

TGACCGTGATACTCAAGATG



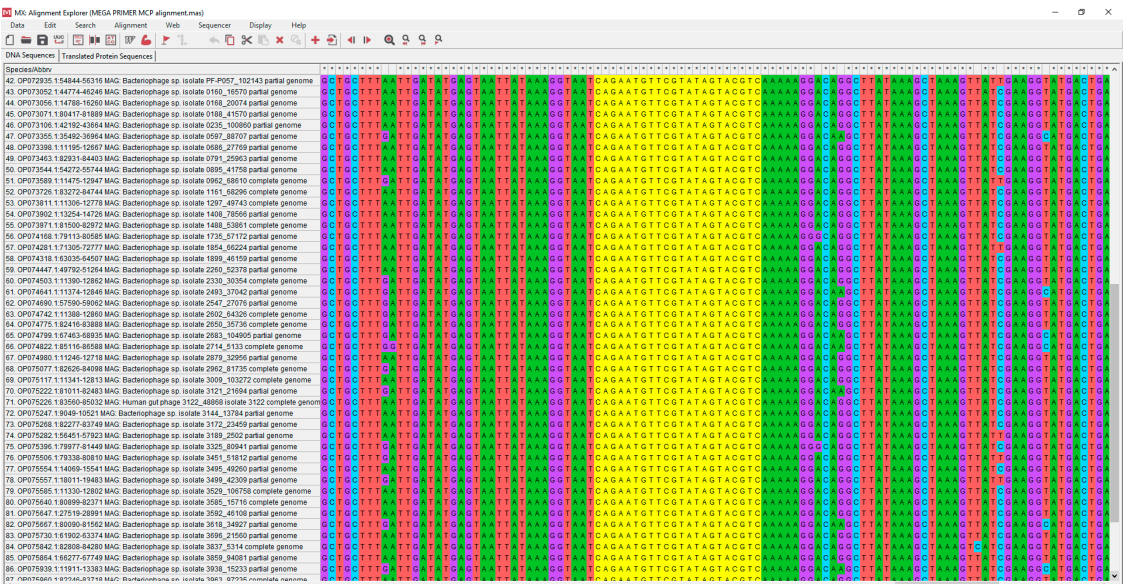
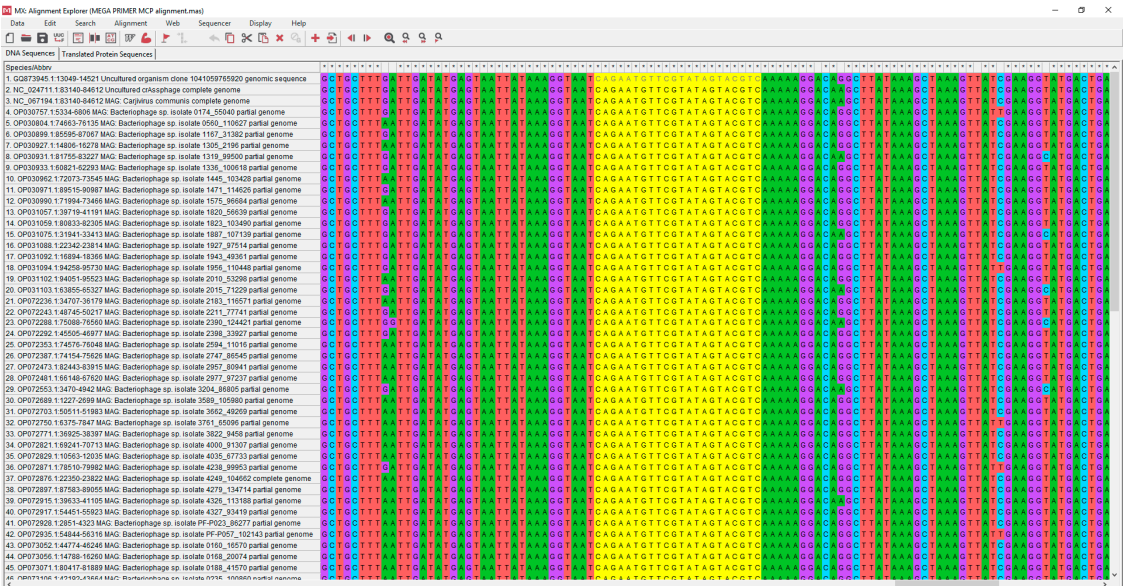
MCP

Reverse primer

GACGTACTATACGAACATTCTG

(Reverse complementary)

CAGAATGTTTCGTATAGTACGTC



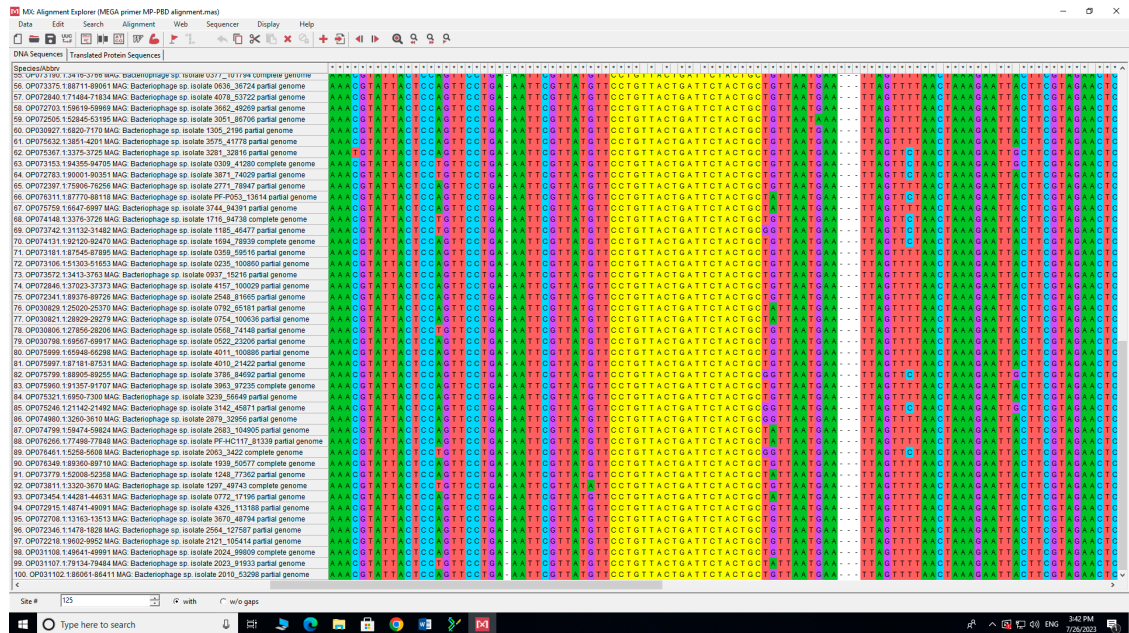
The image displays the MEGA PRIMER-MCL alignment tool interface. The top menu bar includes File, Edit, Search, Alignment, View, Sequencer, Display, and Help. Below the menu is a toolbar with icons for file operations (open, save, print), search (find, replace), alignment (align, unalign), and visualization (zoom, pan). The main window shows a list of DNA sequences on the left, each with an accession number and a species name. The sequences are aligned in a grid format, with each row representing a sequence and each column representing a position in the alignment. The sequences are color-coded: green for 'A', red for 'T', blue for 'C', and yellow for 'G'. The alignment is shown as a series of colored blocks, indicating regions of high similarity. The sequences are listed in ascending order of their accession numbers, starting from L. PVF02068 at the top and ending with L. PVF02448 at the bottom. The alignment is displayed in a grid format, with each row representing a sequence and each column representing a position in the alignment. The sequences are color-coded: green for 'A', red for 'T', blue for 'C', and yellow for 'G'. The alignment is shown as a series of colored blocks, indicating regions of high similarity.

MP-PBD

Forward primer

CCTGTTACYGATTCTACTGC





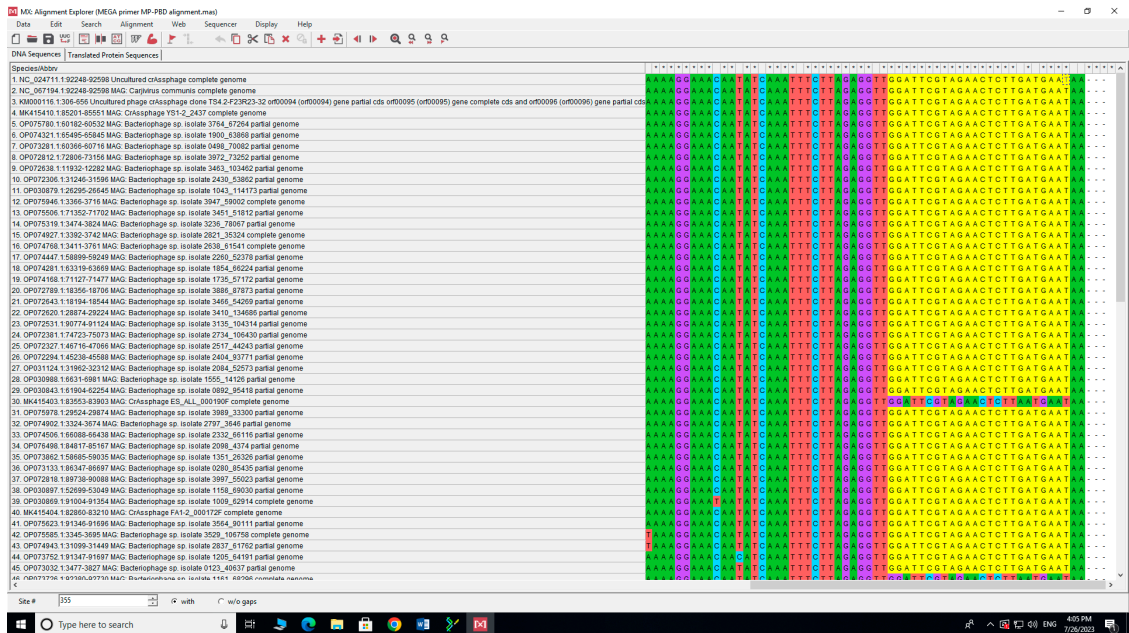
MP-PBD

Reverse primer

ATTCWTRAAGAGTTCTACGAATCC

(Reverse complementary)

GGATTCGTAGAACTCTTRAWGAAT



MEGA Alignment Explorer (MEGA primer MP-PBD alignment.maf)

Species/Isolates

55. OP073105 1.3410-3190 MAG. Bacteriophage sp. isolate 0337_101194 complete genome

56. OP073375 1.88711-89051 MAG. Bacteriophage sp. isolate 0638_36724 partial genome

57. OP072840 1.74484-74834 MAG. Bacteriophage sp. isolate 4078_53722 partial genome

58. OP072703 1.59819-59995 MAG. Bacteriophage sp. isolate 3642_46209 partial genome

59. OP072595 1.52845-53195 MAG. Bacteriophage sp. isolate 3051_86706 partial genome

60. OP039827 1.6820-7170 MAG. Bacteriophage sp. isolate 1305_2195 partial genome

61. OP076832 1.3861-4201 MAG. Bacteriophage sp. isolate 2075_41778 partial genome

62. OP075367 1.3375-3721 MAG. Bacteriophage sp. isolate 3281_32916 partial genome

63. OP073153 1.94355-94705 MAG. Bacteriophage sp. isolate 0309_41280 complete genome

64. OP072783 1.90001-90351 MAG. Bacteriophage sp. isolate 3871_74029 partial genome

65. OP072397 1.75505-75256 MAG. Bacteriophage sp. isolate 2771_73847 partial genome

66. OP076311 1.87770-88118 MAG. Bacteriophage sp. isolate PF-P053_13614 partial genome

67. OP075759 1.6647-6987 MAG. Bacteriophage sp. isolate 3744_94381 partial genome

68. OP074148 1.3375-3721 MAG. Bacteriophage sp. isolate 1716_34738 complete genome

69. OP073742 1.31132-31482 MAG. Bacteriophage sp. isolate 1185_46477 partial genome

70. OP074131 1.92120-92470 MAG. Bacteriophage sp. isolate 1684_78939 complete genome

71. OP073181 1.67545-67895 MAG. Bacteriophage sp. isolate 0359_59619 partial genome

72. OP073105 1.51303-51653 MAG. Bacteriophage sp. isolate 0235_10080 partial genome

73. OP073572 1.3413-3763 MAG. Bacteriophage sp. isolate 0937_15216 partial genome

74. OP073846 1.37623-37373 MAG. Bacteriophage sp. isolate +157_100029 partial genome

75. OP072341 1.89376-89726 MAG. Bacteriophage sp. isolate 2548_31665 partial genome

76. OP030829 1.25020-25370 MAG. Bacteriophage sp. isolate 0792_45181 partial genome

77. OP030621 1.28929-29279 MAG. Bacteriophage sp. isolate 0754_100536 partial genome

78. OP030806 1.27355-26206 MAG. Bacteriophage sp. isolate 0508_71461 partial genome

79. OP030798 1.69567-69917 MAG. Bacteriophage sp. isolate 0522_23200 partial genome

80. OP075999 1.65948-66298 MAG. Bacteriophage sp. isolate 4011_100885 partial genome

81. OP075987 1.87181-87513 MAG. Bacteriophage sp. isolate 4410_71422 partial genome

82. OP075799 1.88905-89255 MAG. Bacteriophage sp. isolate 3785_84692 partial genome

83. OP075960 1.91357-91707 MAG. Bacteriophage sp. isolate 3963_87235 complete genome

84. OP075321 1.6950-7300 MAG. Bacteriophage sp. isolate 3239_55649 partial genome

85. OP075245 1.21142-21482 MAG. Bacteriophage sp. isolate 3142_45871 partial genome

86. OP074880 1.3205-3610 MAG. Bacteriophage sp. isolate 2878_32958 partial genome

87. OP074799 1.59474-59624 MAG. Bacteriophage sp. isolate 2693_104805 partial genome

88. OP076296 1.77498-77848 MAG. Bacteriophage sp. isolate PF-HC117_31133 partial genome

89. OP076461 1.5258-5608 MAG. Bacteriophage sp. isolate 2063_3422 complete genome

90. OP076349 1.69360-69710 MAG. Bacteriophage sp. isolate 1939_50577 complete genome

91. OP073778 1.50008-50256 MAG. Bacteriophage sp. isolate 1248_77261 partial genome

92. OP073811 1.3320-3670 MAG. Bacteriophage sp. isolate 1297_49743 complete genome

93. OP073454 1.44281-44631 MAG. Bacteriophage sp. isolate 0772_17195 partial genome

94. OP073151 1.48741-48971 MAG. Bacteriophage sp. isolate 4326_113105 partial genome

95. OP072708 1.13153-13513 MAG. Bacteriophage sp. isolate 3870_48794 partial genome

96. OP072346 1.1476-1828 MAG. Bacteriophage sp. isolate 2564_12787 partial genome

97. OP072218 1.9902-9952 MAG. Bacteriophage sp. isolate 2121_105414 partial genome

98. OP073108 1.49841-49991 MAG. Bacteriophage sp. isolate 2023_98908 complete genome

99. OP031107 1.79134-79484 MAG. Bacteriophage sp. isolate 2023_91933 partial genome

100. OP031102 1.895091-89411 MAG. Bacteriophage sp. isolate 2010_53299 partial genome

Site # 355

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