +28165 29958	YP_009174075	hypothetical protein [Yellowstone lake mimivirus]	37.4	594	2.4E-85	326.2	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_604 GeneMark.hmm 184_aa +30012 30566	YP_009174076	hypothetical protein [Yellowstone lake mimivirus]	43.2	155	1.2E-27	132.9	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_605 GeneMark.hmm 685_aa +30642 32699	YP_009174077	putative glycosyl transferase [Yellowstone lake mimivirus]	39.1	705	4E-121	445.3	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_606 GeneMark.hmm 258_aa +32686 33462	YP_008052440	ribonuclease HII [Phaeocystis globosa virus]	48.9	231	3.4E-52	214.9	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_607 GeneMark.hmm 728_aa +33572 35758	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_608 GeneMark.hmm 450_aa +35847 37199	YP_009174125	putative replication factor C large subunit [Yellowstone lake mimivirus]	52.5	453	1E-129	473	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_609 GeneMark.hmm 129_aa +37274 37663	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_610 GeneMark.hmm 418_aa +37758 39014	YP_009173339	putative glycosyltransferase [Chrysochromulina ericina virus]	47.4	411	1.4E-90	343.2	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_611 GeneMark.hmm 756_aa +39064 41334	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_612 GeneMark.hmm 554_aa +41412 43076	YP_009174114	putative major capsid protein MCP2 [Yellowstone lake mimivirus]	51.2	563	1E-173	619.4	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_613 GeneMark.hmm 356_aa +43131 44201	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_614 GeneMark.hmm 494_aa +44250 45734	YP_008052392	polyA polymerase catalytic subunit [Phaeocystis globosa virus]	49.3	442	1E-120	443.4	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_615 GeneMark.hmm 612_aa +45832 47667	WP_147530625	ankyrin repeat domain-containing protein [Brachyspira aalborgi]	28.2	571	7.4E-29	138.7	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_616 GeneMark.hmm 232_aa +47741 48439	WP_157151613	ankyrin repeat domain-containing protein [Brachyspira sp. SAP_772]	52.9	157	3.2E-33	151.8	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_617 GeneMark.hmm 239_aa +48533 49252	YP_009173353	hypothetical protein ceV_098 [Chrysochromulina ericina virus]	37.6	125	1.4E-10	76.6	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_618 GeneMark.hmm 86_aa +49316 49576	YP_009174104	hypothetical protein [Yellowstone lake mimivirus]	46.8	77	8.9E-13	82.4	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_619 GeneMark.hmm 86_aa +49606 49866	YP_009174103	hypothetical protein [Yellowstone lake mimivirus]	54.7	75	4.7E-14	86.7	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_620 GeneMark.hmm 447_aa +49874 51217	YP_009173365	hypothetical protein ceV_110 [Chrysochromulina ericina virus]	35.2	176	3.5E-20	109.4	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_621 GeneMark.hmm 498_aa +51272 52768	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_622 GeneMark.hmm 244_aa +52814 53548	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_623 GeneMark.hmm 183_aa +53661 54212	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_624 GeneMark.hmm 266_aa +54263 55063	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_625 GeneMark.hmm 72_aa +55064 55282	no hit	-	-	-	-	-	-
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_626 GeneMark.hmm 304_aa +55392 56306	YP_009173414	hypothetical protein ceV_159 [Chrysochromulina ericina virus]	27.6	192	4.2E-09	72	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_627 GeneMark.hmm 357_aa +56403 57476	YP_009173415	hypothetical protein ceV_160 [Chrysochromulina ericina virus]	38.8	209	1.3E-36	163.7	
MM01_SRX802073_139_dc	Moniruzzaman_MM01_SRX802073_139_dc_000000000007	gene_628 GeneMark.hmm 99_aa +57521 57820	no hit	-	-	-	-	-	-
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_629 GeneMark.hmm 1151_aa +3 3455	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	48.7	1184	0	1099	
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_630 GeneMark.hmm 461_aa +3505 4890	XP_009032967	hypothetical protein AURANDRAFT_20350 [Aureococcus anophagefferens]	45.2	321	3E-75	292.4	
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_631 GeneMark.hmm 207_aa +4927 5550	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	42.4	191	4E-35	157.9	
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_632 GeneMark.hmm 123_aa +5569 5940	no hit	-	-	-	-	-	-
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_633 GeneMark.hmm 137_aa +5987 6400	YP_009173352	dCMP deaminase [Chrysochromulina ericina virus]	64.8	128	2.6E-46	194.5	
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_634 GeneMark.hmm 129_aa +6440 6829	no hit	-	-	-	-	-	-
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_635 GeneMark.hmm 211_aa +6861 7496	WP_135760935	class I SAM-dependent methyltransferase [Leptospira idonii]	31.8	195	1.8E-11	79.3	
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_636 GeneMark.hmm 246_aa +7506 8246	YP_009173624	ERCC4-type nuclease [Chrysochromulina ericina virus]	36.3	248	1.3E-29	139.8	
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_637 GeneMark.hmm 89_aa +8299 8568	no hit	-	-	-	-	-	-
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_638 GeneMark.hmm 331_aa +8606 9601	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	61.3	326	3E-111	411.8	
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_639 GeneMark.hmm 886_aa +9641 12298	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	44.7	828	8E-173	617.5	
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_640 GeneMark.hmm 175_aa +12419 12946	no hit	-	-	-	-	-	-
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_641 GeneMark.hmm 128_aa +12992 13378	no hit	-	-	-	-	-	-
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_642 GeneMark.hmm 162_aa +13482 13970	no hit	-	-	-	-	-	-
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_643 GeneMark.hmm 683_aa +13962 16013	no hit	-	-	-	-	-	-
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_644 GeneMark.hmm 236_aa +16030 16740	no hit	-	-	-	-	-	-
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_645 GeneMark.hmm 316_aa +16773 17723	YP_008052642	thiol protease [Phaeocystis globosa virus]	49.6	264	1.3E-69	273.1	
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_646 GeneMark.hmm 177_aa +17763 18296	YP_008052644	hypothetical protein PGCG_00326 [Phaeocystis globosa virus]	37.2	164	3.6E-16	94.7	
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_647 GeneMark.hmm 228_aa +18331 19017	YP_008052647	hypothetical protein PGCG_00329 [Phaeocystis globosa virus]	34.6	228	1.1E-22	116.7	
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_648 GeneMark.hmm 84_aa +19377 19631	YP_009173734	N-acetylglucosamine-1-phosphate uridylyltransferase [Chrysochromulina ericina virus]	51.6	64	2.9E-08	67.4	
MM01_SRX802073_99_dc	Moniruzzaman_MM01_SRX802073_99_dc_000000000045	gene_649 GeneMark.hmm 163_aa +19606 20097	YP_009173262	dTDP-D-glucose 4,6-dehydratase/N-acetylglucosamine-1-phosphate uridylyltransferase fusio	42.2	154	7.3E-24	120.2	
MM01_SRX802073_									

MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_655 GeneMark.hmm 237_aa +988 1701	YP_008052461	deoxynucleoside kinase [Phaeocystis globosa virus]	40	245	4E-39	171.4
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_656 GeneMark.hmm 522_aa +1711 3279	YP_008052723	DNA methyltransferase [Phaeocystis globosa virus]	28.2	447	7E-36	161.8
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_657 GeneMark.hmm 148_aa +3388 3834	WP_091431419	glycine cleavage system protein GcvH [Aliiviroseovirus sediminilitoris]	34.3	137	1.1E-10	76.3
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_658 GeneMark.hmm 273_aa +3935 4756	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_659 GeneMark.hmm 58_aa +4797 4973	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_660 GeneMark.hmm 191_aa +4978 5553	YP_008052421	hypothetical protein PGCG_00102 [Phaeocystis globosa virus]	57	128	1.4E-37	166
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_661 GeneMark.hmm 211_aa +5589 6224	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_662 GeneMark.hmm 335_aa +6296 7303	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_663 GeneMark.hmm 158_aa +7396 7872	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_664 GeneMark.hmm 226_aa +7875 8555	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_665 GeneMark.hmm 174_aa +8600 9124	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_666 GeneMark.hmm 95_aa +9144 9431	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_667 GeneMark.hmm 169_aa +9457 9966	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_668 GeneMark.hmm 324_aa +10034 11008	YP_009173500	ribonucleoside-diphosphate reductase small subunit [Chrysochromulina ericina virus]	73.4	323	2E-133	485
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_669 GeneMark.hmm 73_aa +11047 11268	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_670 GeneMark.hmm 260_aa +11357 12139	YP_009173496	Beta-4-Galactosyltransferase [Chrysochromulina ericina virus]	39.3	239	5.7E-39	171
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_671 GeneMark.hmm 352_aa +12175 13233	YP_009173464	transcription initiation factor TFIIB [Chrysochromulina ericina virus]	62.5	349	6E-130	473.8
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_672 GeneMark.hmm 416_aa +13300 14550	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_673 GeneMark.hmm 192_aa +14592 15170	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_674 GeneMark.hmm 579_aa +15372 17111	WP_158520294	hypothetical protein, partial [Prochlorococcus sp. HOT208_60m_813B04]	34.2	161	2.4E-13	87
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_675 GeneMark.hmm 196_aa +17245 17835	YP_009173466	hypothetical protein ceV_211 [Chrysochromulina ericina virus]	48.7	195	2.4E-42	181.8
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_676 GeneMark.hmm 291_aa +17887 18762	YP_008052436	patatin-like phospholipase [Phaeocystis globosa virus]	31.8	314	9.6E-43	183.7
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_677 GeneMark.hmm 156_aa +18746 19216	YP_008052437	disulfide isomerase [Phaeocystis globosa virus]	32.1	156	2.3E-11	78.6
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_678 GeneMark.hmm 56_aa +19297 19467	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_679 GeneMark.hmm 198_aa +19506 20102	YP_009173469	Erv1 / Alr family [Chrysochromulina ericina virus]	59.4	187	8.8E-56	226.5
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_680 GeneMark.hmm 214_aa +20133 20777	YP_008052442	exonuclease [Phaeocystis globosa virus]	38.4	219	1.2E-31	146.4
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_681 GeneMark.hmm 80_aa +20842 21084	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_682 GeneMark.hmm 240_aa +21151 21873	YP_009173471	ribonuclease HIII [Chrysochromulina ericina virus]	53.8	212	1.7E-58	235.7
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_683 GeneMark.hmm 297_aa +21955 22848	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_684 GeneMark.hmm 347_aa +22944 23987	XP_017229326	PREDICTED: glutamine synthetase cytosolic isozyme [Daucus carota subsp. sativus]	52.3	342	1E-99	373.2
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_685 GeneMark.hmm 175_aa +24018 24545	YP_009173605	hypothetical protein ceV_350 [Chrysochromulina ericina virus]	30.9	181	1.4E-09	72.8
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_686 GeneMark.hmm 76_aa +24730 24960	YP_003969713	hypothetical protein crov081 [Cafeteria roenbergensis virus BV-PW1]	57.1	70	1.7E-12	81.3
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_687 GeneMark.hmm 475_aa +25042 26469	WP_090257731	ribonuclease R [Fabibacter pacificus]	24.4	373	7.6E-13	85.1
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_688 GeneMark.hmm 351_aa +26510 27565	XP_015772703	PREDICTED: uncharacterized protein LOC107350951 [Acropora digitifera]	50.9	175	3E-51	212.2
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_689 GeneMark.hmm 128_aa +27609 27995	YP_009173385	DUF2177 domain containing protein [Chrysochromulina ericina virus]	37.9	116	9.1E-14	86.3
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_690 GeneMark.hmm 242_aa +28002 28730	YP_007877796	hypothetical protein CPRG_00032 [Cyanophage Syn30]	36.7	166	2.3E-21	112.5
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_691 GeneMark.hmm 332_aa +28738 29736	YP_009173650	MIGE-like protein [Chrysochromulina ericina virus]	34.2	342	2E-44	189.5
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_692 GeneMark.hmm 107_aa +29837 30160	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_693 GeneMark.hmm 238_aa +30123 30839	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_694 GeneMark.hmm 373_aa +30889 32010	WP_052107465	BspA family leucine-rich repeat surface protein [Polaribacter sp. Hel1_33_49]	50.3	147	1.6E-29	140.2
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_695 GeneMark.hmm 343_aa +32109 33140	WP_147102193	GDP-mannose 4,6-dehydratase [Vicingus serpentipes]	58.6	350	9E-115	423.3
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_696 GeneMark.hmm 610_aa +33198 35030	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_697 GeneMark.hmm 308_aa +35138 36064	XP_014156933	cathepsin X [Sphaeroforma arctica JP610]	56.1	278	5.3E-92	347.4
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_698 GeneMark.hmm 80_aa +36094 36336	NP_149711	Invertebrate iridescent virus 6]	50	80	9.4E-09	68.9
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_699 GeneMark.hmm 158_aa +36452 36928	WP_160629538	dUTP diphosphatase [Kiritimatiaellaota bacterium S-5007]	47.5	158	6.2E-28	133.7
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_700 GeneMark.hmm 109_aa +37006 37335	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_701 GeneMark.hmm 385_aa +37456 38613	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_702 GeneMark.hmm 235_aa +38676 39383	WP_068827373	DUF616 domain-containing protein [Wenyngzhuangia fucanilytica]	29.1	220	3.2E-12	82
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_703 GeneMark.hmm 95_aa +39424 39711	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_704 GeneMark.hmm 230_aa +39641 40333	WP_146422880	MULTISPECIES: CYTH domain-containing protein [Candidatus Saccharibacteria]	34.9	169	5.5E-17	97.8
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_705 GeneMark.hmm 201_aa +40370 40975	YP_009173560	hypothetical protein ceV_305 [Chrysochromulina ericina virus]	40.7	177	2.3E-27	132.1
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_706 GeneMark.hmm 1204_aa +41022 44636	YP_009173561	putative helicase [Chrysochromulina ericina virus]	34.3	1270	7E-180	641.3
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_707 GeneMark.hmm 259_aa +44646 45425	YP_009173562	Nudix-like hydrolase [Chrysochromulina ericina virus]	50	262	8.5E-67	263.5
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_708 GeneMark.hmm 139_aa +45467 45886	YP_009173563	Erv1 / Alr family [Chrysochromulina ericina virus]	46.2	143	1.7E-29	138.7
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_709 GeneMark.hmm 488_aa +45907 47373	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_710 GeneMark.hmm 192_aa +47391 47969	YP_009173567	HNH nuclease [Chrysochromulina ericina virus]	49	192	3.6E-46	194.5
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_711 GeneMark.hmm 406_aa +47974 49194	YP_009173568	hypothetical protein ceV_313 [Chrysochromulina ericina virus]	25.7	249	4E-15	92.4
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_712 GeneMark.hmm 233_aa +49222 49923	YP_009173569	hypothetical protein ceV_314 [Chrysochromulina ericina virus]	37.9	214	4.1E-36	161.4
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_713 GeneMark.hmm 281_aa +49951 50796	YP_009173570	hypothetical protein ceV_315 [Chrysochromulina ericina virus]	40.3	283	1.5E-48	203
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_714 GeneMark.hmm 69_aa +50833 51042	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_715 GeneMark.hmm 142_aa +51096 51524	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_716 GeneMark.hmm 132_aa +51530 51928	YP_009173679	Cold-Shock Protein [Chrysochromulina ericina virus]	42.3	123	7E-17	96.7
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_717 GeneMark.hmm 194_aa +51967 52551	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_718 GeneMark.hmm 327_aa +52620 53603	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_719 GeneMark.hmm 255_aa +53658 54425	XP_002182261	proliferating cell nuclear antigen [Phaeodactylum tricornutum CCAP 1055/1]	30	247	7.4E-23	117.5
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_720 GeneMark.hmm 281_aa +54545 55390	YP_008052657	hypothetical protein PGCG_00339 [Phaeocystis globosa virus]	28.1	281	5.6E-24	121.3
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_721 GeneMark.hmm 567_aa +55453 57156	YP_009173669	ribonuclease II family protein [Chrysochromulina ericina virus]	40.3	571	2E-119	439.5
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_722 GeneMark.hmm 82_aa +57157 57405	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_723 GeneMark.hmm 140_aa +57500 57922	YP_008052527	hypothetical protein PGCG_00209 [Phaeocystis globosa virus]	44	100	1.8E-18	102.1
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_724 GeneMark.hmm 145_aa +57950 58387	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_725 GeneMark.hmm 826_aa +58461 60941	YP_009173671	DEAD-like RNA helicase, superfamily II [Chrysochromulina ericina virus]	40.3	866	7E-163	584.3
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_726 GeneMark.hmm 237_aa +61008 61721	YP_008052654	hypothetical protein PGCG_00336 [Phaeocystis globosa virus]	43	149	6.9E-23	117.5
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_727 GeneMark.hmm 271_aa +61762 62577	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_728 GeneMark.hmm 84_aa +62639 62893	XP_024573332	ubiquitin-60s ribosomal protein 140 [Plasmopara halstedii]	92.4	79	3.4E-33	150.2
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_729 GeneMark.hmm 277_aa +62957 63790	YP_009174299	hypothetical protein [Yellowstone lake phycodnavirus 3]	40.1	192	1.2E-29	140.2
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_730 GeneMark.hmm 41_aa +63848 63973	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_731 GeneMark.hmm 111_aa +63942 64277	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_732 GeneMark.hmm 45_aa +64276 64413	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_733 GeneMark.hmm 449_aa +64422 65771	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_734 GeneMark.hmm 230_aa +65907 66599	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_735 GeneMark.hmm 414_aa +66689 67933	WP_108839329	Hint domain-containing protein [Tateyamaria sp. Alg231-49]	30.4	148	5.4E-07	65.5

MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_737 GeneMark.hmm 129_aa +68494 68883	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_738 GeneMark.hmm 77_aa +68983 69216	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_739 GeneMark.hmm 685_aa +69208 71265	YP_009173744	DNA polymerase X/NAD-dependent DNA ligase fusion protein [Chrysochromulina ericina vi	47.8	651	4E-163	584.7	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_740 GeneMark.hmm 378_aa +71353 72486	YP_009173744	DNA polymerase X/NAD-dependent DNA ligase fusion protein [Chrysochromulina ericina vi	48.4	345	2.6E-77	298.9	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_741 GeneMark.hmm 118_aa +72514 72870	YP_008052648	hypothetical protein PGCG_00330 [Phaeocystis globosa virus]	42.9	84	4.8E-09	70.5	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_742 GeneMark.hmm 235_aa +72934 73641	YP_009173630	hypothetical protein ceV_375 [Chrysochromulina ericina virus]	44.8	183	4.4E-38	167.9	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_743 GeneMark.hmm 106_aa +73586 73906	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_744 GeneMark.hmm 565_aa +73952 75649	YP_008052645	asparagine synthetase B [Phaeocystis globosa virus]	51.5	582	6E-156	560.8	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_745 GeneMark.hmm 172_aa +76009 76527	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_746 GeneMark.hmm 290_aa +76604 77476	YP_009173634	C-terminal catalytic domain of Ulp1 protease [Chrysochromulina ericina virus]	41.8	261	1.1E-51	213.4	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_747 GeneMark.hmm 183_aa +77545 78096	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_748 GeneMark.hmm 40_aa +78165 78287	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_749 GeneMark.hmm 2154_aa +78326 84787	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_750 GeneMark.hmm 216_aa +84852 85502	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_751 GeneMark.hmm 242_aa +85517 86245	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_752 GeneMark.hmm 34_aa +86226 86330	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_753 GeneMark.hmm 96_aa +86473 86763	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_754 GeneMark.hmm 116_aa +86767 87117	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_755 GeneMark.hmm 221_aa +87204 87869	YP_009172951	hypothetical protein OmV1_191c [Ostreococcus mediterraneus virus 1]	34.6	185	6.4E-23	117.5	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_756 GeneMark.hmm 1136_aa +87950 91360	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	44.6	1058	3E-230	808.5	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_757 GeneMark.hmm 329_aa +91410 92399	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	62.2	328	1E-120	443	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_758 GeneMark.hmm 195_aa +92521 93108	XP_007508273	predicted protein [Bathycoccus prasinos]	31.4	188	2.1E-14	89	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_759 GeneMark.hmm 303_aa +93117 94028	YP_009173347	MIGE-like and Zn finger domain containing protein [Chrysochromulina ericina virus]	35.6	309	2.5E-38	169.1	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_760 GeneMark.hmm 1676_aa +94351 99381	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_761 GeneMark.hmm 272_aa +99445 100263	XP_008901906	hypothetical protein PPTG_08907 [Phytophthora parasitica INRA-310]	37.7	252	5.1E-38	167.9	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_762 GeneMark.hmm 602_aa +100312 102120	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_763 GeneMark.hmm 54_aa +102240 102404	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_764 GeneMark.hmm 268_aa +102505 103311	YP_009173624	ERCC4-type nuclease [Chrysochromulina ericina virus]	33.6	253	2.6E-26	129	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_765 GeneMark.hmm 105_aa +103333 103650	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_766 GeneMark.hmm 214_aa +103869 104513	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	41.1	190	4.9E-36	161	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_767 GeneMark.hmm 159_aa +104595 105074	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_768 GeneMark.hmm 171_aa +105093 105608	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_769 GeneMark.hmm 48_aa +105758 105904	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_770 GeneMark.hmm 1248_aa +105957 109703	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	50.2	1289	0	1121.7	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_771 GeneMark.hmm 165_aa +109763 110260	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_772 GeneMark.hmm 368_aa +110459 111565	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_773 GeneMark.hmm 327_aa +111624 112607	YP_009173615	ubiquitin specific peptidase C19 [Chrysochromulina ericina virus]	44	334	8.7E-77	297	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_774 GeneMark.hmm 269_aa +112619 113428	YP_009173614	Link (Hyaluronan-binding) domain containing protein [Chrysochromulina ericina virus]	49.3	217	7.7E-55	223.8	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_775 GeneMark.hmm 31_aa +113409 113504	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_776 GeneMark.hmm 108_aa +113491 113817	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_777 GeneMark.hmm 117_aa +113854 114207	YP_008052573	hypothetical protein PGCG_00255 [Phaeocystis globosa virus]	34.8	115	3.5E-12	80.9	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_778 GeneMark.hmm 156_aa +114255 114725	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_779 GeneMark.hmm 75_aa +114749 114976	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_780 GeneMark.hmm 248_aa +115024 115767	YP_009173609	hypothetical protein ceV_354 [Chrysochromulina ericina virus]	37.3	204	6.9E-34	154.1	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_781 GeneMark.hmm 140_aa +115839 116261	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_782 GeneMark.hmm 191_aa +116304 116879	YP_009173608	hypothetical protein ceV_353 [Chrysochromulina ericina virus]	39.1	192	1E-24	123.2	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_783 GeneMark.hmm 197_aa +116941 117534	YP_008052578	metal-dependent hydrolase [Phaeocystis globosa virus]	59.8	194	9.6E-63	249.6	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_784 GeneMark.hmm 1531_aa +117561 122156	YP_009173600	repeat containing protein [Chrysochromulina ericina virus]	27.2	935	3.2E-65	260.8	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_785 GeneMark.hmm 190_aa +122211 122783	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_786 GeneMark.hmm 491_aa +122780 124255	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_787 GeneMark.hmm 1502_aa +124312 128820	YP_009173653	DNA-directed RNA polymerase II, subunit RpB1 [Chrysochromulina ericina virus]	60.8	1510	0	1832.4	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_788 GeneMark.hmm 68_aa +128951 129157	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_789 GeneMark.hmm 66_aa +129141 129341	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_790 GeneMark.hmm 659_aa +129338 131317	YP_009173654	ATP-dependent Lon protease [Chrysochromulina ericina virus]	63.8	387	1E-142	516.9	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_791 GeneMark.hmm 46_aa +131401 131541	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_792 GeneMark.hmm 253_aa +131576 132337	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_793 GeneMark.hmm 120_aa +132458 132820	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_794 GeneMark.hmm 31_aa +132813 132908	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_795 GeneMark.hmm 206_aa +132981 133601	WP_002767298	SGNH/GDSL hydrolase family protein [Microcystis aeruginosa]	27.8	198	4.4E-10	74.7	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_796 GeneMark.hmm 688_aa +133893 135959	WP_113871497	AAA family ATPase [Arcobacter sp. CECT 9188]	25.9	474	4.4E-22	116.3	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_797 GeneMark.hmm 135_aa +135997 136404	YP_008052610	hypothetical protein PGCG_00292 [Phaeocystis globosa virus]	35.6	135	1.2E-19	105.9	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_798 GeneMark.hmm 241_aa +136426 137151	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_799 GeneMark.hmm 576_aa +137197 138927	YP_008052607	MutS 8-like protein [Phaeocystis globosa virus]	40.2	579	1E-110	410.6	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_800 GeneMark.hmm 302_aa +139049 139957	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_801 GeneMark.hmm 92_aa +139986 140264	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_802 GeneMark.hmm 109_aa +140452 140781	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_803 GeneMark.hmm 397_aa +140894 142087	YP_009173595	hypothetical protein ceV_340 [Chrysochromulina ericina virus]	27.1	321	1.1E-25	127.5	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_804 GeneMark.hmm 239_aa +142200 142919	YP_009173598	SWIB-domain containing protein [Chrysochromulina ericina virus]	69.9	143	8.1E-48	200.3	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_805 GeneMark.hmm 356_aa +143040 144110	YP_008052602	hypothetical protein PGCG_00284 [Phaeocystis globosa virus]	36.6	331	9.9E-50	207.2	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_806 GeneMark.hmm 288_aa +144342 145208	YP_009173648	DUF2738 superfamily protein [Chrysochromulina ericina virus]	42.3	253	8E-50	207.2	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_807 GeneMark.hmm 179_aa +146273 146812	XP_032997879	LOW QUALITY PROTEIN: zinc finger protein RFP-like [Lacerta agilis]	47.5	61	4.4E-06	61.2	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_808 GeneMark.hmm 147_aa +146995 147438	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_809 GeneMark.hmm 58_aa +147450 147626	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_810 GeneMark.hmm 299_aa +147650 148549	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_811 GeneMark.hmm 326_aa +148524 149504	YP_009173646	hypothetical protein ceV_391 [Chrysochromulina ericina virus]	33.6	330	1.5E-44	189.9	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_812 GeneMark.hmm 118_aa +149688 150044	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_813 GeneMark.hmm 80_aa +150113 150355	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_814 GeneMark.hmm 966_aa +150422 153322	YP_009173536	MutS7 [Chrysochromulina ericina virus]	40	1006	7E-194	687.6	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_815 GeneMark.hmm 212_aa +153399 154037	XP_001448653	hypothetical protein (macronuclear) [Paramecium tetraurelia strain d4-2]	30.2	172	1.1E-08	70.1	
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_816 GeneMark.hmm 154_aa +154074 154538	no hit	-	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_817 GeneMark.hmm 185_aa +154535 155092	no hit	-					

MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_819 GeneMark.hmm 150_aa - 157456 157908	YP_009173661	hypothetical protein ceV_406 [Chrysochromulina ericina virus]	32.1	159	3.3E-15	91.3
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_820 GeneMark.hmm 220_aa+ 157981 158643	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_821 GeneMark.hmm 314_aa+ 159278 160222	YP_009173639	hypothetical protein ceV_384 [Chrysochromulina ericina virus]	42.6	303	1.4E-63	253.1
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_822 GeneMark.hmm 528_aa+ 160248 161834	YP_009173640	hypothetical protein ceV_385 [Chrysochromulina ericina virus]	30	220	6.6E-18	102.1
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_823 GeneMark.hmm 134_aa+ 161882 162286	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_824 GeneMark.hmm 275_aa+ 162356 163183	YP_008052612	putative Holliday junction resolvase [Phaeocystis globosa virus]	35.1	285	4.1E-35	158.3
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_825 GeneMark.hmm 515_aa+ 163204 164751	YP_008052616	hypothetical protein PGCG_00298 [Phaeocystis globosa virus]	45.8	553	2E-103	386
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_826 GeneMark.hmm 2533_aa - 164833 172434	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_827 GeneMark.hmm 427_aa - 172482 173765	WP_165778057	DNA adenine methylase [Raineya orbicola]	46.6	324	5.1E-77	298.1
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_828 GeneMark.hmm 73_aa - 173835 174056	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_829 GeneMark.hmm 223_aa - 174171 174842	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_830 GeneMark.hmm 303_aa - 174907 175818	YP_009173650	MIGE-like protein [Chrysochromulina ericina virus]	35.2	318	5.1E-47	198
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_831 GeneMark.hmm 55_aa - 175910 176077	no hit	-	-	-	-	-
MM01_SRX802202_64_dc	Moniruzzaman_MM01_SRX802202_64_dc_000000000002	gene_832 GeneMark.hmm 296_aa - 176077 176967	WP_003632250	hydroxymethylglutaryl-CoA lyase [Legionella longbeachae]	32.2	236	1.7E-23	119.8
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_833 GeneMark.hmm 1517_aa+ 180 4733	YP_009173653	DNA-directed RNA polymerase II, subunit RpB1 [Chrysochromulina ericina virus]	43.2	1499	0	1137.5
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_834 GeneMark.hmm 130_aa - 4735 5127	XP_012473741	PREDICTED: structure-specific endonuclease subunit slx1 isoform X1 [Gossypium raimondii]	46.5	71	2.9E-07	64.7
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_835 GeneMark.hmm 306_aa+ 6089 6089	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_836 GeneMark.hmm 119_aa+ 6094 6453	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_837 GeneMark.hmm 210_aa - 6442 7074	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_838 GeneMark.hmm 209_aa - 7476 8105	YP_008052421	hypothetical protein PGCG_00102 [Phaeocystis globosa virus]	38	121	7.2E-16	94
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_839 GeneMark.hmm 314_aa - 8125 9069	YP_009173464	transcription initiation factor TFIIB [Chrysochromulina ericina virus]	41.9	260	1.8E-47	199.5
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_840 GeneMark.hmm 128_aa+ 9127 9513	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_841 GeneMark.hmm 269_aa+ 9586 10395	WP_073282888	3'-5' exonuclease [Anaerospobacter mobilis]	32.8	229	1.6E-12	83.2
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_842 GeneMark.hmm 143_aa - 10388 10819	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_843 GeneMark.hmm 100_aa - 10837 11139	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_844 GeneMark.hmm 99_aa - 11493 11789	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_845 GeneMark.hmm 1119_aa - 11857 15216	YP_009173327	DNA topoisomerase II [Chrysochromulina ericina virus]	45.3	1129	2E-263	918.7
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_846 GeneMark.hmm 431_aa - 15258 16553	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_847 GeneMark.hmm 105_aa+ 16631 16948	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_848 GeneMark.hmm 121_aa+ 16954 17319	YP_008052516	DNA-directed RNA polymerase II subunit RPB9 [Phaeocystis globosa virus]	32.5	126	9.3E-08	66.2
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_849 GeneMark.hmm 218_aa+ 17386 18042	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_850 GeneMark.hmm 285_aa+ 18103 18960	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_851 GeneMark.hmm 120_aa+ 19011 19373	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_852 GeneMark.hmm 195_aa+ 19472 20056	YP_009507580	major capsid protein [Heterosigma akashiwo virus 01]	50	200	4.2E-42	181
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_853 GeneMark.hmm 168_aa+ 20388 20891	YP_009052173	putative capsid protein [Aureococcus anophagefferens virus]	33.5	245	8.6E-20	106.7
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_854 GeneMark.hmm 240_aa - 21394 22116	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_855 GeneMark.hmm 1668_aa - 22473 27476	no hit	-	-	-	-	-
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_856 GeneMark.hmm 203_aa+ 27519 28130	YP_008052578	metal-dependent hydrolase [Phaeocystis globosa virus]	34.9	189	3.3E-18	101.7
MM05_ERX552270_36_dc	Moniruzzaman_MM05_ERX552270_36_dc_000000000003	gene_857 GeneMark.hmm 1199_aa+ 28218 31817	YP_009052217	putative B family DNA polymerase [Aureococcus anophagefferens virus]	31.2	1367	3E-155	559.7
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_858 GeneMark.hmm 230_aa+ 2 694	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_859 GeneMark.hmm 190_aa+ 691 1263	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_860 GeneMark.hmm 194_aa+ 1459 2043	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_861 GeneMark.hmm 1214_aa+ 12124 5768	YP_009052217	putative B family DNA polymerase [Aureococcus anophagefferens virus]	47.2	1407	0	1187.9
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_862 GeneMark.hmm 477_aa+ 5880 7313	WP_166411343	hypothetical protein [Sphingomonas sp. HDW15B]	50.5	99	6E-18	102.1
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_863 GeneMark.hmm 402_aa+ 7346 8554	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_864 GeneMark.hmm 245_aa+ 8617 9354	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_865 GeneMark.hmm 147_aa+ 9502 9945	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_866 GeneMark.hmm 138_aa+ 10008 10424	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_867 GeneMark.hmm 323_aa+ 10450 11421	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_868 GeneMark.hmm 217_aa+ 11437 12090	YP_009052192	hypothetical protein AaV_116 [Aureococcus anophagefferens virus]	46.6	174	1.5E-40	176
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_869 GeneMark.hmm 76_aa+ 12102 12332	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_870 GeneMark.hmm 274_aa+ 12313 13137	YP_008052558	NUDIX-like hydrolase [Phaeocystis globosa virus]	35.3	249	3.1E-27	132.1
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_871 GeneMark.hmm 1450_aa+ 13236 17588	YP_009173653	DNA-directed RNA polymerase II, subunit RpB1 [Chrysochromulina ericina virus]	40.9	1458	7E-307	1063.5
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_872 GeneMark.hmm 215_aa+ 17647 18294	YP_008052570	extracellular link domain-containing protein [Phaeocystis globosa virus]	41	166	1.7E-28	136
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_873 GeneMark.hmm 238_aa+ 18329 19045	YP_003970126	putative ubiquitin-conjugating enzyme E2 [Cafeteria roenbergensis virus BV-PW1]	42.6	176	2.5E-25	125.6
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_874 GeneMark.hmm 158_aa+ 19094 19570	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_875 GeneMark.hmm 205_aa+ 19612 20229	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_876 GeneMark.hmm 142_aa+ 20232 20660	YP_009174128	hypothetical protein [Yellowstone lake mimivirus]	38.5	122	3.5E-14	87.8
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_877 GeneMark.hmm 252_aa+ 20735 21493	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_878 GeneMark.hmm 459_aa+ 21490 22869	YP_009052194	putative translation elongation factor EF-1 alpha [Aureococcus anophagefferens virus]	68.8	448	6E-190	673.3
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_879 GeneMark.hmm 206_aa+ 22915 23535	WP_118257111	ATP-dependent Clp protease proteolytic subunit [Eubacterium] rectale	35.3	173	4.9E-17	97.8
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_880 GeneMark.hmm 117_aa+ 23589 23942	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_881 GeneMark.hmm 290_aa+ 23961 24833	no hit	-	-	-	-	-
MM09_ERX555978_20_dc	Moniruzzaman_MM09_ERX555978_20_dc_000000000007	gene_882 GeneMark.hmm 228_aa+ 24974 25660	WP_069304799	2,3-diphosphoglycerate-dependent phosphoglycerate mutase [Pelagibacteraceae bacterium]	35.3	232	5.8E-35	157.5
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_883 GeneMark.hmm 115_aa+ 2 346	no hit	-	-	-	-	-
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_884 GeneMark.hmm 206_aa+ 400 1020	WP_118257111	ATP-dependent Clp protease proteolytic subunit [Eubacterium] rectale	35.3	173	4.9E-17	97.8
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_885 GeneMark.hmm 459_aa+ 1066 2445	YP_009052194	putative translation elongation factor EF-1 alpha [Aureococcus anophagefferens virus]	68.8	448	6E-190	673.3
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_886 GeneMark.hmm 252_aa+ 2442 3200	no hit	-	-	-	-	-
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_887 GeneMark.hmm 142_aa+ 3275 3703	YP_009174128	hypothetical protein [Yellowstone lake mimivirus]	38.5	122	3.5E-14	87.8
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_888 GeneMark.hmm 205_aa+ 3706 4323	no hit	-	-	-	-	-
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_889 GeneMark.hmm 158_aa+ 4365 4841	no hit	-	-	-	-	-
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_890 GeneMark.hmm 238_aa+ 4890 5606	YP_003970126	putative ubiquitin-conjugating enzyme E2 [Cafeteria roenbergensis virus BV-PW1]	42.6	176	2.5E-25	125.6
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_891 GeneMark.hmm 215_aa+ 5641 6288	YP_008052570	extracellular link domain-containing protein [Phaeocystis globosa virus]	41	166	1.7E-28	136
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_892 GeneMark.hmm 1450_aa+ 6347 10699	YP_009173653	DNA-directed RNA polymerase II, subunit RpB1 [Chrysochromulina ericina virus]	40.9	1458	7E-307	1063.5
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_893 GeneMark.hmm 274_aa+ 10798 11622	YP_008052558	NUDIX-like hydrolase [Phaeocystis globosa virus]	35.3	249	3.1E-27	132.1
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_894 GeneMark.hmm 76_aa+ 11603 11833	no hit	-	-	-	-	-
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_895 GeneMark.hmm 217_aa+ 11845 12498	YP_009052192	hypothetical protein AaV_116 [Aureococcus anophagefferens virus]	46.6	174	1.5E-40	176
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000							

MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_901 GeneMark.hmm 477_aa - 16622 18055	WP_166411343	hypothetical protein [Sphingomonas sp. HDW15B]	50.5	99	6E-18	102.1
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_902 GeneMark.hmm 1214_aa+ 18167 21811	YP_009052217	putative B family DNA polymerase [Aureococcus anophagefferens virus]	47.1	1407	0	1185.2
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_903 GeneMark.hmm 194_aa+ 21892 22476	no hit	-	-	-	-	-
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_904 GeneMark.hmm 190_aa+ 22672 23244	no hit	-	-	-	-	-
MM09_ERX556015_14_dc	Moniruzzaman_MM09_ERX556015_14_dc_000000000011	gene_905 GeneMark.hmm 200_aa+ 23241 23843	no hit	-	-	-	-	-
MM09_ERX556103_23_dc	Moniruzzaman_MM09_ERX556103_23_dc_000000000006	gene_906 GeneMark.hmm 91_aa+ 343 618	no hit	-	-	-	-	-
MM09_ERX556103_23_dc	Moniruzzaman_MM09_ERX556103_23_dc_000000000006	gene_907 GeneMark.hmm 1562_aa+ 675 5363	YP_009052217	putative B family DNA polymerase [Aureococcus anophagefferens virus]	52.1	1560	0	1479.5
MM09_ERX556103_23_dc	Moniruzzaman_MM09_ERX556103_23_dc_000000000006	gene_908 GeneMark.hmm 474_aa+ 5498 6922	XP_009032625	hypothetical protein AURANDRAFT_60746 [Aureococcus anophagefferens]	27.2	390	1.1E-24	124.4
MM09_ERX556103_23_dc	Moniruzzaman_MM09_ERX556103_23_dc_000000000006	gene_909 GeneMark.hmm 217_aa+ 7000 7653	YP_003970082	putative mitochondrial carrier protein [Cafeteria roenbergensis virus BV-PW1]	39	200	1E-28	136.7
MM09_ERX556103_23_dc	Moniruzzaman_MM09_ERX556103_23_dc_000000000006	gene_910 GeneMark.hmm 61_aa+ 7705 7890	no hit	-	-	-	-	-
MM09_ERX556103_23_dc	Moniruzzaman_MM09_ERX556103_23_dc_000000000006	gene_911 GeneMark.hmm 142_aa+ 7925 8353	XP_018432894	PREDICTED: eukaryotic translation initiation factor 1A-like [Raphanus sativus]	54.9	142	9.8E-33	149.4
MM09_ERX556103_23_dc	Moniruzzaman_MM09_ERX556103_23_dc_000000000006	gene_912 GeneMark.hmm 301_aa+ 8513 9418	no hit	-	-	-	-	-
MM09_ERX556103_23_dc	Moniruzzaman_MM09_ERX556103_23_dc_000000000006	gene_913 GeneMark.hmm 836_aa+ 9457 11967	YP_009052451	putative fucosylgalactoside 3-alpha-galactosyltransferase [Aureococcus anophagefferens v	45.8	827	3E-198	701.8
MM09_ERX556103_23_dc	Moniruzzaman_MM09_ERX556103_23_dc_000000000006	gene_914 GeneMark.hmm 125_aa+ 12057 12434	no hit	-	-	-	-	-
MM09_ERX556103_23_dc	Moniruzzaman_MM09_ERX556103_23_dc_000000000006	gene_915 GeneMark.hmm 38_aa+ 12916 13032	no hit	-	-	-	-	-
MM09_ERX556103_23_dc	Moniruzzaman_MM09_ERX556103_23_dc_000000000006	gene_916 GeneMark.hmm 41_aa+ 13016 13141	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_917 GeneMark.hmm 175_aa+ 2 526	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_918 GeneMark.hmm 187_aa+ 689 1252	YP_009173478	hypothetical protein ceV_223 [Chrysochromulina ericina virus]	45	120	2.5E-20	108.6
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_919 GeneMark.hmm 273_aa+ 1293 2114	YP_009173374	replication factor C small subunit [Chrysochromulina ericina virus]	51.7	263	7.6E-58	233.8
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_920 GeneMark.hmm 333_aa+ 2119 3120	YP_009174071	hypothetical protein [Yellowstone lake mimivirus]	69.9	289	1.6E-78	302.8
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_921 GeneMark.hmm 88_aa+ 3176 3442	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_922 GeneMark.hmm 635_aa+ 3504 5411	YP_008052712	NAD-dependent DNA ligase [Phaeocystis globosa virus]	47.4	643	5E-155	557.8
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_923 GeneMark.hmm 46_aa+ 5412 5552	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_924 GeneMark.hmm 578_aa+ 5626 7362	YP_009173379	putative phosphotransferase [Chrysochromulina ericina virus]	46.5	550	1E-96	364
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_925 GeneMark.hmm 278_aa+ 7499 8335	YP_009173380	putative VV A32-like packaging ATPase [Chrysochromulina ericina virus]	77	278	2E-129	471.9
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_926 GeneMark.hmm 443_aa+ 8379 9710	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_927 GeneMark.hmm 285_aa+ 9754 10611	YP_009173458	hypothetical protein ceV_203 [Chrysochromulina ericina virus]	47.6	267	3.4E-69	271.6
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_928 GeneMark.hmm 83_aa+ 10709 10960	YP_009174055	hypothetical protein [Yellowstone lake mimivirus]	67.1	79	8E-19	102.4
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_929 GeneMark.hmm 83_aa+ 11052 11303	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_930 GeneMark.hmm 199_aa+ 11300 11899	YP_009173607	hypothetical protein ceV_352 [Chrysochromulina ericina virus]	59.8	194	8.5E-59	236.5
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_931 GeneMark.hmm 139_aa+ 11979 12398	YP_009173608	hypothetical protein ceV_353 [Chrysochromulina ericina virus]	40	110	3.5E-11	77.8
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_932 GeneMark.hmm 399_aa+ 12553 13752	YP_009173609	hypothetical protein ceV_354 [Chrysochromulina ericina virus]	39.7	398	4.2E-33	152.1
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_933 GeneMark.hmm 161_aa+ 14107 14592	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_934 GeneMark.hmm 134_aa+ 14640 15044	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_935 GeneMark.hmm 116_aa+ 15066 15416	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_936 GeneMark.hmm 213_aa+ 15413 16054	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_937 GeneMark.hmm 129_aa+ 16057 16446	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_938 GeneMark.hmm 414_aa+ 16498 17742	YP_009173614	Link (Hyaluronan-binding) domain containing protein [Chrysochromulina ericina virus]	42.9	156	1.6E-35	160.2
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_939 GeneMark.hmm 348_aa+ 17761 18807	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	49.7	348	3E-102	381.7
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_940 GeneMark.hmm 333_aa+ 18861 19862	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_941 GeneMark.hmm 1317_aa+ 19926 23879	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	45.8	1309	0	1088.6
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_942 GeneMark.hmm 163_aa+ 23995 24486	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_943 GeneMark.hmm 237_aa+ 24553 25266	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	39.1	207	3.6E-32	148.3
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_944 GeneMark.hmm 292_aa+ 25300 26178	YP_009173624	ERCC4-type nuclease [Chrysochromulina ericina virus]	33.1	275	1.3E-26	130.2
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_945 GeneMark.hmm 83_aa+ 26233 26484	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_946 GeneMark.hmm 202_aa+ 26547 27155	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_947 GeneMark.hmm 300_aa+ 27271 28278	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	62.7	316	6E-116	427.2
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_948 GeneMark.hmm 1200_aa+ 28347 31949	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	42.3	1050	2E-211	746.5
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_949 GeneMark.hmm 504_aa+ 32016 33530	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_950 GeneMark.hmm 89_aa+ 33671 33994	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_951 GeneMark.hmm 118_aa+ 34038 34394	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_952 GeneMark.hmm 164_aa+ 34444 34938	YP_008052395	hypothetical protein PGCG_00076 [Phaeocystis globosa virus]	52.4	164	1.9E-32	148.7
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_953 GeneMark.hmm 268_aa+ 34997 35803	YP_009173324	proliferating cell nuclear antigen [Chrysochromulina ericina virus]	62.2	262	3.9E-91	344.4
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_954 GeneMark.hmm 310_aa+ 35885 36817	WP_074755194	SDR family oxidoreductase [Butyrivibrio fibrisolvens]	63.4	309	2E-112	415.6
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_955 GeneMark.hmm 727_aa+ 36851 39034	WP_038653660	glycosyltransferase family 4 protein [Prochlorococcus sp. MIT 0801]	30.4	405	6.7E-37	165.6
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_956 GeneMark.hmm 341_aa+ 39012 40037	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_957 GeneMark.hmm 300_aa+ 40021 40923	XP_001748117	uncharacterized protein MONBRDRAFT_38123 [Monosiga brevicollis MX1]	31.2	208	6E-16	94.7
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_958 GeneMark.hmm 117_aa+ 40950 41303	YP_009173484	DUF814 domain containing protein [Chrysochromulina ericina virus]	38.7	106	6E-12	80.1
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_959 GeneMark.hmm 170_aa+ 41358 41870	YP_009173322	eukaryotic initiation factor 4E [Chrysochromulina ericina virus]	54.3	151	4E-41	177.6
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_960 GeneMark.hmm 284_aa+ 41925 42779	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_961 GeneMark.hmm 474_aa+ 42969 44393	YP_009173584	hypothetical protein ceV_329 [Chrysochromulina ericina virus]	36	483	7.9E-63	251.1
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_962 GeneMark.hmm 318_aa+ 44407 45363	YP_009173585	hypothetical protein ceV_330 [Chrysochromulina ericina virus]	38.6	308	5.2E-34	154.8
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_963 GeneMark.hmm 169_aa+ 45573 46082	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_964 GeneMark.hmm 243_aa+ 46127 46858	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_965 GeneMark.hmm 209_aa+ 46937 47566	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_966 GeneMark.hmm 345_aa+ 47603 48640	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_967 GeneMark.hmm 321_aa+ 48689 49654	YP_008052564	hypothetical protein PGCG_00246 [Phaeocystis globosa virus]	39.8	284	4.3E-44	188.3
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_968 GeneMark.hmm 233_aa+ 49697 50398	YP_009173569	hypothetical protein ceV_314 [Chrysochromulina ericina virus]	27	222	1.6E-08	69.7
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_969 GeneMark.hmm 395_aa+ 50413 51600	no hit	-	-	-	-	-
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_970 GeneMark.hmm 204_aa+ 51646 52260	YP_009173567	HNH nuclease [Chrysochromulina ericina virus]	49.5	194	3.4E-47	198
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_971 GeneMark.hmm 142_aa+ 52272 52700	YP_009173563	Erv1 / Alr family [Chrysochromulina ericina virus]	52.5	139	7.2E-36	159.8
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_972 GeneMark.hmm 269_aa+ 52792 53601	YP_009173562	Nudix-like hydrolase [Chrysochromulina ericina virus]	56.9	260	2E-79	305.4
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_973 GeneMark.hmm 1403_aa+ 53657 57868	YP_009173561	putative helicase [Chrysochromulina ericina virus]	43.1	1221	2E-256	896
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_974 GeneMark.hmm 170_aa+ 57947 58459	YP_009173560	hypothetical protein ceV_305 [Chrysochromulina ericina virus]	43.7	167	1.1E-33	152.9
GVMAG-M-3300024261-61	GVMAG-M-3300024261-61 Ga0233439_10000491	gene_975 GeneMark						

GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_983 GeneMark.hmm 216_aa -5155 5805	YP_009173469	Erv1 / Alr family [Chrysochromulina ericina virus]	53.3	184	1.3E-52	216.1
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_984 GeneMark.hmm 167_aa +5913 6416	YP_009173468	Protein Disulfide Isomerase (PDIa) [Chrysochromulina ericina virus]	42.2	90	2.1E-10	75.5
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_985 GeneMark.hmm 325_aa -6434 7411	YP_008052436	patatin-like phospholipase [Phaeocystis globosa virus]	31.8	308	5E-40	174.9
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_986 GeneMark.hmm 193_aa +7489 8070	YP_008052435	hypothetical protein PGCG_00116 [Phaeocystis globosa virus]	43.5	191	4E-37	164.5
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_987 GeneMark.hmm 418_aa -8199 9455	YP_008052570	extracellular link domain-containing protein [Phaeocystis globosa virus]	33.6	280	7.3E-36	161.4
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_988 GeneMark.hmm 348_aa -9477 10523	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	49.3	345	2E-102	382.5
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_989 GeneMark.hmm 257_aa +17776 18549	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_990 GeneMark.hmm 1669_aa -12032 17041	YP_009173620	DNA polymerase B [Chrysochromulina ericina virus]	49.8	1682	0	1559.7
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_991 GeneMark.hmm 197_aa -17163 17756	XP_011445708	PREDICTED: protein disulfide-isomerase [Crassostrea gigas]	34	97	4.4E-07	64.7
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_992 GeneMark.hmm 257_aa +17776 18549	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	38.8	206	4.5E-28	134.8
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_993 GeneMark.hmm 141_aa +18609 19034	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_994 GeneMark.hmm 189_aa -19075 19644	XP_005770693	hypothetical protein EMIHURAFT_447996 [Emiliania huxleyi CCMP1516]	38.9	113	3.4E-09	71.6
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_995 GeneMark.hmm 307_aa -19677 20600	YP_009173624	ERCC4-type nuclease [Chrysochromulina ericina virus]	28	307	1.4E-20	110.2
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_996 GeneMark.hmm 83_aa -20691 20942	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_997 GeneMark.hmm 335_aa +21061 22068	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	62.7	316	4E-116	427.6
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_998 GeneMark.hmm 656_aa -22328 24298	YP_008052380	DNA methylase [Phaeocystis globosa virus]	79.6	269	2E-123	453.4
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_999 GeneMark.hmm 331_aa +24698 25693	YP_008052348	hypothetical protein PGCG_00029 [Phaeocystis globosa virus]	30.3	330	3.9E-32	148.7
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1000 GeneMark.hmm 330_aa +25999 26991	YP_008052591	hypothetical protein PGCG_00273 [Phaeocystis globosa virus]	29.2	343	2.1E-30	142.9
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1001 GeneMark.hmm 1193_aa +27056 30637	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	40.9	1032	6E-208	734.6
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1002 GeneMark.hmm 263_aa -30715 31506	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1003 GeneMark.hmm 110_aa -31613 31945	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1004 GeneMark.hmm 268_aa +32241 33047	YP_009173324	proliferating cell nuclear antigen [Chrysochromulina ericina virus]	62.4	263	6E-92	347.1
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1005 GeneMark.hmm 235_aa +33109 33816	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1006 GeneMark.hmm 117_aa -33836 34189	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1007 GeneMark.hmm 41_aa +34275 34400	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1008 GeneMark.hmm 170_aa -34397 34909	YP_009173322	eukaryotic initiation factor 4E [Chrysochromulina ericina virus]	55.2	154	2.1E-42	181.8
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1009 GeneMark.hmm 259_aa -34974 35753	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1010 GeneMark.hmm 129_aa +36151 36540	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1011 GeneMark.hmm 63_aa +36708 36899	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1012 GeneMark.hmm 495_aa -36993 38480	YP_009173584	hypothetical protein ceV_329 [Chrysochromulina ericina virus]	35.1	502	5.4E-62	248.4
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1013 GeneMark.hmm 320_aa -38492 39454	YP_009173585	hypothetical protein ceV_330 [Chrysochromulina ericina virus]	36.7	316	3.3E-36	162.2
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1014 GeneMark.hmm 176_aa -39503 40033	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1015 GeneMark.hmm 263_aa -40098 40889	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1016 GeneMark.hmm 214_aa +40993 41637	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1017 GeneMark.hmm 321_aa +41710 42675	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1018 GeneMark.hmm 85_aa -42629 42886	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1019 GeneMark.hmm 273_aa +42969 43790	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1020 GeneMark.hmm 334_aa -43803 44807	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1021 GeneMark.hmm 325_aa -44829 45806	YP_008052564	hypothetical protein PGCG_00246 [Phaeocystis globosa virus]	37.5	285	3.3E-36	162.2
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1022 GeneMark.hmm 290_aa -45853 46725	no hit	-	-	-	-	-
GVMAG-M-3300024299-4	GVMAG-M-3300024299-4 Ga0233448_1000411	gene_1023 GeneMark.hmm 193_aa -46745 47326	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1024 GeneMark.hmm 174_aa +220 744	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1025 GeneMark.hmm 70_aa -741 953	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1026 GeneMark.hmm 370_aa -993 2105	XP_008869517	hypothetical protein H310_06290 [Aphanomyces invadans]	43.1	348	1.1E-67	266.9
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1027 GeneMark.hmm 576_aa -2143 3873	YP_009173669	ribonuclease II family protein [Chrysochromulina ericina virus]	40.3	583	1E-107	400.2
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1028 GeneMark.hmm 83_aa +3945 4196	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1029 GeneMark.hmm 775_aa +4241 6568	YP_009173643	DNA topoisomerase IA [Chrysochromulina ericina virus]	41.8	779	6E-172	614.4
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1030 GeneMark.hmm 205_aa +6585 7202	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1031 GeneMark.hmm 369_aa +7240 8349	YP_009173646	hypothetical protein ceV_391 [Chrysochromulina ericina virus]	41.5	364	3.3E-56	228.8
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1032 GeneMark.hmm 293_aa +8327 9208	WP_007699490	molecular chaperone DnaJ [Campylobacter jejuni]	43.5	62	3.2E-06	62.4
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1033 GeneMark.hmm 456_aa +9230 10600	WP_087592255	carotenoid oxygenase family protein [unicellular cyanobacterium SU3]	27.2	323	5.9E-15	92
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1034 GeneMark.hmm 239_aa +10622 11341	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1035 GeneMark.hmm 68_aa +11342 11548	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1036 GeneMark.hmm 637_aa +11526 13439	XP_012750470	hypothetical protein SAMD00019534_095490 [Acytostelium subglobosum LB1]	43.8	614	4E-139	505
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1037 GeneMark.hmm 191_aa +13518 14093	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1038 GeneMark.hmm 382_aa -14110 15258	XP_023216006	uridine 5'-monophosphate synthase-like [Centruroides sculpturatus]	31.7	461	4.6E-53	218.4
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1039 GeneMark.hmm 117_aa -15411 15764	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1040 GeneMark.hmm 275_aa +15835 16662	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1041 GeneMark.hmm 212_aa -16652 17290	WP_111371127	hypothetical protein [Arcticibacterium luteifluviastionis]	30.9	162	1.6E-07	66.2
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1042 GeneMark.hmm 324_aa -17402 18376	YP_009173648	DUF2738 superfamily protein [Chrysochromulina ericina virus]	41.9	229	9.3E-47	197.2
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1043 GeneMark.hmm 363_aa +18518 19609	YP_008052602	hypothetical protein PGCG_00284 [Phaeocystis globosa virus]	33.2	364	8.5E-41	177.6
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1044 GeneMark.hmm 201_aa +19698 20303	YP_009173598	SWIB-domain containing protein [Chrysochromulina ericina virus]	58.5	135	1.1E-32	149.8
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1045 GeneMark.hmm 293_aa +20436 21308	WP_075066345	glycosyltransferase family 2 protein [Candidatus Berkiella aquae]	39.4	264	3E-44	188.7
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1046 GeneMark.hmm 329_aa -21300 22289	YP_009173596	PIN domain of flap Endonuclease 1 [Chrysochromulina ericina virus]	40.2	333	1.4E-58	236.5
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1047 GeneMark.hmm 383_aa +22332 23483	YP_009173595	hypothetical protein ceV_340 [Chrysochromulina ericina virus]	29.3	382	7.2E-22	114.8
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1048 GeneMark.hmm 240_aa -23530 24252	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1049 GeneMark.hmm 671_aa -24329 26344	YP_008052605	hypothetical protein PGCG_00287 [Phaeocystis globosa virus]	28.3	707	2.3E-47	200.3
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1050 GeneMark.hmm 291_aa -26391 27266	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1051 GeneMark.hmm 377_aa +27359 28492	YP_009173589	Helicase 45 [Chrysochromulina ericina virus]	53.5	368	1E-108	403.3
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1052 GeneMark.hmm 604_aa +28531 30345	YP_008052607	MutS 8-like protein [Phaeocystis globosa virus]	36.3	601	6E-101	378.3
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1053 GeneMark.hmm 163_aa -30373 30864	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1054 GeneMark.hmm 226_aa +30938 31618	WP_051954494	hypothetical protein [Methylobacter whittenburyi]	35.4	226	3.2E-22	115.2
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1055 GeneMark.hmm 191_aa +31637 32212	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1056 GeneMark.hmm 383_aa -32209 33360	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1057 GeneMark.hmm 180_aa -33832 34374	WP_112896994	DNA/RNA non-specific endonuclease [Photobacter				

GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1065 GeneMark.hmm 290_aa - 39109 39981	YP_009173630	hypothetical protein ceV_375 [Chrysochromulina ericina virus]	33	267	3.1E-25	125.6
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1066 GeneMark.hmm 205_aa - 40019 40636	YP_008052700	deoxyuridine 5'-triphosphate nucleotidohydrolase [Phaeocystis globosa virus]	34.4	209	1.2E-15	93.2
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1067 GeneMark.hmm 166_aa - 40674 41174	YP_009173661	hypothetical protein ceV_406 [Chrysochromulina ericina virus]	38.1	160	5.3E-22	114
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1068 GeneMark.hmm 147_aa - 41262 41705	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1069 GeneMark.hmm 258_aa - 41742 42518	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1070 GeneMark.hmm 81_aa - 42580 42825	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1071 GeneMark.hmm 114_aa - 42907 43251	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1072 GeneMark.hmm 72_aa - 43259 43477	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1073 GeneMark.hmm 158_aa - 43478 43954	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1074 GeneMark.hmm 770_aa - 43986 46298	YP_009173654	ATP-dependent Lon protease [Chrysochromulina ericina virus]	58.4	404	5E-133	485
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1075 GeneMark.hmm 1507_aa - 46403 50926	YP_009173653	DNA-directed RNA polymerase II, subunit RpB1 [Chrysochromulina ericina virus]	58.5	1511	0	1768.8
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1076 GeneMark.hmm 97_aa - 50984 51277	XP_008880703	polyubiquitin [Aphanomyces invadans]	96.1	77	1.3E-33	151.8
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1077 GeneMark.hmm 447_aa - 51305 52648	YP_008052667	protein kinase [Phaeocystis globosa virus]	36.1	432	1.7E-54	223.4
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1078 GeneMark.hmm 1903_aa - 52699 58410	YP_008052580	hypothetical protein PGCG_00262 [Phaeocystis globosa virus]	28.4	1997	2E-141	514.2
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1079 GeneMark.hmm 513_aa - 58457 59998	XP_023344854	probable mitochondrial chaperone BCS1-A [Eurytemora affinis]	36.3	300	1.4E-41	180.6
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1080 GeneMark.hmm 159_aa - 60041 60520	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1081 GeneMark.hmm 199_aa - 60508 61107	YP_009173607	hypothetical protein ceV_352 [Chrysochromulina ericina virus]	63	192	3.7E-62	247.7
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1082 GeneMark.hmm 440_aa - 61151 62473	WP_018589635	insulinase family protein [Terrisporobacter glycolicus]	32.1	402	5.9E-44	188.3
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1083 GeneMark.hmm 157_aa - 62524 62997	YP_009173608	hypothetical protein ceV_353 [Chrysochromulina ericina virus]	53.7	95	8.3E-17	96.7
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1084 GeneMark.hmm 395_aa - 63103 64290	YP_009173609	hypothetical protein ceV_354 [Chrysochromulina ericina virus]	42.6	390	8.7E-31	144.4
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1085 GeneMark.hmm 103_aa - 64276 64587	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1086 GeneMark.hmm 314_aa - 64607 65551	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1087 GeneMark.hmm 68_aa - 65573 65779	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1088 GeneMark.hmm 104_aa - 65787 66101	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1089 GeneMark.hmm 123_aa - 66123 66494	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1090 GeneMark.hmm 166_aa - 66537 67037	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1091 GeneMark.hmm 447_aa - 67198 68541	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1092 GeneMark.hmm 377_aa - 68607 69740	YP_008052432	transcription initiation factor IIB [Phaeocystis globosa virus]	51.6	384	7E-104	387.1
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1093 GeneMark.hmm 61_aa - 69792 69977	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1094 GeneMark.hmm 48_aa - 70019 70165	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1095 GeneMark.hmm 249_aa - 70196 70945	YP_009173496	Beta-4-Galactosyltransferase [Chrysochromulina ericina virus]	47	215	3.4E-49	204.9
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1096 GeneMark.hmm 160_aa - 70938 71420	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1097 GeneMark.hmm 97_aa - 71493 71786	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1098 GeneMark.hmm 268_aa - 71817 72623	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1099 GeneMark.hmm 267_aa - 72620 73423	YP_009173556	FtsJ-like methyltransferase [Chrysochromulina ericina virus]	47.2	246	2.3E-59	238.8
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1100 GeneMark.hmm 115_aa - 73478 73825	YP_009173556	FtsJ-like methyltransferase [Chrysochromulina ericina virus]	53	115	4.3E-23	117.1
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1101 GeneMark.hmm 1146_aa - 73877 73717	YP_008052553	mRNA capping enzyme [Phaeocystis globosa virus]	44.7	1086	1E-262	916.4
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1102 GeneMark.hmm 262_aa - 77367 78155	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1103 GeneMark.hmm 107_aa - 78139 78462	YP_008052555	hypothetical protein PGCG_00237 [Phaeocystis globosa virus]	37.6	85	2.6E-06	61.2
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1104 GeneMark.hmm 86_aa - 78512 78772	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1105 GeneMark.hmm 183_aa - 78774 79325	YP_009173560	hypothetical protein ceV_305 [Chrysochromulina ericina virus]	45.1	182	3E-34	154.8
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1106 GeneMark.hmm 1588_aa - 79387 84153	YP_009173561	putative helicase [Chrysochromulina ericina virus]	40.5	1256	2E-237	832.8
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1107 GeneMark.hmm 269_aa - 84189 84998	YP_009173562	Nudix-like hydrolase [Chrysochromulina ericina virus]	53.2	263	5.1E-75	290.8
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1108 GeneMark.hmm 142_aa - 85054 85482	YP_009173563	Erv1 / Alr family [Chrysochromulina ericina virus]	59.3	108	2.3E-34	154.8
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1109 GeneMark.hmm 196_aa - 85505 86095	YP_009173567	HNH nuclease [Chrysochromulina ericina virus]	50.5	192	9.9E-44	186.4
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1110 GeneMark.hmm 401_aa - 86126 87331	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1111 GeneMark.hmm 232_aa - 87352 88050	YP_009173569	hypothetical protein ceV_314 [Chrysochromulina ericina virus]	29	245	3.8E-10	75.1
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1112 GeneMark.hmm 313_aa - 88087 89028	YP_008052564	hypothetical protein PGCG_00246 [Phaeocystis globosa virus]	34	291	3.5E-35	158.7
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1113 GeneMark.hmm 467_aa - 89056 90459	WP_155505370	hypothetical protein [K189A clade bacterium]	40	115	3.1E-11	79.7
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1114 GeneMark.hmm 308_aa - 90456 91382	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1115 GeneMark.hmm 205_aa - 91423 92040	YP_009173572	hypothetical protein ceV_317 [Chrysochromulina ericina virus]	45.6	57	2.7E-07	65.5
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1116 GeneMark.hmm 262_aa - 92156 92944	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1117 GeneMark.hmm 172_aa - 92996 93514	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1118 GeneMark.hmm 294_aa - 93565 94449	YP_009173585	hypothetical protein ceV_330 [Chrysochromulina ericina virus]	40.5	289	9.7E-43	183.7
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1119 GeneMark.hmm 460_aa - 94461 95843	YP_008052616	hypothetical protein PGCG_00298 [Phaeocystis globosa virus]	35.5	502	7.7E-63	251.1
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1120 GeneMark.hmm 207_aa - 95889 96512	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1121 GeneMark.hmm 96_aa - 96555 96845	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1122 GeneMark.hmm 365_aa - 96879 97976	XP_005855718	rieske (2fe-2s) domain protein [Nannochloropsis gaditana CCMP526]	33.6	333	5E-41	178.3
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1123 GeneMark.hmm 676_aa - 98079 100109	YP_008052571	ATP-dependent zinc metalloprotease [Phaeocystis globosa virus]	51.9	509	2E-132	482.6
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1124 GeneMark.hmm 156_aa - 100157 100627	XP_002140586	MORN repeat domain-containing protein [Cryptosporidium muris RN66]	32	200	7.2E-21	110.2
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1125 GeneMark.hmm 170_aa - 100630 101142	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1126 GeneMark.hmm 115_aa - 101108 101455	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1127 GeneMark.hmm 115_aa - 101527 101874	WP_0020729301	iron-sulfur cluster insertion protein ErpA [Mesorhizobium loti]	41	105	4.8E-14	87
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1128 GeneMark.hmm 92_aa - 101876 102154	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1129 GeneMark.hmm 298_aa - 102195 103091	NP_048517	ate transcarbamylase [Paramecium bursaria Chlorella virus 1]	43.9	301	4.5E-56	228
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1130 GeneMark.hmm 87_aa - 103141 103404	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1131 GeneMark.hmm 133_aa - 103481 103882	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1132 GeneMark.hmm 308_aa - 103974 104900	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1133 GeneMark.hmm 253_aa - 104890 105651	XP_033655684	proliferating cell nuclear antigen [Westerdykella ornata]	29.7	256	5.2E-21	111.3
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1134 GeneMark.hmm 330_aa - 105847 106839	WP_088400110	hypothetical protein [Flavobacterium columnare]	41.7	300	1.8E-53	219.5
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1135 GeneMark.hmm 421_aa - 106912 108177	YP_008052395	hypothetical protein PGCG_00076 [Phaeocystis globosa virus]	55.6	153	2.4E-31	146.4
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1136 GeneMark.hmm 42_aa - 108177 108305	no hit	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1137 GeneMark.hmm 454_aa - 108313 109677	WP_151966966	deoxyribodipyrimidine photo-lyase [Planctomycetes bacterium SRT547]	44	457	5E-100	374.8
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1138 GeneMark.hmm 449_aa - 109716 111065	XP_024402118	uncharacterized protein LOC112295134 [Physcomitrella patens]	21.8	455</		

GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1147 GeneMark.hmm 110_aa + 115756 116088	no hit	-	-	-	-	-	-
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1148 GeneMark.hmm 1192_aa + 116117 119695	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	40.9	1048	3E-202	715.7	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1149 GeneMark.hmm 281_aa + 119786 120631	XP_001699203	hypothetical protein CHLREDRAFT_206136 [Chlamydomonas reinhardtii]	28	336	5.5E-19	104.8	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1150 GeneMark.hmm 78_aa + 120807 121043	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1151 GeneMark.hmm 164_aa + 121215 121709	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1152 GeneMark.hmm 335_aa + 121712 122719	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	60.8	316	1E-112	416.4	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1153 GeneMark.hmm 78_aa + 122800 123036	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1154 GeneMark.hmm 268_aa + 123084 123890	YP_009173624	ERCC4-type nuclease [Chrysochromulina ericina virus]	34.7	268	2.1E-28	136	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1155 GeneMark.hmm 215_aa + 123905 124552	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1156 GeneMark.hmm 109_aa + 124549 124878	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1157 GeneMark.hmm 76_aa + 124973 125203	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1158 GeneMark.hmm 301_aa + 125251 126156	XP_001015761	oxidoreductase (short-chain dehydrogenase family) [Tetrahymena thermophila SB210]	44	282	9.5E-54	220.3	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1159 GeneMark.hmm 57_aa + 126232 126405	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1160 GeneMark.hmm 234_aa + 126428 127132	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	37.6	205	3.4E-30	141.7	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1161 GeneMark.hmm 159_aa + 127190 127669	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1162 GeneMark.hmm 1318_aa + 127763 131719	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	46.5	1324	0	1084.7	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1163 GeneMark.hmm 558_aa + 131743 133419	XP_009042027	hypothetical protein AURANDRAFT_60367 [Aureococcus anophagefferens]	33.8	527	2E-73	286.6	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1164 GeneMark.hmm 449_aa + 133446 134795	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1165 GeneMark.hmm 351_aa + 134841 135896	YP_009173615	ubiquitin specific peptidase C19 [Chrysochromulina ericina virus]	46.9	350	4.9E-86	327.8	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1166 GeneMark.hmm 411_aa + 135909 137144	YP_009173614	Link (Hyaluronan-binding) domain containing protein [Chrysochromulina ericina virus]	43.8	169	4.4E-33	152.1	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1167 GeneMark.hmm 192_aa + 137169 137747	YP_008052435	hypothetical protein PGCG_00116 [Phaeocystis globosa virus]	38.9	185	2.3E-29	138.7	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1168 GeneMark.hmm 300_aa + 137798 138700	YP_009173467	patatin-like phospholipase [Chrysochromulina ericina virus]	36.8	280	3.2E-41	178.7	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1169 GeneMark.hmm 158_aa + 138665 139141	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1170 GeneMark.hmm 198_aa + 139211 139807	YP_008052438	Erv family thiol oxidoreductase [Phaeocystis globosa virus]	51.3	193	2.7E-49	204.9	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1171 GeneMark.hmm 262_aa + 139862 140650	YP_009173366	hypothetical protein ceV_111 [Chrysochromulina ericina virus]	39.1	230	2.3E-35	159.1	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1172 GeneMark.hmm 192_aa + 140748 141326	YP_009174082	hypothetical protein [Yellowstone lake mimivirus]	42.9	177	5.2E-29	137.5	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1173 GeneMark.hmm 215_aa + 141369 142016	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1174 GeneMark.hmm 157_aa + 142007 142480	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1175 GeneMark.hmm 119_aa + 142514 142873	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1176 GeneMark.hmm 119_aa + 142833 143192	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1177 GeneMark.hmm 1421_aa + 143271 147536	no hit	-	-	-	-	-	
GVMAG-M-3300024314-16	GVMAG-M-3300024314-16 Ga0228657_1000014	gene_1178 GeneMark.hmm 580_aa + 147606 149348	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1179 GeneMark.hmm 343_aa + 111032	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1180 GeneMark.hmm 237_aa + 1093 1806	YP_008052461	deoxynucleoside kinase [Phaeocystis globosa virus]	40	245	4E-39	171.4	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1181 GeneMark.hmm 522_aa + 1816 3384	YP_008052723	DNA methyltransferase [Phaeocystis globosa virus]	28.2	447	7E-36	161.8	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1182 GeneMark.hmm 148_aa + 3493 3939	WP_091431419	glycine cleavage system protein GcvH [Aliiroseovarius sediminilitoris]	34.3	137	1.1E-10	76.3	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1183 GeneMark.hmm 273_aa + 4040 4861	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1184 GeneMark.hmm 58_aa + 4902 5078	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1185 GeneMark.hmm 191_aa + 5083 5658	YP_008052421	hypothetical protein PGCG_00102 [Phaeocystis globosa virus]	57	128	1.4E-37	166	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1186 GeneMark.hmm 238_aa + 5694 6410	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1187 GeneMark.hmm 335_aa + 6482 7489	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1188 GeneMark.hmm 158_aa + 7582 8058	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1189 GeneMark.hmm 226_aa + 8061 8741	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1190 GeneMark.hmm 174_aa + 8786 9310	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1191 GeneMark.hmm 95_aa + 9330 9617	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1192 GeneMark.hmm 169_aa + 9643 10152	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1193 GeneMark.hmm 324_aa + 10220 11194	YP_009173500	ribonucleoside-diphosphate reductase small subunit [Chrysochromulina ericina virus]	73.4	323	2E-133	485	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1194 GeneMark.hmm 73_aa + 11233 11454	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1195 GeneMark.hmm 260_aa + 11543 12325	YP_009173496	Beta-4-Galactosyltransferase [Chrysochromulina ericina virus]	39.3	239	5.7E-39	171	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1196 GeneMark.hmm 352_aa + 12361 13419	YP_009173464	transcription initiation factor TFIIB [Chrysochromulina ericina virus]	62.5	349	6E-130	473.8	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1197 GeneMark.hmm 416_aa + 13486 14736	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1198 GeneMark.hmm 192_aa + 14778 15356	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1199 GeneMark.hmm 579_aa + 15558 17297	WP_158520294	hypothetical protein, partial [Prochlorococcus sp. HOT208_60m_813B04]	34.2	161	2.4E-13	87	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1200 GeneMark.hmm 196_aa + 17431 18021	YP_009173466	hypothetical protein ceV_211 [Chrysochromulina ericina virus]	48.7	195	2.4E-42	181.8	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1201 GeneMark.hmm 291_aa + 18073 18948	YP_008052436	patatin-like phospholipase [Phaeocystis globosa virus]	31.8	314	9.6E-43	183.7	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1202 GeneMark.hmm 156_aa + 18932 19402	YP_008052437	disulfide isomerase [Phaeocystis globosa virus]	32.1	156	2.3E-11	78.6	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1203 GeneMark.hmm 56_aa + 19483 19653	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1204 GeneMark.hmm 198_aa + 19692 20288	YP_009173469	Erv / Alr family [Chrysochromulina ericina virus]	59.4	187	8.8E-56	226.5	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1205 GeneMark.hmm 214_aa + 20319 20963	YP_008052442	exonuclease [Phaeocystis globosa virus]	38.4	219	1.2E-31	146.4	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1206 GeneMark.hmm 80_aa + 21028 21270	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1207 GeneMark.hmm 240_aa + 21337 22059	YP_009173471	ribonuclease HIII [Chrysochromulina ericina virus]	53.8	212	1.7E-58	235.7	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1208 GeneMark.hmm 297_aa + 22141 23034	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1209 GeneMark.hmm 347_aa + 23130 24173	XP_017229326	PREDICTED: glutamine synthetase cytosolic isozyme [Daucus carota subsp. sativus]	52.3	342	1E-99	373.2	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1210 GeneMark.hmm 175_aa + 24204 24731	YP_009173605	hypothetical protein ceV_350 [Chrysochromulina ericina virus]	30.9	181	1.4E-09	72.8	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1211 GeneMark.hmm 76_aa + 24916 25146	YP_003969713	hypothetical protein crov081 [Cafeteria roenbergensis virus BV-PW1]	57.1	70	1.7E-12	81.3	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1212 GeneMark.hmm 475_aa + 25228 26655	WP_090257731	ribonuclease R [Fabibacter pacificus]	24.4	373	7.6E-13	85.1	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1213 GeneMark.hmm 351_aa + 26696 27751	XP_015772703	PREDICTED: uncharacterized protein LOC107350951 [Acropora digitifera]	50.9	175	3E-51	212.2	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1214 GeneMark.hmm 128_aa + 27795 28181	YP_009173385	DUF2177 domain containing protein [Chrysochromulina ericina virus]	37.9	116	9.1E-14	86.3	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1215 GeneMark.hmm 242_aa + 28188 28916	YP_007877796	hypothetical protein CPRG_00032 [Cyanophage Syn30]	36.7	166	2.3E-21	112.5	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1216 GeneMark.hmm 332_aa + 28924 29922	YP_009173650	MIGE-like protein [Chrysochromulina ericina virus]	34.2	342	2E-44	189.5	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1217 GeneMark.hmm 107_aa + 30023 30346	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1218 GeneMark.hmm 238_aa + 30309 31025	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1219 GeneMark.hmm 373_aa + 31075 32196	WP_052107465	BspA family leucine-rich repeat surface protein [Polaribacter sp. Hel1_33_49]	50.3	147	1.6E-29	140.2	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1220 GeneMark.hmm 343_aa + 32295 33326	WP_147102193	GDP-mannose 4,6-dehydratase [Vicingus serpentes]	58.6	350	9E-115	423.3	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1221 GeneMark.hmm 610_aa + 33384 35216	no hit	-	-	-	-	-	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1222 GeneMark.hmm 308_aa + 35324 36250	XP_014156933	cathepsin X [Sphaeroforma arctica JP610]	56.1	278	5.3E-92	347.4	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1223 GeneMark.hmm 80_aa + 36280 36522	NP_149711	Invertebrate iridescent virus 6]	50	80	9.4E-09	68.9	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1224 GeneMark.hmm 158_aa + 36638 37114	WP_160629538	dUTP diphosphatase [Kiritimatiaellaeota bacterium S-5007]	47.5	158	6.2E-28	133.7	
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1225 GeneMark.hmm 109_aa + 37192 37521	no hit	-	-	-	-		

GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1229 GeneMark.hmm 230_aa - 39827 40519	WP_146422880	MULTISPECIES: CYTH domain-containing protein [Candidatus Saccharibacteria]	34.9	169	5.5E-17	97.8
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1230 GeneMark.hmm 201_aa - 40556 41161	YP_009173560	hypothetical protein ceV_305 [Chrysochromulina ericina virus]	40.7	177	2.3E-27	132.1
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1231 GeneMark.hmm 1204_aa - 41208 44822	YP_009173561	putative helicase [Chrysochromulina ericina virus]	34.3	1270	7E-180	641.3
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1232 GeneMark.hmm 259_aa - 44832 45611	YP_009173562	Nudix-like hydrolase [Chrysochromulina ericina virus]	50	262	8.5E-67	263.5
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1233 GeneMark.hmm 139_aa+ 45653 46072	YP_009173563	Erv1 / Alr family [Chrysochromulina ericina virus]	46.2	143	1.7E-29	138.7
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1234 GeneMark.hmm 488_aa+ 46093 47559	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1235 GeneMark.hmm 192_aa+ 47577 48155	YP_009173567	HNH nuclease [Chrysochromulina ericina virus]	49	192	3.6E-46	194.5
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1236 GeneMark.hmm 406_aa+ 48160 49380	YP_009173568	hypothetical protein ceV_313 [Chrysochromulina ericina virus]	25.7	249	4E-15	92.4
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1237 GeneMark.hmm 233_aa+ 49408 50109	YP_009173569	hypothetical protein ceV_314 [Chrysochromulina ericina virus]	37.9	214	4.1E-36	161.4
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1238 GeneMark.hmm 281_aa+ 50137 50982	YP_009173570	hypothetical protein ceV_315 [Chrysochromulina ericina virus]	40.3	283	1.5E-48	203
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1239 GeneMark.hmm 69_aa+ 51019 51228	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1240 GeneMark.hmm 142_aa+ 51282 51710	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1241 GeneMark.hmm 132_aa+ 51716 52114	YP_009173679	Cold-Shock Protein [Chrysochromulina ericina virus]	42.3	123	7E-17	96.7
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1242 GeneMark.hmm 194_aa+ 52153 52737	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1243 GeneMark.hmm 327_aa+ 52806 53789	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1244 GeneMark.hmm 255_aa+ 53844 54611	XP_002182261	proliferating cell nuclear antigen [Phaeodactylum tricornutum CCAP 1055/1]	30	247	7.4E-23	117.5
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1245 GeneMark.hmm 281_aa+ 54731 55576	YP_008052657	hypothetical protein PGCG_00339 [Phaeocystis globosa virus]	28.1	281	5.6E-24	121.3
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1246 GeneMark.hmm 567_aa+ 55639 57342	YP_009173669	ribonuclease II family protein [Chrysochromulina ericina virus]	40.3	571	2E-119	439.5
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1247 GeneMark.hmm 82_aa+ 57343 57591	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1248 GeneMark.hmm 140_aa+ 57686 58108	YP_008052527	hypothetical protein PGCG_00209 [Phaeocystis globosa virus]	44	100	1.8E-18	102.1
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1249 GeneMark.hmm 145_aa+ 58136 58573	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1250 GeneMark.hmm 826_aa+ 58647 61127	YP_009173671	DEAD-like RNA helicase, superfamily II [Chrysochromulina ericina virus]	40.3	866	7E-163	584.3
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1251 GeneMark.hmm 271_aa+ 61194 61907	YP_008052654	hypothetical protein PGCG_00336 [Phaeocystis globosa virus]	43	149	6.9E-23	117.5
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1252 GeneMark.hmm 271_aa+ 61948 62763	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1253 GeneMark.hmm 84_aa+ 62825 63079	XP_024573332	ubiquitin-60s ribosomal protein I40 [Plasmodium falciparum]	92.4	79	3.4E-33	150.2
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1254 GeneMark.hmm 277_aa+ 63143 63976	YP_009174299	hypothetical protein [Yellowstone lake phycodnavirus 3]	40.1	192	1.2E-29	140.2
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1255 GeneMark.hmm 41_aa+ 64034 64159	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1256 GeneMark.hmm 111_aa+ 64128 64463	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1257 GeneMark.hmm 45_aa+ 64462 64599	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1258 GeneMark.hmm 449_aa+ 64608 65957	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1259 GeneMark.hmm 230_aa+ 66093 66785	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1260 GeneMark.hmm 414_aa+ 66875 68119	WP_108839329	Hint domain-containing protein [Tateyamaria sp. Alg231-49]	30.4	148	5.4E-07	65.5
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1261 GeneMark.hmm 140_aa+ 68193 68615	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1262 GeneMark.hmm 129_aa+ 68680 69069	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1263 GeneMark.hmm 77_aa+ 69169 69402	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1264 GeneMark.hmm 1084_aa+ 69394 72648	YP_009173744	DNA polymerase X/NAD-dependent DNA ligase fusion protein [Chrysochromulina ericina vi	48.5	1085	8E-241	843.6
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1265 GeneMark.hmm 118_aa+ 72676 73032	YP_008052648	hypothetical protein PGCG_00330 [Phaeocystis globosa virus]	42.9	84	4.8E-09	70.5
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1266 GeneMark.hmm 235_aa+ 73096 73803	YP_009173630	hypothetical protein ceV_375 [Chrysochromulina ericina virus]	44.8	183	4.4E-38	167.9
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1267 GeneMark.hmm 106_aa+ 73748 74068	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1268 GeneMark.hmm 565_aa+ 74114 75811	YP_008052645	asparagine synthetase B [Phaeocystis globosa virus]	51.5	582	6E-156	560.8
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1269 GeneMark.hmm 172_aa+ 76171 76689	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1270 GeneMark.hmm 290_aa+ 76766 77638	YP_009173634	C-terminal catalytic domain of Ulp1 protease [Chrysochromulina ericina virus]	41.8	261	1.1E-51	213.4
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1271 GeneMark.hmm 183_aa+ 77707 78258	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1272 GeneMark.hmm 40_aa+ 78327 78449	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1273 GeneMark.hmm 2407_aa+ 78488 85711	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1274 GeneMark.hmm 242_aa+ 85726 86454	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1275 GeneMark.hmm 34_aa+ 86435 86539	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1276 GeneMark.hmm 96_aa+ 86682 86972	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1277 GeneMark.hmm 116_aa+ 86976 87326	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1278 GeneMark.hmm 221_aa+ 87413 88078	YP_009172951	hypothetical protein OmV1_191c [Ostreococcus mediterraneus virus 1]	34.6	185	6.4E-23	117.5
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1279 GeneMark.hmm 1136_aa+ 88159 91569	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	44.6	1058	3E-230	808.5
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1280 GeneMark.hmm 329_aa+ 91619 92608	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	62.2	328	1E-120	443
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1281 GeneMark.hmm 195_aa+ 92730 93317	XP_007508273	predicted protein [Bathycoccus prasinos]	31.4	188	2.1E-14	89
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1282 GeneMark.hmm 303_aa+ 93326 94237	YP_009173347	MIGE-like and Zn finger domain containing protein [Chrysochromulina ericina virus]	35.6	309	2.5E-38	169.1
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1283 GeneMark.hmm 1676_aa+ 94560 99590	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1284 GeneMark.hmm 272_aa+ 99654 100472	XP_008901906	hypothetical protein PPTG_08907 [Phytophthora parasitica INRA-310]	37.7	252	5.1E-38	167.9
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1285 GeneMark.hmm 602_aa+ 100521 102329	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1286 GeneMark.hmm 54_aa+ 102449 102613	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1287 GeneMark.hmm 268_aa+ 102714 103520	YP_009173624	ERCC4-type nuclease [Chrysochromulina ericina virus]	33.6	253	2.6E-26	129
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1288 GeneMark.hmm 105_aa+ 103542 103859	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1289 GeneMark.hmm 214_aa+ 104078 104722	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	41.1	190	4.9E-36	161
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1290 GeneMark.hmm 159_aa+ 104804 105283	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1291 GeneMark.hmm 171_aa+ 105302 105817	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1292 GeneMark.hmm 48_aa+ 105967 106113	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1293 GeneMark.hmm 1248_aa+ 106166 109912	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	50.2	1289	0	1121.7
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1294 GeneMark.hmm 165_aa+ 109972 110469	no hit	-	-	-	-	-
GVMAG-S-1016713-123	GVMAG-S-1016713-123 1016713_contig_39	gene_1295 GeneMark.hmm 36_aa+ 110543 110650	no hit	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1296 GeneMark.hmm 29_aa+ 2 91	no hit	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1297 GeneMark.hmm 203_aa+ 221 832	no hit	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1298 GeneMark.hmm 190_aa+ 975 1547	no hit	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1299 GeneMark.hmm 80_aa+ 2900 3142	no hit	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1300 GeneMark.hmm 501_aa+ 3291 4796	no hit	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1301 GeneMark.hmm 135_aa+ 4971 5378	no hit	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1302 GeneMark.hmm 92_aa+ 5863 6141	no hit	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1303 GeneMark.hmm 197_aa+ 6167 6760	no hit	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1304 GeneMark.hmm 69_aa+ 6846 7055	no hit	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1305 GeneMark.hmm 204_aa+ 7102 7716	WP_034422991	ribonuclease HII [Candidatus Entotheonella palauensis]	56	182	1.8E-43	185.7
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1306 GeneMark.hmm 350_aa+ 7708 8760	no hit	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1307 GeneMark.hmm 262_aa+ 9235 10023	no hit	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1308 GeneMark.hmm 69_aa+ 10181 10390	no hit	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-101							

GVMAGs (high and medium qualities)

GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1311 GeneMark.hmm 143_aa + 12067 12498	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1312 GeneMark.hmm 364_aa - 15767 16861	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1313 GeneMark.hmm 106_aa - 17626 17946	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1314 GeneMark.hmm 227_aa + 18637 19320	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1315 GeneMark.hmm 630_aa - 19948 21840	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1316 GeneMark.hmm 297_aa + 22533 23426	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1317 GeneMark.hmm 183_aa + 23574 24125	XP_014507782	DNA-directed RNA polymerases II and IV subunit 5A [Vigna radiata var. radiata]	32.8	195	9E-15	90.1	
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1318 GeneMark.hmm 483_aa + 24176 25627	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1319 GeneMark.hmm 169_aa - 25683 26192	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1320 GeneMark.hmm 133_aa + 26790 27191	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1321 GeneMark.hmm 148_aa - 27553 27999	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1322 GeneMark.hmm 145_aa - 29508 29945	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1323 GeneMark.hmm 386_aa - 30076 31236	YP_294161	etical protein EhV403 [Emiliania huxleyi virus 86]	40	220	2.5E-38	169.5	
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1324 GeneMark.hmm 232_aa + 31338 32036	WP_067861258	ATP-dependent Clp protease proteolytic subunit [Nocardia shimofusensis]	29.6	169	9.1E-12	80.5	
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1325 GeneMark.hmm 331_aa - 32276 33271	WP_123131756	ribonucleotide-diphosphate reductase subunit beta [Rubifacter immobilis]	55.4	316	6.7E-93	350.5	
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1326 GeneMark.hmm 226_aa + 33579 34259	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1327 GeneMark.hmm 178_aa - 34288 34824	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1328 GeneMark.hmm 105_aa - 35625 35942	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1329 GeneMark.hmm 223_aa - 35917 36588	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1330 GeneMark.hmm 237_aa - 36648 37361	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1331 GeneMark.hmm 182_aa - 37457 38005	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1332 GeneMark.hmm 360_aa - 38085 39167	YP_293900	etical protein EhV147 [Emiliania huxleyi virus 86]	35.4	144	2.2E-12	83.2	
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1333 GeneMark.hmm 121_aa + 39166 39531	no hit	-	-	-	-	-	-
GVMAG-S-1016713-165	GVMAG-S-1016713-165 1016713_contig_440	gene_1334 GeneMark.hmm 58_aa - 39957 40133	no hit	-	-	-	-	-	-
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1335 GeneMark.hmm 495_aa + 83 1570	no hit	-	-	-	-	-	-
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1336 GeneMark.hmm 1989_aa - 1630 7599	YP_009173600	repeat containing protein [Chrysochromulina ericina virus]	40.2	1953	6E-280	974.5	
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1337 GeneMark.hmm 220_aa + 7640 8302	YP_009173602	Dihydrofolate reductase [Chrysochromulina ericina virus]	46.5	142	5.9E-29	137.5	
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1338 GeneMark.hmm 199_aa - 8328 8927	YP_008052578	metal-dependent hydrolase [Phaeocystis globosa virus]	56.7	194	2E-60	241.9	
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1339 GeneMark.hmm 189_aa - 8971 9540	YP_009173608	hypothetical protein ceV_353 [Chrysochromulina ericina virus]	54.1	122	1.3E-27	132.9	
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1340 GeneMark.hmm 427_aa - 9627 10910	YP_009173609	hypothetical protein ceV_354 [Chrysochromulina ericina virus]	48.4	399	3.3E-44	189.1	
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1341 GeneMark.hmm 76_aa + 10986 11216	no hit	-	-	-	-	-	-
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1342 GeneMark.hmm 152_aa + 11229 11687	no hit	-	-	-	-	-	-
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1343 GeneMark.hmm 132_aa + 11762 12160	no hit	-	-	-	-	-	-
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1344 GeneMark.hmm 520_aa + 12220 13782	XP_018136077	ankyrin repeat-containing protein [Pochonia chlamyosporia 170]	50	116	1.2E-19	107.8	
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1345 GeneMark.hmm 1248_aa + 13917 17663	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	50.9	1274	0	1191.4	
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1346 GeneMark.hmm 93_aa - 17721 18002	no hit	-	-	-	-	-	-
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1347 GeneMark.hmm 358_aa - 18042 19118	no hit	-	-	-	-	-	-
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1348 GeneMark.hmm 346_aa + 19192 20232	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	50	342	5.2E-96	360.9	
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1349 GeneMark.hmm 287_aa + 20249 21112	YP_009173614	Link (Hyaluronan-binding) domain containing protein [Chrysochromulina ericina virus]	52.2	205	4.5E-61	244.6	
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1350 GeneMark.hmm 90_aa - 21084 21356	no hit	-	-	-	-	-	-
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1351 GeneMark.hmm 127_aa - 21394 21777	no hit	-	-	-	-	-	-
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1352 GeneMark.hmm 115_aa - 21792 22139	YP_008052573	hypothetical protein PGCG_00255 [Phaeocystis globosa virus]	40.9	110	8.2E-14	86.3	
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1353 GeneMark.hmm 404_aa - 22180 23394	XP_022904221	thioredoxin domain-containing protein 5 homolog [Onthophagus taurus]	30.1	103	8.1E-08	68.2	
GVMAG-S-1096102-67	GVMAG-S-1096102-67 1096102_contig_1086	gene_1354 GeneMark.hmm 232_aa + 23435 24133	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	45.6	215	1.1E-38	169.9	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1355 GeneMark.hmm 232_aa + 1 699	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1356 GeneMark.hmm 357_aa - 746 1819	YP_009173415	hypothetical protein ceV_160 [Chrysochromulina ericina virus]	42.6	197	2.9E-33	152.5	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1357 GeneMark.hmm 328_aa - 1906 2892	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1358 GeneMark.hmm 434_aa + 3255 4559	YP_008052499	hypothetical protein PGCG_00181 [Phaeocystis globosa virus]	29.9	365	1.1E-26	131	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1359 GeneMark.hmm 157_aa + 4577 5050	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1360 GeneMark.hmm 138_aa + 5118 5534	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1361 GeneMark.hmm 77_aa + 5560 5793	YP_009173355	hypothetical protein ceV_100 [Chrysochromulina ericina virus]	42.1	76	1.3E-10	75.1	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1362 GeneMark.hmm 102_aa + 5819 6127	YP_008052487	hypothetical protein PGCG_00169 [Phaeocystis globosa virus]	36.7	79	2.1E-08	68.2	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1363 GeneMark.hmm 226_aa + 6166 6846	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1364 GeneMark.hmm 504_aa - 6878 8392	YP_009173345	putative polyA polymerase catalytic subunit [Chrysochromulina ericina virus]	50.5	424	7E-116	427.6	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1365 GeneMark.hmm 353_aa - 8423 9484	YP_009173344	putative phosphoinositide-specific phospholipase C-beta2 [Chrysochromulina ericina virus]	24.7	360	3.6E-20	109	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1366 GeneMark.hmm 549_aa + 9555 11204	YP_009174114	putative major capsid protein MCP2 [Yellowstone lake mimivirus]	51	563	5E-162	580.9	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1367 GeneMark.hmm 563_aa + 11262 12953	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1368 GeneMark.hmm 424_aa + 12988 14262	YP_009173339	putative glycosyltransferase [Chrysochromulina ericina virus]	49.9	399	3E-100	375.6	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1369 GeneMark.hmm 206_aa - 14311 14931	WP_101762060	glycosyltransferase family 25 protein [Pantoea endophytica]	32.4	207	5.2E-19	104.4	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1370 GeneMark.hmm 453_aa - 14984 16345	YP_009174125	putative replication factor C large subunit [Yellowstone lake mimivirus]	50	450	2E-117	432.6	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1371 GeneMark.hmm 647_aa - 16418 18361	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1372 GeneMark.hmm 236_aa + 18524 19234	YP_008052440	ribonuclease HIII [Phaeocystis globosa virus]	47.6	210	6.8E-47	197.2	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1373 GeneMark.hmm 676_aa - 19183 21213	YP_009174077	putative glycosyl transferase [Yellowstone lake mimivirus]	39.3	682	5E-114	421.8	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1374 GeneMark.hmm 194_aa + 21305 21889	YP_009174076	hypothetical protein [Yellowstone lake mimivirus]	41.3	155	2.7E-25	125.2	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1375 GeneMark.hmm 600_aa + 21959 23761	YP_009174075	hypothetical protein [Yellowstone lake mimivirus]	36.7	602	6.5E-86	328.2	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1376 GeneMark.hmm 272_aa - 23812 24630	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1377 GeneMark.hmm 64_aa + 24695 24889	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1378 GeneMark.hmm 310_aa - 24954 25886	YP_008052591	hypothetical protein PGCG_00273 [Phaeocystis globosa virus]	38.2	283	9.2E-36	160.6	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1379 GeneMark.hmm 37_aa - 26696 26809	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1380 GeneMark.hmm 431_aa + 27102 28397	WP_105939792	ankyrin repeat domain-containing protein [Arcobacter cryaerophilus]	36.2	312	1.2E-44	190.7	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1381 GeneMark.hmm 190_aa - 28394 28966	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1382 GeneMark.hmm 226_aa - 29035 29715	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1383 GeneMark.hmm 129_aa - 29806 30195	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1384 GeneMark.hmm 389_aa + 30252 31421	XP_002305073	senescence-specific cysteine protease SAG12 [Populus trichocarpa]	33.9	322	1.3E-42	183.7	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1385 GeneMark.hmm 160_aa + 31477 31959	XP_011400216	Structure-specific endonuclease subunit SLX1-like protein [Auxenochlorella protothecoides]	38.9	131	1.5E-10	75.9	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1386 GeneMark.hmm 101_aa - 31956 32261	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1387 GeneMark.hmm 1269_aa - 32306 36115	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	38.7	1025	2E-185	659.8	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1388 GeneMark.hmm 352_aa - 36230 37288	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	61.7	334	3E-116	428.3	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1389 GeneMark.hmm 93_aa + 37303 37584	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1390 GeneMark.hmm 275_aa + 37655 38482	YP_009173624	ERCC4-type nuclease [Chrysochromulina ericina virus]	31.5	276	3.2E-24	122.1	
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1391 GeneMark.hmm 390_aa - 38484 39656	no hit	-	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1392 GeneMark.hmm 234_aa - 39962 40666	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	38.5	205	5.7E		

GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1393 GeneMark.hmm 173_aa + 40716 41237	XP_022183857	protein disulfide-isomerase [Nilaparvata lugens]	36.2	94	5.9E-08	67.4
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1394 GeneMark.hmm 1391_aa + 41330 445505	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	45.9	1327	4E-284	988
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1395 GeneMark.hmm 150_aa + 45556 46008	no hit	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1396 GeneMark.hmm 410_aa + 45997 47229	no hit	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1397 GeneMark.hmm 352_aa + 47318 48376	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	38.9	350	2.6E-66	262.3
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1398 GeneMark.hmm 367_aa + 48388 49491	YP_008052570	extracellular link domain-containing protein [Phaeocystis globosa virus]	33	282	6.8E-38	167.9
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1399 GeneMark.hmm 103_aa + 49548 49859	no hit	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1400 GeneMark.hmm 126_aa + 49884 50264	no hit	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1401 GeneMark.hmm 392_aa + 50672 51850	YP_009173609	hypothetical protein ceV_354 [Chrysochromulina ericina virus]	35.9	195	7.1E-25	124.8
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1402 GeneMark.hmm 155_aa + 51925 52392	YP_009173608	hypothetical protein ceV_353 [Chrysochromulina ericina virus]	50.5	107	5.3E-16	94
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1403 GeneMark.hmm 200_aa + 52513 53115	YP_009173607	hypothetical protein ceV_352 [Chrysochromulina ericina virus]	63.8	199	1.8E-64	255.4
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1404 GeneMark.hmm 87_aa + 53210 53473	YP_009174055	hypothetical protein [Yellowstone lake mimivirus]	60.3	78	6E-17	96.3
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1405 GeneMark.hmm 292_aa + 53538 54416	YP_009173458	hypothetical protein ceV_203 [Chrysochromulina ericina virus]	50	272	5.8E-72	280.8
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1406 GeneMark.hmm 67_aa + 54511 56535	no hit	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1407 GeneMark.hmm 278_aa + 56557 57393	YP_009173380	putative VV A32-like packaging ATPase [Chrysochromulina ericina virus]	79.1	278	5E-131	476.9
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1408 GeneMark.hmm 574_aa + 57510 59234	YP_009173379	putative phosphotransferase [Chrysochromulina ericina virus]	46.6	558	3E-101	379
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1409 GeneMark.hmm 135_aa + 59226 59633	no hit	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1410 GeneMark.hmm 979_aa + 59689 62628	YP_009173744	DNA polymerase X/NAD-dependent DNA ligase fusion protein [Chrysochromulina ericina vi	43.6	1040	6E-225	790.8
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1411 GeneMark.hmm 87_aa + 62736 62999	no hit	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1412 GeneMark.hmm 360_aa + 63033 64115	YP_009174071	hypothetical protein [Yellowstone lake mimivirus]	68.5	178	2.2E-65	259.2
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1413 GeneMark.hmm 283_aa + 64124 64975	YP_009173374	replication factor C small subunit [Chrysochromulina ericina virus]	44.3	271	1.4E-54	223
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1414 GeneMark.hmm 174_aa + 64984 65508	YP_009173478	hypothetical protein ceV_223 [Chrysochromulina ericina virus]	39.2	153	5.8E-19	104
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1415 GeneMark.hmm 138_aa + 65576 65992	YP_008052450	hypothetical protein PGCV_00131 [Phaeocystis globosa virus]	41.6	113	8.3E-13	83.2
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1416 GeneMark.hmm 493_aa + 66072 67553	YP_009173475	YqaJ-like viral recombinase [Chrysochromulina ericina virus]	36.3	402	1.6E-69	273.5
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1417 GeneMark.hmm 1155_aa + 67640 71107	YP_009173474	Ribonucleotide reductase large subunit [Chrysochromulina ericina virus]	40.4	1685	0	1198
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1418 GeneMark.hmm 458_aa + 71146 72522	no hit	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1419 GeneMark.hmm 276_aa + 72609 73439	YP_008052442	exonuclease [Phaeocystis globosa virus]	28.4	268	2.1E-15	92.8
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1420 GeneMark.hmm 565_aa + 73545 75242	WP_165123127	glycosyltransferase family 2 protein [Bradyrhizobium sp. 6(2017)]	27.6	261	3.5E-09	73.2
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1421 GeneMark.hmm 827_aa + 75277 77760	no hit	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1422 GeneMark.hmm 418_aa + 77804 79060	no hit	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1423 GeneMark.hmm 36_aa + 79912 80022	no hit	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1424 GeneMark.hmm 76_aa + 82945 83175	no hit	-	-	-	-	-
GVMAG-S-ERX555943-30	GVMAG-S-ERX555943-30 ERX555943_contig_11	gene_1425 GeneMark.hmm 61_aa + 84533 84715	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1426 GeneMark.hmm 967_aa + 82902 83175	YP_009173561	putative helicase [Chrysochromulina ericina virus]	39.8	940	2E-158	570.1
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1427 GeneMark.hmm 290_aa + 82907 83179	YP_009173562	Nudix-like hydrolase [Chrysochromulina ericina virus]	45.5	257	2E-56	229.2
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1428 GeneMark.hmm 103_aa + 83763 84074	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1429 GeneMark.hmm 1031_aa + 84202 84979	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1430 GeneMark.hmm 52_aa + 84747 85055	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1431 GeneMark.hmm 41_aa + 85021 85146	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1432 GeneMark.hmm 59_aa + 84888 85667	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1433 GeneMark.hmm 532_aa + 87231 88321	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1434 GeneMark.hmm 322_aa + 10305 11273	YP_009173569	hypothetical protein ceV_314 [Chrysochromulina ericina virus]	28	214	5.8E-17	98.2
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1435 GeneMark.hmm 388_aa + 11307 12473	YP_009173570	hypothetical protein ceV_315 [Chrysochromulina ericina virus]	35.6	289	1.2E-35	160.6
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1436 GeneMark.hmm 1525_aa + 12482 17059	YP_009173620	DNA polymerase B [Chrysochromulina ericina virus]	45.7	1635	0	1322.4
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1437 GeneMark.hmm 209_aa + 17129 17758	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1438 GeneMark.hmm 181_aa + 17792 18337	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1439 GeneMark.hmm 72_aa + 18327 18545	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1440 GeneMark.hmm 156_aa + 18711 19181	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1441 GeneMark.hmm 89_aa + 19209 19478	XP_003392364	beta-ketoacyl-CoA synthase [Leishmania infantum JPCM5]	44.7	76	8.3E-06	59.3
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1442 GeneMark.hmm 151_aa + 19480 19935	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1443 GeneMark.hmm 275_aa + 20368 21195	WP_069541546	LlaMI family restriction endonuclease [Vibrio parahaemolyticus]	42.7	255	9.3E-48	200.3
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1444 GeneMark.hmm 406_aa + 21179 22399	WP_123615812	DNA cytosine methyltransferase [Muriabaculaceae bacterium Isolate-080 (Janvier)]	35.9	354	2.4E-44	189.5
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1445 GeneMark.hmm 388_aa + 22527 23735	WP_147757921	N-6 DNA methylase [Brachyspira aalborgi]	31.8	406	3.6E-40	175.6
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1446 GeneMark.hmm 124_aa + 23792 24166	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1447 GeneMark.hmm 338_aa + 24322 25368	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1448 GeneMark.hmm 132_aa + 25444 25842	WP_013159164	sulfite exporter TauE/SafE family protein [Meiothermus silvanus]	39.4	109	7.7E-08	66.6
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1449 GeneMark.hmm 125_aa + 25895 26272	no hit	-	-	-	-	-
GVMAG-S-ERX555967-113	GVMAG-S-ERX555967-113 ERX555967_contig_1026	gene_1450 GeneMark.hmm 212_aa + 26313 26951	no hit	-	-	-	-	-
GVMAG-S-ERX555967-93	GVMAG-S-ERX555967-93 ERX555967_contig_3023	gene_1451 GeneMark.hmm 319_aa + 31959	no hit	-	-	-	-	-
GVMAG-S-ERX555967-93	GVMAG-S-ERX555967-93 ERX555967_contig_3023	gene_1452 GeneMark.hmm 155_aa + 9811 1448	YP_004894627	hypothetical protein MegaChil_gp0576 [Megavirus chiliensis]	46.7	122	5.5E-21	110.5
GVMAG-S-ERX555967-93	GVMAG-S-ERX555967-93 ERX555967_contig_3023	gene_1453 GeneMark.hmm 1807_aa + 1481 6904	YP_007354471	hypothetical protein Moutou_00501 [Acanthamoeba polyphaga moutouovirus]	31.6	2100	9E-253	884
GVMAG-S-ERX555967-93	GVMAG-S-ERX555967-93 ERX555967_contig_3023	gene_1454 GeneMark.hmm 197_aa + 6924 7517	YP_004894629	putative metalloproteinase WLM domain protein [Megavirus chiliensis]	41.2	199	6.7E-32	147.1
GVMAG-S-ERX555967-93	GVMAG-S-ERX555967-93 ERX555967_contig_3023	gene_1455 GeneMark.hmm 210_aa + 7584 8216	no hit	-	-	-	-	-
GVMAG-S-ERX555967-93	GVMAG-S-ERX555967-93 ERX555967_contig_3023	gene_1456 GeneMark.hmm 1177_aa + 8225 11758	YP_003970183	putative DNA-dependent DNA polymerase family B [Cafeteria roenbergensis virus BV-PW1	35.2	1331	1E-201	713.8
GVMAG-S-ERX555967-93	GVMAG-S-ERX555967-93 ERX555967_contig_3023	gene_1457 GeneMark.hmm 193_aa + 11845 12426	no hit	-	-	-	-	-
GVMAG-S-ERX555967-93	GVMAG-S-ERX555967-93 ERX555967_contig_3023	gene_1458 GeneMark.hmm 536_aa + 12477 14087	XP_022856058	ubiquitin carboxyl-terminal hydrolase 10-like [Olea europaea var. sylvestris]	40.4	156	6.3E-24	122.1
GVMAG-S-ERX555967-93	GVMAG-S-ERX555967-93 ERX555967_contig_3023	gene_1459 GeneMark.hmm 344_aa + 14185 15219	YP_003986821	probable DNA polymerase family X [Acanthamoeba polyphaga mimivirus]	42.7	349	9.5E-58	233.8
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1460 GeneMark.hmm 291_aa + 358 1233	XP_019638167	PREDICTED: ankyrin-3-like [Branchiostoma belcheri]	52.7	188	4.7E-42	181.4
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1461 GeneMark.hmm 37_aa + 1319 1432	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1462 GeneMark.hmm 170_aa + 1422 1934	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1463 GeneMark.hmm 609_aa + 2089 3918	XP_021874351	FAD binding domain-domain-containing protein [Kockovaella imperatae]	66.7	598	2E-229	804.7
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1464 GeneMark.hmm 242_aa + 4020 4748	XP_009826543	succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial [Aphanomyces ast	68	228	2.4E-84	321.6
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1465 GeneMark.hmm 107_aa + 4741 5064	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1466 GeneMark.hmm 152_aa + 5148 5606	XP_004367486	succinate dehydrogenase, cytochrome b556 subunit protein [Acanthamoeba castellanii str.	40.2	112	2.5E-10	75.1
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1467 GeneMark.hmm 294_aa + 5615 6499	XP_006390629	casein kinase 1-like protein 2 [Eutrema salsugineum]	33.3	261	1E-31	147.1
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1468 GeneMark.hmm 115_aa + 6686 7033	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG							

GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1475 GeneMark.hmm 273_aa - 16418 17239	YP_008052380	DNA methylase [Phaeocystis globosa virus]	82.2	258	2E-126	461.8
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1476 GeneMark.hmm 725_aa+ 17340 19517	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1477 GeneMark.hmm 908_aa+ 19611 22337	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1478 GeneMark.hmm 83_aa+ 22394 22645	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1479 GeneMark.hmm 177_aa - 22654 23187	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1480 GeneMark.hmm 318_aa+ 24224 25180	YP_008052744	hypothetical protein PGCG_00433 [Phaeocystis globosa virus]	32.6	304	1.2E-35	160.2
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1481 GeneMark.hmm 322_aa+ 25331 26299	YP_009174067	putative site-specific DNA methyltransferase [Yellowstone lake mimivirus]	69.3	306	5E-123	450.7
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1482 GeneMark.hmm 208_aa - 26296 26922	YP_009254762	hypothetical protein [Tokyovirus A1]	35.7	185	9.6E-21	110.2
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1483 GeneMark.hmm 250_aa - 26983 27735	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1484 GeneMark.hmm 160_aa - 27794 28276	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1485 GeneMark.hmm 239_aa+ 28416 29135	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1486 GeneMark.hmm 256_aa - 29191 29961	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1487 GeneMark.hmm 241_aa - 30007 30732	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1488 GeneMark.hmm 299_aa+ 30924 31823	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1489 GeneMark.hmm 286_aa+ 31871 32731	WP_146921314	FkbM family methyltransferase [Algoriphagus aquimarinus]	34.7	167	5.7E-16	94.7
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1490 GeneMark.hmm 846_aa+ 32865 35405	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1491 GeneMark.hmm 181_aa+ 35463 36008	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1492 GeneMark.hmm 599_aa - 36117 37916	YP_009173669	ribonuclease II family protein [Chrysochromulina ericina virus]	38.3	592	4E-111	411.8
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1493 GeneMark.hmm 376_aa - 38030 39160	YP_008052657	hypothetical protein PGCG_00339 [Phaeocystis globosa virus]	28.2	291	1.7E-15	93.6
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1494 GeneMark.hmm 245_aa - 39222 39959	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1495 GeneMark.hmm 494_aa - 39994 41478	YP_009173609	hypothetical protein ceV_354 [Chrysochromulina ericina virus]	37.9	203	6.2E-34	155.2
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1496 GeneMark.hmm 114_aa+ 41471 41815	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1497 GeneMark.hmm 162_aa+ 41845 42333	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1498 GeneMark.hmm 113_aa+ 42454 42795	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1499 GeneMark.hmm 112_aa+ 42834 43172	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1500 GeneMark.hmm 208_aa+ 43248 43874	WP_035004769	class II aldolase/adducin family protein, partial [Betaproteobacteria bacterium MOLA814]	31.9	216	8.7E-14	87
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1501 GeneMark.hmm 369_aa+ 43876 44985	YP_009173614	Link (Hyaluronan-binding) domain containing protein [Chrysochromulina ericina virus]	53.3	150	1.3E-44	190.3
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1502 GeneMark.hmm 348_aa+ 45005 46051	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	53.5	340	5E-105	391
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1503 GeneMark.hmm 621_aa+ 46121 47986	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1504 GeneMark.hmm 136_aa+ 48020 48430	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1505 GeneMark.hmm 1156_aa - 48513 51983	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	39.1	1180	6E-208	734.6
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1506 GeneMark.hmm 335_aa - 52068 53075	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	62.3	324	7E-122	446.8
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1507 GeneMark.hmm 93_aa+ 53190 53471	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1508 GeneMark.hmm 280_aa+ 53578 54420	YP_008052636	ERCC4-type DNA repair nuclease [Phaeocystis globosa virus]	36.8	285	1.7E-28	136.3
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1509 GeneMark.hmm 112_aa+ 54566 54904	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1510 GeneMark.hmm 140_aa+ 54972 55394	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1511 GeneMark.hmm 269_aa+ 55494 56303	YP_008052632	hypothetical protein PGCG_00314 [Phaeocystis globosa virus]	30.9	256	7E-24	120.9
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1512 GeneMark.hmm 289_aa+ 56387 57256	YP_009173390	hypothetical protein ceV_135 [Chrysochromulina ericina virus]	47.5	101	2.2E-15	92.8
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1513 GeneMark.hmm 150_aa+ 57289 57741	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1514 GeneMark.hmm 1311_aa+ 57803 61738	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	50.2	1314	0	1153.3
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1515 GeneMark.hmm 110_aa+ 61794 62126	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1516 GeneMark.hmm 288_aa+ 62201 63067	WP_169975941	NAD-dependent deacetylase [Campylobacter sp. RM16191]	36.6	284	1.7E-44	189.5
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1517 GeneMark.hmm 159_aa+ 63069 63548	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1518 GeneMark.hmm 377_aa+ 63581 64714	YP_009448291	UV damage endonuclease UvdE [Orpheovirus IHUMI-LCC2]	46.5	316	2E-80	309.3
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1519 GeneMark.hmm 505_aa+ 64888 66405	WP_117784804	ribonuclease R [Clostridium sp. AF15-31]	25.7	354	1.5E-14	90.9
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1520 GeneMark.hmm 316_aa+ 66562 67512	XP_002178029	predicted protein [Phaeodactylum tricornutum CCAP 1055/1]	32.4	188	3.1E-15	92.4
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1521 GeneMark.hmm 329_aa+ 67622 68611	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1522 GeneMark.hmm 315_aa+ 68726 69673	YP_009173634	C-terminal catalytic domain of Ulp1 protease [Chrysochromulina ericina virus]	49.4	259	7.4E-65	257.3
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1523 GeneMark.hmm 168_aa+ 69725 70231	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1524 GeneMark.hmm 628_aa+ 70354 72240	YP_009173631	asparagine synthetase B [Chrysochromulina ericina virus]	47.3	636	2E-142	516.2
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1525 GeneMark.hmm 108_aa+ 72353 72679	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1526 GeneMark.hmm 176_aa+ 72771 73301	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1527 GeneMark.hmm 118_aa+ 73331 73687	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1528 GeneMark.hmm 107_aa+ 73774 74097	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1529 GeneMark.hmm 643_aa+ 74285 76216	XP_024572007	acyl-dehydrogenase [Plasmopara halstedii]	39.7	544	6E-108	401.4
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1530 GeneMark.hmm 304_aa+ 76254 77168	XP_001450879	hypothetical protein (macronuclear) [Paramecium tetraurelia strain d4-2]	44.4	279	2.1E-53	219.2
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1531 GeneMark.hmm 215_aa+ 77252 77899	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1532 GeneMark.hmm 60_aa+ 78170 78352	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1533 GeneMark.hmm 365_aa+ 78566 79663	XP_006364102	PREDICTED: uncharacterized protein LOC102586362 [Solanum tuberosum]	39.9	283	3.3E-40	175.6
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1534 GeneMark.hmm 154_aa+ 79660 80124	XP_026424758	glucosamine 6-phosphate N-acetyltransferase-like [Papaver somniferum]	42.9	154	1.8E-19	105.5
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1535 GeneMark.hmm 278_aa+ 80209 81045	YP_008052649	hypothetical protein PGCG_00331 [Phaeocystis globosa virus]	32.3	257	4.9E-28	134.8
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1536 GeneMark.hmm 82_aa+ 81118 81366	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1537 GeneMark.hmm 120_aa+ 81467 81829	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1538 GeneMark.hmm 140_aa+ 81918 82340	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1539 GeneMark.hmm 240_aa+ 82458 83180	YP_008052654	hypothetical protein PGCG_00336 [Phaeocystis globosa virus]	39.1	138	4.8E-24	121.3
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1540 GeneMark.hmm 284_aa+ 83268 84122	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1541 GeneMark.hmm 172_aa+ 84233 84751	YP_009173608	hypothetical protein ceV_353 [Chrysochromulina ericina virus]	47	83	6.5E-07	63.9
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1542 GeneMark.hmm 201_aa+ 84833 85438	YP_008052578	metal-dependent hydrolase [Phaeocystis globosa virus]	57.5	193	1.2E-57	232.6
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1543 GeneMark.hmm 187_aa+ 85505 86068	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1544 GeneMark.hmm 276_aa+ 86158 86988	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1545 GeneMark.hmm 138_aa+ 87030 87446	WP_048089435	ribonuclease HI family protein [Candidatus Methanoperedens nitroreducens]	46	126	7.5E-22	113.2
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1546 GeneMark.hmm 141_aa+ 87585 88010	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1547 GeneMark.hmm 153_aa+ 88046 88507	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1548 GeneMark.hmm 1787_aa+ 88659 94022	YP_009173600	repeat containing protein [Chrysochromulina ericina virus]	30.9	957	4E-112	416.8
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1549 GeneMark.hmm 108_aa+ 94063 94389	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1550 GeneMark.hmm 223_aa+ 94448 95119	WP_108864097	FAD-dependent thymidylate synthase [Rhodobacteraceae bacterium Water-Bin34]	59.6	228	3E-68	268.1
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1551 GeneMark.hmm 972_aa+ 95216 98134	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1552 GeneMark.hmm 71_aa+ 98230 98445	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1553 GeneMark.hmm 78_aa+ 98473 98709	YP_009052202	hypothetical protein AaV_126 [Aureococcus anophagefferens virus]	65.6	64	7.5E-19	102.4
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1554 GeneMark.hmm 1488_aa+ 98796 103262	YP_0091					

GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1557 GeneMark.hmm 229_aa + 106878 107567	YP_008052647	hypothetical protein PGCG_00329 [Phaeocystis globosa virus]	35.1	222	6.9E-20	107.5
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1558 GeneMark.hmm 284_aa + 107622 108476	YP_009173576	N-4 cytosine/N-6 adenine -specific DNA methylase [Chrysochromulina ericina virus]	67.5	277	5E-108	400.6
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1559 GeneMark.hmm 777_aa + 108590 110923	YP_009173654	ATP-dependent Lon protease [Chrysochromulina ericina virus]	64.5	397	8E-148	534.3
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1560 GeneMark.hmm 115_aa + 111053 111400	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1561 GeneMark.hmm 113_aa + 111472 111813	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1562 GeneMark.hmm 560_aa + 112052 113734	YP_009173639	hypothetical protein ceV_384 [Chrysochromulina ericina virus]	32	147	1E-08	71.6
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1563 GeneMark.hmm 296_aa + 113764 114654	YP_009173639	hypothetical protein ceV_384 [Chrysochromulina ericina virus]	38.2	301	5E-55	224.6
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1564 GeneMark.hmm 174_aa + 114745 115269	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1565 GeneMark.hmm 162_aa + 115371 115859	YP_009173661	hypothetical protein ceV_406 [Chrysochromulina ericina virus]	43.8	160	2.4E-27	131.7
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1566 GeneMark.hmm 353_aa + 116557 117618	YP_008052348	hypothetical protein PGCG_00029 [Phaeocystis globosa virus]	33.4	311	1.9E-29	139.8
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1567 GeneMark.hmm 191_aa + 117670 118245	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1568 GeneMark.hmm 148_aa + 118289 118735	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1569 GeneMark.hmm 291_aa + 118866 119741	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1570 GeneMark.hmm 79_aa + 119854 120093	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1571 GeneMark.hmm 99_aa + 120151 120450	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1572 GeneMark.hmm 86_aa + 121074 121334	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1573 GeneMark.hmm 827_aa + 121428 123911	YP_009173643	DNA topoisomerase IA [Chrysochromulina ericina virus]	41.7	803	3E-159	572.4
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1574 GeneMark.hmm 584_aa + 123993 125747	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1575 GeneMark.hmm 204_aa + 125821 126435	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1576 GeneMark.hmm 56_aa + 126514 126684	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1577 GeneMark.hmm 162_aa + 126685 127173	YP_008052597	hypothetical protein PGCG_00279 [Phaeocystis globosa virus]	29.9	164	1.1E-11	79.7
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1578 GeneMark.hmm 321_aa + 127275 128240	YP_009173646	hypothetical protein ceV_391 [Chrysochromulina ericina virus]	39.4	327	8E-59	237.3
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1579 GeneMark.hmm 317_aa + 128307 129260	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1580 GeneMark.hmm 234_aa + 129275 129979	XP_005794348	hypothetical protein EMIHUDDRAFT_431867 [Emiliania huxleyi CCMP1516]	31.7	208	1.6E-11	79.7
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1581 GeneMark.hmm 311_aa + 130234 131169	YP_009173648	DUF2738 superfamily protein [Chrysochromulina ericina virus]	37.5	261	1.3E-32	150.2
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1582 GeneMark.hmm 403_aa + 131356 132567	YP_008052602	hypothetical protein PGCG_00284 [Phaeocystis globosa virus]	36.4	346	4.4E-54	221.9
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1583 GeneMark.hmm 207_aa + 132768 133391	YP_009173598	SWIB-domain containing protein [Chrysochromulina ericina virus]	63.7	135	2.8E-36	161.8
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1584 GeneMark.hmm 239_aa + 133553 134272	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1585 GeneMark.hmm 305_aa + 134333 135250	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1586 GeneMark.hmm 301_aa + 135410 136315	YP_009173596	PIN domain of flap Endonuclease 1 [Chrysochromulina ericina virus]	37.2	298	6E-48	201.1
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1587 GeneMark.hmm 459_aa + 136399 137778	YP_009173595	hypothetical protein ceV_340 [Chrysochromulina ericina virus]	28.2	294	5.6E-29	138.7
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1588 GeneMark.hmm 75_aa + 137768 137995	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1589 GeneMark.hmm 181_aa + 138071 138616	YP_009174655	hypothetical protein [Yellowstone lake phycodnavirus 2]	29.4	160	6.6E-10	73.9
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1590 GeneMark.hmm 59_aa + 138663 138842	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1591 GeneMark.hmm 669_aa + 138890 140899	YP_008052605	hypothetical protein PGCG_00287 [Phaeocystis globosa virus]	28.5	698	5E-55	225.7
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1592 GeneMark.hmm 155_aa + 141050 141517	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1593 GeneMark.hmm 335_aa + 141571 142578	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1594 GeneMark.hmm 423_aa + 142779 144050	YP_009173589	Helicase 45 [Chrysochromulina ericina virus]	57.2	374	3E-124	455.3
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1595 GeneMark.hmm 598_aa + 144113 145909	YP_009173588	MutS8 [Chrysochromulina ericina virus]	36.6	579	4E-100	375.6
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1596 GeneMark.hmm 288_aa + 145994 146860	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1597 GeneMark.hmm 136_aa + 146894 147304	YP_008052610	hypothetical protein PGCG_00292 [Phaeocystis globosa virus]	36	139	1E-07	66.2
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1598 GeneMark.hmm 274_aa + 147513 148337	YP_008052612	putative Holliday junction resolvase [Phaeocystis globosa virus]	39.4	277	3.1E-43	185.3
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1599 GeneMark.hmm 495_aa + 148407 149894	YP_009173584	hypothetical protein ceV_329 [Chrysochromulina ericina virus]	43.6	518	4.2E-91	345.1
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1600 GeneMark.hmm 193_aa + 150040 150621	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1601 GeneMark.hmm 440_aa + 150650 151972	YP_008052619	2-polyphenylphenol 6-hydroxylase [Phaeocystis globosa virus]	25.7	377	6.3E-22	115.2
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1602 GeneMark.hmm 2197_aa + 152054 158647	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1603 GeneMark.hmm 91_aa + 158748 159023	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1604 GeneMark.hmm 192_aa + 159058 159636	YP_009173581	hypothetical protein ceV_326 [Chrysochromulina ericina virus]	42.2	116	1.7E-19	105.9
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1605 GeneMark.hmm 252_aa + 159779 160537	YP_008052624	hypothetical protein PGCG_00306 [Phaeocystis globosa virus]	53.6	69	9.9E-12	80.5
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1606 GeneMark.hmm 124_aa + 160611 160985	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1607 GeneMark.hmm 408_aa + 161033 162259	YP_009173579	N-acyltransferase/N-myristoyltransferase [Chrysochromulina ericina virus]	30.9	405	3E-42	182.6
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1608 GeneMark.hmm 56_aa + 162362 162532	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1609 GeneMark.hmm 315_aa + 162559 163506	YP_009173574	SAM dependent methyltransferase domain containing protein [Chrysochromulina ericina virus]	41.9	265	3.1E-47	198.7
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1610 GeneMark.hmm 367_aa + 163567 164670	YP_009173573	hypothetical protein ceV_318 [Chrysochromulina ericina virus]	32.3	359	8.1E-55	224.2
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1611 GeneMark.hmm 132_aa + 164702 165100	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1612 GeneMark.hmm 175_aa + 165099 165626	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1613 GeneMark.hmm 345_aa + 165700 166737	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1614 GeneMark.hmm 297_aa + 166822 167715	YP_009173570	hypothetical protein ceV_315 [Chrysochromulina ericina virus]	38.4	292	3.5E-48	201.8
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1615 GeneMark.hmm 258_aa + 167825 168601	YP_009173569	hypothetical protein ceV_314 [Chrysochromulina ericina virus]	31.3	262	1.2E-25	126.7
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1616 GeneMark.hmm 801_aa + 168697 171102	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1617 GeneMark.hmm 201_aa + 171154 171759	YP_009173567	HNH nuclease [Chrysochromulina ericina virus]	48.5	200	8.3E-46	193.4
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1618 GeneMark.hmm 448_aa + 171786 173132	YP_009173564	hypothetical protein ceV_309 [Chrysochromulina ericina virus]	30.7	342	2.3E-35	159.8
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1619 GeneMark.hmm 143_aa + 173188 173619	YP_009173563	Erv1 / Alr family [Chrysochromulina ericina virus]	44.1	143	2.2E-32	148.3
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1620 GeneMark.hmm 297_aa + 173678 174571	YP_009173562	Nudix-like hydrolase [Chrysochromulina ericina virus]	52.1	257	2.8E-74	288.5
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1621 GeneMark.hmm 1269_aa + 174586 178395	YP_009173561	putative helicase [Chrysochromulina ericina virus]	41	1250	1E-242	849.7
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1622 GeneMark.hmm 97_aa + 178439 178732	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1623 GeneMark.hmm 180_aa + 178825 179367	YP_009173560	hypothetical protein ceV_305 [Chrysochromulina ericina virus]	47.9	165	2.7E-35	158.3
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1624 GeneMark.hmm 127_aa + 179489 179872	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1625 GeneMark.hmm 263_aa + 179902 180693	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1626 GeneMark.hmm 1181_aa + 180776 184321	YP_008052553	mRNA capping enzyme [Phaeocystis globosa virus]	47.3	1056	2E-274	955.3
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1627 GeneMark.hmm 368_aa + 184393 185499	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1628 GeneMark.hmm 326_aa + 185554 186534	XP_012940436	PREDICTED: chymotrypsin inhibitor-like [Aplysia californica]	52.9	70	2.5E-07	66.2
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1629 GeneMark.hmm 89_aa + 186591 186860	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1630 GeneMark.hmm 105_aa + 187005 187322	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1631 GeneMark.hmm 115_aa + 187384 187731	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1632 GeneMark.hmm 250_aa + 187788 188540	no hit	-	-	-	-	-
GVMAG-S-ERX556106-38	GVMAG-S-ERX556106-38 ERX556106_contig_4	gene_1633 GeneMark.hmm 64_aa + 188605 188796						

GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1639 GeneMark.hmm 166_aa+ 3156 3656	YP_008052437	disulfide isomerase [Phaeocystis globosa virus]	39.4	94	3.2E-11	78.2
GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1640 GeneMark.hmm 300_aa- 3648 4550	YP_008052436	patatin-like phospholipase [Phaeocystis globosa virus]	38.1	247	7.8E-40	174.1
GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1641 GeneMark.hmm 197_aa+ 4611 5204	YP_008052435	hypothetical protein PGCG_00116 [Phaeocystis globosa virus]	41.2	194	1.1E-34	156.4
GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1642 GeneMark.hmm 63_aa+ 5244 5435	no hit	-	-	-	-	-
GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1643 GeneMark.hmm 147_aa- 5432 5875	no hit	-	-	-	-	-
GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1644 GeneMark.hmm 399_aa- 5942 7141	YP_008052570	extracellular link domain-containing protein [Phaeocystis globosa virus]	38.4	294	1.5E-38	170.2
GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1645 GeneMark.hmm 348_aa- 7162 8208	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	47.1	346	1.2E-92	349.7
GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1646 GeneMark.hmm 371_aa+ 8264 9379	no hit	-	-	-	-	-
GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1647 GeneMark.hmm 67_aa- 9376 9579	no hit	-	-	-	-	-
GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1648 GeneMark.hmm 1296_aa- 9649 13539	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	46.8	1292	0	1124.4
GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1649 GeneMark.hmm 177_aa- 13596 14129	XP_022118461	protein disulfide-isomerase A3 [Pteris rapae]	32.4	105	1.1E-06	63.2
GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1650 GeneMark.hmm 225_aa+ 14211 14888	YP_009173622	hypothetical protein ceV_367 [Chrysochromulina ericina virus]	42.1	171	3.9E-28	134.8
GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1651 GeneMark.hmm 276_aa- 14880 15710	YP_009173624	ERCC4-type nuclease [Chrysochromulina ericina virus]	33.2	280	8.8E-30	140.6
GVMAG-M-3300021960-2	GVMAG-M-3300021960-2 Ga0222715_10002631	gene_1652 GeneMark.hmm 38_aa+ 16172 16285	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	77.8	36	5.5E-07	62
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1653 GeneMark.hmm 57_aa- 2 172	no hit	-	-	-	-	-
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1654 GeneMark.hmm 381_aa+ 318 1463	WP_013455790	DNA cytosine methyltransferase [Marivirga tractuosa]	38.2	356	5.4E-46	194.9
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1655 GeneMark.hmm 259_aa- 1447 2226	WP_086183151	LlaMI family restriction endonuclease [Acinetobacter sp. ANC 4558]	37.1	256	3.7E-38	168.3
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1656 GeneMark.hmm 113_aa- 2274 2615	no hit	-	-	-	-	-
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1657 GeneMark.hmm 262_aa- 2638 3426	XP_017244334	PREDICTED: uncharacterized protein LOC108216159 [Daucus carota subsp. sativus]	27.8	252	1.3E-17	100.1
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1658 GeneMark.hmm 73_aa- 3451 3672	no hit	-	-	-	-	-
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1659 GeneMark.hmm 258_aa- 3714 4490	no hit	-	-	-	-	-
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1660 GeneMark.hmm 116_aa- 4487 4837	YP_007676303	hypothetical protein MPVG_00239 [Micromonas pusilla virus 12T]	49.6	115	9.1E-21	109.4
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1661 GeneMark.hmm 237_aa- 4908 5621	YP_008052442	exonuclease [Phaeocystis globosa virus]	35.8	218	2.6E-22	115.5
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1662 GeneMark.hmm 268_aa- 5682 6488	YP_009174414	hypothetical protein [Yellowstone lake phycodnavirus 3]	30.9	223	1.1E-11	80.5
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1663 GeneMark.hmm 388_aa+ 6658 7824	no hit	-	-	-	-	-
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1664 GeneMark.hmm 534_aa+ 7908 9512	no hit	-	-	-	-	-
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1665 GeneMark.hmm 285_aa- 9574 10431	no hit	-	-	-	-	-
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1666 GeneMark.hmm 121_aa+ 10508 10873	no hit	-	-	-	-	-
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1667 GeneMark.hmm 233_aa- 10882 11583	YP_009173510	Deoxyribonucleoside kinase [Chrysochromulina ericina virus]	39.1	197	1.2E-32	149.8
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1668 GeneMark.hmm 98_aa- 11656 11952	no hit	-	-	-	-	-
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1669 GeneMark.hmm 1323_aa- 12003 15974	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	45.4	1332	0	1104
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1670 GeneMark.hmm 145_aa+ 16074 16511	no hit	-	-	-	-	-
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1671 GeneMark.hmm 147_aa- 16558 17001	no hit	-	-	-	-	-
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1672 GeneMark.hmm 310_aa+ 17069 18001	YP_008052632	hypothetical protein PGCG_00314 [Phaeocystis globosa virus]	30	213	3.9E-10	75.5
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1673 GeneMark.hmm 247_aa- 18004 18747	YP_009173624	ERCC4-type nuclease [Chrysochromulina ericina virus]	37.5	251	1.3E-35	159.8
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1674 GeneMark.hmm 99_aa- 18802 19101	no hit	-	-	-	-	-
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1675 GeneMark.hmm 348_aa+ 19218 20264	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	64.6	314	3E-119	438.3
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1676 GeneMark.hmm 90_aa+ 22660 22932	no hit	-	-	-	-	-
GVMAG-S-1016713-148	GVMAG-S-1016713-148 1016713_contig_1229	gene_1677 GeneMark.hmm 81_aa+ 23790 24032	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1678 GeneMark.hmm 30_aa+ 1 93	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1679 GeneMark.hmm 255_aa+ 153 920	XP_002182261	proliferating cell nuclear antigen [Phaeodactylum tricornutum CCAP 1055/1]	29.4	248	1.6E-22	116.3
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1680 GeneMark.hmm 281_aa+ 1017 1862	YP_008052657	hypothetical protein PGCG_00339 [Phaeocystis globosa virus]	28.3	283	1.5E-24	123.2
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1681 GeneMark.hmm 567_aa+ 1924 3627	YP_009173669	ribonuclease II family protein [Chrysochromulina ericina virus]	41	571	2E-122	449.1
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1682 GeneMark.hmm 82_aa- 3628 3876	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1683 GeneMark.hmm 46_aa- 3889 4029	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1684 GeneMark.hmm 56_aa- 4075 4245	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1685 GeneMark.hmm 78_aa+ 4244 4480	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1686 GeneMark.hmm 145_aa- 4811 5248	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1687 GeneMark.hmm 826_aa- 5317 7797	YP_009173671	DEAD-like RNA helicase, superfamily II [Chrysochromulina ericina virus]	40.6	881	1E-162	583.6
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1688 GeneMark.hmm 234_aa+ 7864 8568	YP_008052654	hypothetical protein PGCG_00336 [Phaeocystis globosa virus]	43	149	3E-23	118.6
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1689 GeneMark.hmm 271_aa+ 8609 9424	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1690 GeneMark.hmm 97_aa- 9592 9885	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1691 GeneMark.hmm 441_aa- 9993 11318	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1692 GeneMark.hmm 230_aa- 11454 12146	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1693 GeneMark.hmm 413_aa- 12229 13470	WP_012040184	Hint domain-containing protein [Acidiphilium cryptum]	32.7	147	1.2E-06	64.3
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1694 GeneMark.hmm 140_aa+ 13543 13965	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1695 GeneMark.hmm 107_aa+ 14083 14406	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1696 GeneMark.hmm 1076_aa- 14398 17628	YP_009173744	DNA polymerase X/NAD-dependent DNA ligase fusion protein [Chrysochromulina ericina vi	49	1076	6E-242	847.4
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1697 GeneMark.hmm 117_aa- 17656 18009	YP_008052648	hypothetical protein PGCG_00330 [Phaeocystis globosa virus]	42.9	84	4E-08	67.4
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1698 GeneMark.hmm 235_aa+ 18074 18781	YP_009173630	hypothetical protein ceV_375 [Chrysochromulina ericina virus]	39.1	233	1.2E-38	169.9
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1699 GeneMark.hmm 106_aa- 18726 19046	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1700 GeneMark.hmm 565_aa- 19092 20789	YP_008052645	asparagine synthetase B [Phaeocystis globosa virus]	51.4	582	2E-156	562.4
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1701 GeneMark.hmm 172_aa+ 21147 21665	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1702 GeneMark.hmm 290_aa+ 21742 22614	YP_009173634	C-terminal catalytic domain of Ulp1 protease [Chrysochromulina ericina virus]	42.1	261	5E-52	214.5
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1703 GeneMark.hmm 192_aa- 22687 23265	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1704 GeneMark.hmm 1052_aa+ 23333 26491	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1705 GeneMark.hmm 242_aa+ 26537 27265	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1706 GeneMark.hmm 143_aa- 27381 27812	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1707 GeneMark.hmm 111_aa+ 27966 28301	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1708 GeneMark.hmm 118_aa- 28305 28661	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1709 GeneMark.hmm 220_aa- 28705 29367	YP_293886	ve ATP-dependent protease proteolytic subunit [Emiliania huxleyi virus 86]	35.3	167	1.2E-21	113.2
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1710 GeneMark.hmm 1139_aa- 29449 32868	YP_008052639	NPH-I transcription termination factor [Phaeocystis globosa virus]	43.8	1081	1E-229	806.6
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1711 GeneMark.hmm 329_aa- 32917 33906	YP_009173638	dsRNA-specific ribonuclease [Chrysochromulina ericina virus]	61.9	328	1E-119	439.5
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1712 GeneMark.hmm 195_aa+ 34028 34615	XP_002499992	hypothetical protein MICPUN_107781 [Micromonas commoda]	42.6	108	4.8E-14	87.8
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1713 GeneMark.hmm 321_aa- 34624 35589	YP_009173347	MIGE-like and Zn finger domain containing protein [Chrysochromulina ericina virus]	33	324	1.2E-35	160.2
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1714 GeneMark.hmm 1533_aa+ 35927 40528	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1715 GeneMark.hmm 272_aa- 40595 41413	XP_008901906	hypothetical protein PPTG_08907 [Phytophthora parasitica INRA-310]	37.3	252	9.6E-37	163.7
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1716 GeneMark.hmm 606_aa- 41462 43282	no hit	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1717 GeneMark.hmm 133_aa- 43356 43757	no hit	-	-	-	-	-

GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1721 GeneMark.hmm 159_aa + 45926 46405	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1722 GeneMark.hmm 163_aa + 46412 46903	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1723 GeneMark.hmm 43_aa + 47051 47182	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1724 GeneMark.hmm 1248_aa + 47236 50982	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	50.2	1294	0	1119	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1725 GeneMark.hmm 165_aa + 51042 51539	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1726 GeneMark.hmm 42_aa + 51611 51739	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1727 GeneMark.hmm 431_aa + 51736 53031	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1728 GeneMark.hmm 327_aa + 53090 54073	YP_009173615	ubiquitin specific peptidase C19 [Chrysochromulina ericina virus]	44	334	8.7E-77	297	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1729 GeneMark.hmm 265_aa + 54087 54884	YP_009173614	Link (Hyaluronan-binding) domain containing protein [Chrysochromulina ericina virus]	42.9	280	5.3E-56	227.6	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1730 GeneMark.hmm 108_aa + 54943 55269	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1731 GeneMark.hmm 117_aa + 55308 55661	YP_008052573	hypothetical protein PGCG_00255 [Phaeocystis globosa virus]	34.8	115	2.3E-11	78.2	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1732 GeneMark.hmm 137_aa + 55709 56122	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1733 GeneMark.hmm 75_aa + 56146 56373	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1734 GeneMark.hmm 377_aa + 56436 57569	YP_009173609	hypothetical protein ceV_354 [Chrysochromulina ericina virus]	30.3	333	1.5E-32	150.2	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1735 GeneMark.hmm 191_aa + 57612 58187	YP_009173608	hypothetical protein ceV_353 [Chrysochromulina ericina virus]	39.1	192	1.7E-24	122.5	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1736 GeneMark.hmm 197_aa + 58244 58837	YP_008052578	metal-dependent hydrolase [Phaeocystis globosa virus]	60.3	194	1.3E-62	249.2	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1737 GeneMark.hmm 1531_aa + 58864 63459	YP_009173600	repeat containing protein [Chrysochromulina ericina virus]	28.7	755	1.6E-64	258.5	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1738 GeneMark.hmm 197_aa + 63493 64086	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1739 GeneMark.hmm 500_aa + 64083 65585	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1740 GeneMark.hmm 1502_aa + 65634 70142	YP_009173653	DNA-directed RNA polymerase II, subunit RpB1 [Chrysochromulina ericina virus]	61.3	1502	0	1833.9	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1741 GeneMark.hmm 68_aa + 70302 70508	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1742 GeneMark.hmm 663_aa + 70691 72682	YP_009173654	ATP-dependent Lon protease [Chrysochromulina ericina virus]	62.3	398	4E-142	515	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1743 GeneMark.hmm 115_aa + 72775 73230	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1744 GeneMark.hmm 270_aa + 73377 74189	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1745 GeneMark.hmm 128_aa + 74287 74673	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1746 GeneMark.hmm 198_aa + 74851 75447	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1747 GeneMark.hmm 697_aa + 75623 77716	WP_113871497	AAA family ATPase [Arcobacter sp. CECT 9188]	25.9	474	2E-22	117.5	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1748 GeneMark.hmm 135_aa + 77755 78162	YP_008052610	hypothetical protein PGCG_00292 [Phaeocystis globosa virus]	36.3	135	6.9E-20	106.7	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1749 GeneMark.hmm 235_aa + 78184 78891	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1750 GeneMark.hmm 576_aa + 78937 80667	YP_008052607	MutS 8-like protein [Phaeocystis globosa virus]	40.2	579	8E-115	424.1	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1751 GeneMark.hmm 302_aa + 80828 81736	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1752 GeneMark.hmm 117_aa + 81865 82218	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1753 GeneMark.hmm 397_aa + 82552 83745	YP_009173595	hypothetical protein ceV_340 [Chrysochromulina ericina virus]	27.3	392	9.1E-28	134.4	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1754 GeneMark.hmm 239_aa + 83844 84563	YP_009173598	SWIB-domain containing protein [Chrysochromulina ericina virus]	64	164	1.1E-47	199.9	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1755 GeneMark.hmm 359_aa + 84684 85763	YP_008052602	hypothetical protein PGCG_00284 [Phaeocystis globosa virus]	37.3	324	7.6E-50	207.6	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1756 GeneMark.hmm 289_aa + 86001 86870	YP_009173648	DUF2738 superfamily protein [Chrysochromulina ericina virus]	42.3	253	1E-49	206.8	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1757 GeneMark.hmm 45_aa + 87388 87525	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1758 GeneMark.hmm 152_aa + 87690 88148	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1759 GeneMark.hmm 59_aa + 88165 88344	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1760 GeneMark.hmm 299_aa + 88368 89267	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1761 GeneMark.hmm 326_aa + 89242 90222	YP_009173646	hypothetical protein ceV_391 [Chrysochromulina ericina virus]	34.8	330	6.7E-45	191	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1762 GeneMark.hmm 118_aa + 90413 90769	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1763 GeneMark.hmm 83_aa + 90851 91102	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1764 GeneMark.hmm 966_aa + 91222 94122	YP_009173536	MutS7 [Chrysochromulina ericina virus]	40.1	1006	1E-193	686.8	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1765 GeneMark.hmm 211_aa + 94199 94834	XP_001448653	hypothetical protein (macronuclear) [Paramecium tetraurelia strain d4-2]	30.3	175	1.9E-08	69.3	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1766 GeneMark.hmm 154_aa + 94871 95335	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1767 GeneMark.hmm 185_aa + 95332 95889	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1768 GeneMark.hmm 776_aa + 95912 98242	YP_009173643	DNA topoisomerase IA [Chrysochromulina ericina virus]	44.3	783	7E-176	627.5	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1769 GeneMark.hmm 150_aa + 98269 98721	YP_009173661	hypothetical protein ceV_406 [Chrysochromulina ericina virus]	32.1	159	4.3E-15	90.9	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1770 GeneMark.hmm 213_aa + 98794 99435	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1771 GeneMark.hmm 314_aa + 99975 100919	YP_009173639	hypothetical protein ceV_384 [Chrysochromulina ericina virus]	42.6	303	1.1E-63	253.4	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1772 GeneMark.hmm 528_aa + 100945 102531	YP_009173640	hypothetical protein ceV_385 [Chrysochromulina ericina virus]	28.6	245	1.7E-18	104	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1773 GeneMark.hmm 134_aa + 102580 102984	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1774 GeneMark.hmm 275_aa + 103053 103880	YP_009173585	hypothetical protein ceV_330 [Chrysochromulina ericina virus]	36.6	279	9.4E-32	147.1	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1775 GeneMark.hmm 515_aa + 103901 105448	YP_008052616	hypothetical protein PGCG_00298 [Phaeocystis globosa virus]	45.2	553	2E-102	382.9	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1776 GeneMark.hmm 2493_aa + 105529 113010	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1777 GeneMark.hmm 427_aa + 113058 114341	WP_165778057	DNA adenine methylase [Raineya orbicola]	46.6	324	8.7E-77	297.4	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1778 GeneMark.hmm 72_aa + 114391 114609	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1779 GeneMark.hmm 303_aa + 114660 115571	YP_009173650	MIGE-like protein [Chrysochromulina ericina virus]	36.2	318	1E-47	200.3	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1780 GeneMark.hmm 55_aa + 115663 115830	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1781 GeneMark.hmm 296_aa + 115830 116720	WP_053590688	hydroxymethylglutaryl-CoA lyase [Bacillus sp. FJAT-22090]	31.6	250	2.9E-23	119	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1782 GeneMark.hmm 230_aa + 116749 117441	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1783 GeneMark.hmm 144_aa + 117464 117898	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1784 GeneMark.hmm 195_aa + 117952 118539	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1785 GeneMark.hmm 191_aa + 118604 119179	YP_009173580	hypothetical protein ceV_325 [Chrysochromulina ericina virus]	36.7	139	4E-13	84.7	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1786 GeneMark.hmm 394_aa + 119176 120360	YP_009173579	N-acyltransferase/N-myristoyltransferase [Chrysochromulina ericina virus]	29.2	391	2.8E-29	139.4	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1787 GeneMark.hmm 312_aa + 120406 121344	YP_009173574	SAM dependent methyltransferase domain containing protein [Chrysochromulina ericina vir	39.6	280	6.4E-45	191	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1788 GeneMark.hmm 350_aa + 121408 122460	YP_009173573	hypothetical protein ceV_318 [Chrysochromulina ericina virus]	41.4	345	4.3E-74	288.1	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1789 GeneMark.hmm 202_aa + 122468 123076	no hit	-	-	-	-	-	-
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1790 GeneMark.hmm 261_aa + 123097 123882	YP_009173572	hypothetical protein ceV_317 [Chrysochromulina ericina virus]	56.1	57	1.6E-09	73.2	
GVMAG-S-1074262-51	GVMAG-S-1074262-51 1074262_contig_17	gene_1791 GeneMark.hmm 892_aa + 123934 126612	YP_003969992	hypothetical protein crov359 [Cafeteria roenbergensis virus BV-PW1]	31.8	245	4.1E-28	136.7	
GVMAG-S-3300000226-21	GVMAG-S-3300000226-21 3300000226.a:SI34jun09_135mDRAF	gene_1792 GeneMark.hmm 1091_aa + 1 3276	YP_008052566	DNA polymerase [Phaeocystis globosa virus]	47	1087	2E-248	869	
GVMAG-S-3300000226-21	GVMAG-S-3300000226-21 3300000226.a:SI34jun09_135mDRAF	gene_1793 GeneMark.hmm 147_aa + 3365 3808	no hit	-	-	-	-	-	-
GVMAG-S-3300000226-21	GVMAG-S-3300000226-21 3300000226.a:SI34jun09_135mDRAF	gene_1794 GeneMark.hmm 427_aa + 3784 5067	no hit	-	-	-	-	-	-
GVMAG-S-3300000226-21	GVMAG-S-3300000226-21 3300000226.a:SI34jun09_135mDRAF	gene_1795 GeneMark.hmm 352_aa + 5162 6220	YP_008052569	ubiquitin specific peptidase C19 [Phaeocystis globosa virus]	38.6	350	1.1E-66	263.5	
GVMAG-S-3300000226-21	GVMAG-S-3300000226-21 3300000226.a:SI34jun09_135mDRAF	gene_1796 GeneMark.hmm 376_aa + 6213 7343	YP_008052570	extracellular link domain-containing protein [Phaeocystis globosa virus]	32.9	283	5.9E-37	164.9	
GVMAG-S-3300000226-21	GVMAG-S-3300000226-21 3300000226.a:SI34jun09_135mDRAF	gene_1797 GeneMark.hmm 106_aa + 7426 7746	no hit	-	-	-	-	-	-
GVMAG-S-3300000226-21	GVMAG-S-3300000226-21 3300000226.a:SI34jun09_135mDRAF	gene_1798 GeneMark.hmm 126_aa + 7771 8151	no hit	-	-	-	-	-	-
GVMAG-S-3300000226-21	GVMAG-S-3300000226-21 3300000226.a:SI34jun09_135mDRAF	gene_1799 GeneMark.hmm 418_aa + 8569 9825	no hit	-	-	-	-	-	-
GVMAG-S-3300000226-21	GVMAG-S-3300000226-21 3300000226.a:SI34jun09_135mDRAF	gene_1800 GeneMark.hmm 155_aa + 9900 10367	YP_009173608	hypothetical protein ceV_353 [Chrysochromulina ericina virus]	50.9	106	2E-15	92	
GVMAG-S-3300000226-21	GVMAG-S-3300000226-21 3300000226.a:SI34jun09_135mDRAF	gene_1801 GeneMark.hmm 200_aa + 10493 11095	YP_009173607	hypothetical protein ceV_352 [Chrysochromulina ericina virus]	64.8	199	1.4E-64	255.8	
GVMAG-S-3300000226-21	GVMAG-S-33								

