LOCUS PaqCI\_12-part\_T7\_Assembly 39777 bp DNA circular UNA 03-AUG-2023

DEFINITION .

ACCESSION urn.local...1rw-gl13bms

VERSION urn.local...1rw-gl13bms

KEYWORDS .

SOURCE

ORGANISM .

FEATURES Location/Qualifiers

repeat\_region 1..160

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="Terminal Repeat"

regulatory 224

/regulatory\_class="promoter"

/note="E. coli promoter A0 (leftward)"

/standard\_name="E. coli promoter A0 (leftward) regulatory"

regulatory 405

/regulatory\_class="promoter"

/note="T7 promoter phiOL"

/standard\_name="T7 promoter phiOL regulatory"

regulatory 498

/regulatory\_class="promoter"

/note="E. coli promoter A1"

/standard\_name="E. coli promoter A1 regulatory"

regulatory 626

/regulatory\_class="promoter"

/note="E. coli promoter A2"

/standard\_name="E. coli promoter A2 regulatory"

regulatory 750

/regulatory\_class="promoter"

/note="E. coli promoter A3"

/standard\_name="E. coli promoter A3 regulatory"

misc\_structure 890

/note="RNase III site R0.3"

/standard\_name="RNase III site R0.3 misc structure"

mRNA 891..1468

/product="0.3 mRNA"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="0.3 mRNA"

CDS 925..1278

/note="unnamed protein product; gene 0.3, inhibits EcoB

and EcoK host restriction"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24384.1"

/db\_xref="InterPro:IPR014798"

/db\_xref="PDB:1S7Z"

/db\_xref="UniProtKB/Swiss-Prot:P03775"

/standard\_name="CDS"

CDS 1278..1433

/note="unnamed protein product; gene 0.4"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24385.1"

/db\_xref="UniProtKB/Swiss-Prot:P03776"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="unnamed protein product; gene 0.4 CDS"

misc\_structure 1468

/note="RNase III site R0.5"

/standard\_name="RNase III site R0.5 misc structure"

mRNA 1469..3138

/product="0.7 mRNA"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="0.7 mRNA"

CDS 1496..1639

/note="unnamed protein product; gene 0.5"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24386.1"

/db\_xref="UniProtKB/Swiss-Prot:P03777"

/standard\_name="unnamed protein product; gene 0.5 CDS"

regulatory 1514

/regulatory\_class="promoter"

/note="E. coli B promoter"

/standard\_name="E. coli B promoter regulatory"

CDS join(1636..1794,1796..1972)

/note="unnamed protein product; possible gene 0.6B"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24388.1"

/db\_xref="UniProtKB/Swiss-Prot:P03778"

/standard\_name="CDS"

CDS 1636..1797

/note="unnamed protein product; gene 0.6A"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24387.1"

/db\_xref="UniProtKB/Swiss-Prot:P03778"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="unnamed protein product; gene 0.6A CDS"

CDS 2021..3100

/note="unnamed protein product; gene 0.7, protein kinase"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24389.1"

/db\_xref="GOA:P00513"

/db\_xref="InterPro:IPR014374"

/db\_xref="UniProtKB/Swiss-Prot:P00513"

/standard\_name="CDS"

regulatory 3113

/regulatory\_class="promoter"

/note="E. coli C promoter"

/standard\_name="E. coli C promoter regulatory"

misc\_structure 3138

/note="RNase III site R1"

/standard\_name="RNase III site R1 misc structure"

mRNA 3139..5887

/product="1 mRNA"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="1 mRNA"

CDS 3171..5822

/note="unnamed protein product; gene 1, T7 RNA polymerase"

/codon\_start=1

/transl\_table=11

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/db\_xref="GOA:P00573"

/db\_xref="InterPro:IPR002092"

/db\_xref="PDB:1ARO"

/db\_xref="PDB:1CEZ"

/db\_xref="PDB:1H38"

/db\_xref="PDB:1MSW"

/db\_xref="PDB:1QLN"

/db\_xref="PDB:1S0V"

/db\_xref="PDB:1S76"

/db\_xref="PDB:1S77"

/db\_xref="PDB:2PI4"

/db\_xref="PDB:2PI5"

/db\_xref="PDB:3E2E"

/db\_xref="PDB:3E3J"

/db\_xref="PDB:4RNP"

/db\_xref="UniProtKB/Swiss-Prot:P00573"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

primer\_bind complement(3921..3946)

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F4-RP"

misc\_feature 3943..8777

/note="Geneious type: Concatenated sequence"

/standard\_name="PaqCI-12-F2"

misc\_feature 3943..3946

/note="Geneious type: ligation"

/standard\_name="Ligation"

primer\_bind 3943..3965

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F5-FP"

misc\_difference 3944

/standard\_name="3,944 A  T"

regulatory 5848

/regulatory\_class="promoter"

/note="T7 promoter phi1.1A"

/standard\_name="T7 promoter phi1.1A regulatory"

misc\_structure 5887

/note="RNase III site R1.1"

/standard\_name="RNase III site R1.1 misc structure"

mRNA 5888..6448

/product="1.1 mRNA"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="1.1 mRNA"

regulatory 5923

/regulatory\_class="promoter"

/note="T7 promoter phi1.1B"

/standard\_name="T7 promoter phi1.1B regulatory"

CDS 6007..6135

/note="unnamed protein product; gene 1.1"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24391.1"

/db\_xref="InterPro:IPR013232"

/db\_xref="UniProtKB/Swiss-Prot:P03779"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="unnamed protein product; gene 1.1 CDS"

CDS 6137..6394

/note="unnamed protein product; gene 1.2, inhibits host

dGTP triphosphohydrolase [8] /target for F plasmid

exclusion [11]"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24392.1"

/db\_xref="GOA:P03780"

/db\_xref="InterPro:IPR020147"

/db\_xref="UniProtKB/Swiss-Prot:P03780"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

regulatory 6409

/regulatory\_class="promoter"

/note="T7 promoter phi1.3"

/standard\_name="T7 promoter phi1.3 regulatory"

misc\_structure 6448

/note="RNase III site R1.3"

/standard\_name="RNase III site R1.3 misc structure"

mRNA 6449..7588

/product="1.3 mRNA"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="1.3 mRNA"

CDS 6475..7554

/note="unnamed protein product; gene 1.3, DNA ligase"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24393.1"

/db\_xref="GOA:P00969"

/db\_xref="InterPro:IPR012310"

/db\_xref="InterPro:IPR012340"

/db\_xref="InterPro:IPR016027"

/db\_xref="InterPro:IPR016059"

/db\_xref="InterPro:IPR016306"

/db\_xref="PDB:1A0I"

/db\_xref="UniProtKB/Swiss-Prot:P00969"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

regulatory 7588

/regulatory\_class="terminator"

/note="E. coli transcription terminator TE"

/standard\_name="regulatory"

CDS 7608..7763

/note="unnamed protein product; gene 1.4"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24394.1"

/db\_xref="UniProtKB/Swiss-Prot:P03791"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="unnamed protein product; gene 1.4 CDS"

regulatory 7778

/regulatory\_class="promoter"

/note="T7 promoter phi1.5"

/standard\_name="T7 promoter phi1.5 regulatory"

CDS 7791..7880

/note="unnamed protein product; gene 1.5"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24395.1"

/db\_xref="UniProtKB/Swiss-Prot:P03792"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="unnamed protein product; gene 1.5 CDS"

regulatory 7895

/regulatory\_class="promoter"

/note="T7 promoter phi1.6"

/standard\_name="T7 promoter phi1.6 regulatory"

CDS 7906..8166

/note="unnamed protein product; gene 1.6"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24396.1"

/db\_xref="InterPro:IPR018015"

/db\_xref="UniProtKB/Swiss-Prot:P03793"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="unnamed protein product; gene 1.6 CDS"

CDS 8166..8756

/note="unnamed protein product; gene 1.7"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24397.1"

/db\_xref="InterPro:IPR021739"

/db\_xref="UniProtKB/Swiss-Prot:P03781"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="unnamed protein product; gene 1.7 CDS"

CDS 8749..8895

/note="unnamed protein product; gene 1.8"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24398.1"

/db\_xref="UniProtKB/Swiss-Prot:P03794"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="unnamed protein product; gene 1.8 CDS"

primer\_bind complement(8751..8777)

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F8-RP"

misc\_feature 8774..9389

/note="Geneious type: Concatenated sequence"

/standard\_name="PaqCI-12-F3"

misc\_feature 8774..8777

/note="Geneious type: ligation"

/standard\_name="Ligation"

primer\_bind 8774..8793

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F9-FP"

misc\_difference 8775

/standard\_name="8,775 T  A"

CDS 8898..9092

/note="unnamed protein product; gene 2, inhibits E. coli

RNA polymerase"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24399.1"

/db\_xref="InterPro:IPR016412"

/db\_xref="PDB:2WNM"

/db\_xref="UniProtKB/Swiss-Prot:P03704"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

regulatory 9107

/regulatory\_class="promoter"

/note="T7 promoter phi2.5"

/standard\_name="T7 promoter phi2.5 regulatory"

CDS 9158..9856

/note="unnamed protein product; gene 2.5, single-stranded

DNA-binding protein"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24400.1"

/db\_xref="GOA:P03696"

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/db\_xref="InterPro:IPR016027"

/db\_xref="InterPro:IPR016411"

/db\_xref="PDB:1JE5"

/db\_xref="UniProtKB/Swiss-Prot:P03696"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

primer\_bind complement(9364..9389)

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F9-RP"

misc\_feature 9386..9955

/note="Geneious type: Concatenated sequence"

/standard\_name="PaqCI-12-F4"

misc\_feature 9386..9389

/note="Geneious type: ligation"

/standard\_name="Ligation"

primer\_bind 9386..9404

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F10-FP"

misc\_difference 9388

/standard\_name="9,388 A  T"

CDS 9857..10276

/note="unnamed protein product; gene 2.8"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24401.1"

/db\_xref="UniProtKB/Swiss-Prot:P03795"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="unnamed protein product; gene 2.8 CDS"

primer\_bind complement(9937..9955)

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F10-RP"

misc\_feature 9952..15582

/note="Geneious type: Concatenated sequence"

/standard\_name="PaqCI-12-F5"

misc\_feature 9952..9955

/note="Geneious type: ligation"

/standard\_name="Ligation"

primer\_bind 9952..9976

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F11-FP"

misc\_difference 9955

/standard\_name="9,955 G  C"

CDS 10257..10706

/note="unnamed protein product; gene 3, endonuclease"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24402.1"

/db\_xref="GOA:P00641"

/db\_xref="InterPro:IPR008029"

/db\_xref="InterPro:IPR011335"

/db\_xref="InterPro:IPR011578"

/db\_xref="PDB:1FZR"

/db\_xref="PDB:1M0D"

/db\_xref="PDB:1M0I"

/db\_xref="PDB:2PFJ"

/db\_xref="PDB:3CAE"

/db\_xref="UniProtKB/Swiss-Prot:P00641"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

CDS 10706..11161

/note="unnamed protein product; gene 3.5,

lysozyme/inhibits T7 RNA polymerase [7]"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24403.1"

/db\_xref="GOA:P00806"

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/db\_xref="InterPro:IPR015510"

/db\_xref="PDB:1ARO"

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/db\_xref="UniProtKB/Swiss-Prot:P00806"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

regulatory 11180

/regulatory\_class="promoter"

/note="T7 promoter phi3.8"

/standard\_name="T7 promoter phi3.8 regulatory"

misc\_structure 11203

/note="possible RNase III site R3.8"

/standard\_name="possible RNase III site R3.8 misc

structure"

CDS 11225..11590

/note="unnamed protein product; gene 3.8"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24404.1"

/db\_xref="GOA:P03797"

/db\_xref="InterPro:IPR002711"

/db\_xref="InterPro:IPR003615"

/db\_xref="UniProtKB/Swiss-Prot:P03797"

/standard\_name="unnamed protein product; gene 3.8 CDS"

CDS 11565..13265

/note="unnamed protein product; gene 4A, primase/helicase

[14,15]"

/codon\_start=1

/transl\_table=11

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/db\_xref="GOA:P03692"

/db\_xref="InterPro:IPR006171"

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/db\_xref="InterPro:IPR013237"

/db\_xref="PDB:1CR0"

/db\_xref="PDB:1CR1"

/db\_xref="PDB:1CR2"

/db\_xref="PDB:1CR4"

/db\_xref="PDB:1E0J"

/db\_xref="PDB:1E0K"

/db\_xref="PDB:1NUI"

/db\_xref="PDB:1Q57"

/db\_xref="UniProtKB/Swiss-Prot:P03692"

/standard\_name="CDS"

CDS 11635..11757

/note="unnamed protein product; gene 4.1"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24406.1"

/db\_xref="UniProtKB/Swiss-Prot:P03782"

/standard\_name="unnamed protein product; gene 4.1 CDS"

CDS 11754..13265

/note="unnamed protein product; gene 4B/helicase [14,15]"

/codon\_start=1

/transl\_table=11

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/db\_xref="GOA:P03692"

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/db\_xref="InterPro:IPR007694"

/db\_xref="InterPro:IPR013237"

/db\_xref="PDB:1CR0"

/db\_xref="PDB:1CR1"

/db\_xref="PDB:1CR2"

/db\_xref="PDB:1CR4"

/db\_xref="PDB:1E0J"

/db\_xref="PDB:1E0K"

/db\_xref="PDB:1NUI"

/db\_xref="PDB:1Q57"

/db\_xref="UniProtKB/Swiss-Prot:P03692"

/standard\_name="CDS"

regulatory 12671

/regulatory\_class="promoter"

/note="T7 promoter phi4c"

/standard\_name="T7 promoter phi4c regulatory"

CDS 12988..13326

/note="unnamed protein product; gene 4.2"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24408.1"

/db\_xref="UniProtKB/Swiss-Prot:P03783"

/standard\_name="unnamed protein product; gene 4.2 CDS"

regulatory 13341

/regulatory\_class="promoter"

/note="T7 promoter phi4.3"

/standard\_name="T7 promoter phi4.3 regulatory"

CDS 13352..13564

/note="unnamed protein product; gene 4.3"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24409.1"

/db\_xref="UniProtKB/Swiss-Prot:P03784"

/standard\_name="unnamed protein product; gene 4.3 CDS"

CDS 13584..13853

/note="unnamed protein product; gene 4.5"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24410.1"

/db\_xref="UniProtKB/Swiss-Prot:P03785"

/standard\_name="unnamed protein product; gene 4.5 CDS"

misc\_structure 13892

/note="RNase III site R4.7"

/standard\_name="RNase III site R4.7 misc structure"

regulatory 13915

/regulatory\_class="promoter"

/note="T7 promoter phi4.7"

/standard\_name="T7 promoter phi4.7 regulatory"

CDS 13927..14334

/note="unnamed protein product; gene 4.7"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24411.1"

/db\_xref="UniProtKB/Swiss-Prot:P03786"

/standard\_name="unnamed protein product; gene 4.7 CDS"

CDS 14353..16467

/note="unnamed protein product; gene 5, DNA polymerase"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24412.1"

/db\_xref="GOA:P00581"

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/db\_xref="InterPro:IPR002298"

/db\_xref="InterPro:IPR012337"

/db\_xref="InterPro:IPR019760"

/db\_xref="PDB:1SKR"

/db\_xref="PDB:1SKS"

/db\_xref="PDB:1SKW"

/db\_xref="PDB:1SL0"

/db\_xref="PDB:1SL1"

/db\_xref="PDB:1SL2"

/db\_xref="PDB:1T7P"

/db\_xref="PDB:1T8E"

/db\_xref="PDB:1TK0"

/db\_xref="PDB:1TK5"

/db\_xref="PDB:1TK8"

/db\_xref="PDB:1TKD"

/db\_xref="PDB:1X9M"

/db\_xref="PDB:1X9S"

/db\_xref="PDB:1X9W"

/db\_xref="PDB:1ZYQ"

/db\_xref="PDB:2AJQ"

/db\_xref="UniProtKB/Swiss-Prot:P00581"

/standard\_name="CDS"

primer\_bind complement(15555..15582)

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F14-RP"

misc\_feature 15579..17734

/note="Geneious type: Concatenated sequence"

/standard\_name="PaqCI-12-F6"

misc\_feature 15579..15582

/note="Geneious type: ligation"

/standard\_name="Ligation"

primer\_bind 15579..15601

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F15-FP"

CDS 16483..16839

/note="unnamed protein product; gene 5.3"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24413.1"

/db\_xref="UniProtKB/Swiss-Prot:P03798"

/standard\_name="unnamed protein product; gene 5.3 CDS"

CDS join(16851..17147,17147..17359)

/note="unnamed protein product; possible gene 5.5-5.7"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24415.1"

/db\_xref="InterPro:IPR022611"

/db\_xref="UniProtKB/Swiss-Prot:P03787"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

CDS 16851..17150

/note="unnamed protein product; gene 5.5, permits growth

on lambda lysogens [13] /binds host nucleoid protein H-NS

[16]"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24414.1"

/db\_xref="InterPro:IPR022611"

/db\_xref="UniProtKB/Swiss-Prot:P03787"

/standard\_name="CDS"

CDS 17150..17359

/note="unnamed protein product; gene 5.7"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24416.1"

/db\_xref="InterPro:IPR022611"

/db\_xref="UniProtKB/Swiss-Prot:P03787"

/standard\_name="unnamed protein product; gene 5.7 CDS"

CDS 17359..17517

/note="unnamed protein product; gene 5.9, inhibits host

recBCD nuclease [13]"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24417.1"

/db\_xref="UniProtKB/Swiss-Prot:P20406"

/standard\_name="CDS"

CDS 17504..18406

/note="unnamed protein product; gene 6, exonuclease"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24418.1"

/db\_xref="GOA:P00638"

/db\_xref="InterPro:IPR020046"

/db\_xref="UniProtKB/Swiss-Prot:P00638"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

primer\_bind complement(17716..17734)

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F16-RP"

misc\_difference 17731

/standard\_name="17,731 A  T"

misc\_feature 17731..23298

/note="Geneious type: Concatenated sequence"

/standard\_name="PaqCI-12-F7"

misc\_feature 17731..17734

/note="Geneious type: ligation"

/standard\_name="Ligation"

primer\_bind 17731..17751

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F17-FP"

CDS 18394..18507

/note="unnamed protein product; gene 6.3"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24419.1"

/db\_xref="UniProtKB/Swiss-Prot:P03799"

/standard\_name="unnamed protein product; gene 6.3 CDS"

regulatory 18545

/regulatory\_class="promoter"

/note="T7 promoter phi6.5"

/standard\_name="T7 promoter phi6.5 regulatory"

misc\_structure 18563

/note="RNase III site R6.5"

/standard\_name="RNase III site R6.5 misc structure"

CDS 18605..18859

/note="unnamed protein product; gene 6.5"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24420.1"

/db\_xref="InterPro:IPR020121"

/db\_xref="UniProtKB/Swiss-Prot:P03800"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="unnamed protein product; gene 6.5 CDS"

CDS 18864..19130

/note="unnamed protein product; gene 6.7"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24421.1"

/db\_xref="InterPro:IPR020134"

/db\_xref="UniProtKB/Swiss-Prot:P03801"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="unnamed protein product; gene 6.7 CDS"

CDS 19130..19531

/note="unnamed protein product; gene 7, host range"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24422.1"

/db\_xref="UniProtKB/Swiss-Prot:P03750"

/standard\_name="CDS"

CDS 19535..19834

/note="unnamed protein product; gene 7.3, host range"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24423.1"

/db\_xref="UniProtKB/Swiss-Prot:P03751"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

CDS 19848..20240

/note="unnamed protein product; gene 7.7"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24424.1"

/db\_xref="InterPro:IPR003615"

/db\_xref="UniProtKB/Swiss-Prot:P03796"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="unnamed protein product; gene 7.7 CDS"

CDS 20240..21850

/note="unnamed protein product; gene 8, head-tail

connector protein"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24425.1"

/db\_xref="GOA:P03728"

/db\_xref="InterPro:IPR020991"

/db\_xref="UniProtKB/Swiss-Prot:P03728"

/standard\_name="CDS"

regulatory 21865

/regulatory\_class="promoter"

/note="T7 promoter phi9"

/standard\_name="T7 promoter phi9 regulatory"

CDS 21950..22873

/note="unnamed protein product; gene 9, scaffolding

protein"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24426.1"

/db\_xref="GOA:P03716"

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/db\_xref="UniProtKB/Swiss-Prot:P03716"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

regulatory 22904

/regulatory\_class="promoter"

/note="T7 promoter phi10"

/standard\_name="T7 promoter phi10 regulatory"

CDS join(22967..23989,23989..24162)

/note="unnamed protein product; gene 10B, minor capsid

protein [12]"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24428.1"

/db\_xref="GOA:P19727"

/db\_xref="UniProtKB/Swiss-Prot:P19727"

/standard\_name="CDS"

CDS 22967..24004

/note="unnamed protein product; gene 10A, major capsid

protein"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24427.1"

/db\_xref="GOA:P19726"

/db\_xref="UniProtKB/Swiss-Prot:P19726"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

primer\_bind complement(23269..23298)

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F21-RP"

misc\_feature 23295..26636

/note="Geneious type: Concatenated sequence"

/standard\_name="PaqCI-12-F8"

misc\_feature 23295..23298

/note="Geneious type: ligation"

/standard\_name="Ligation"

primer\_bind 23295..23314

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F22-FP"

regulatory 24210

/regulatory\_class="terminator"

/note="T7 transcription terminator Tphi"

/standard\_name="T7 transcription terminator Tphi

regulatory"

CDS 24228..24818

/note="unnamed protein product; gene 11, tail protein"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24429.1"

/db\_xref="UniProtKB/Swiss-Prot:P03746"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

CDS 24842..27226

/note="unnamed protein product; gene 12, tail protein"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24430.1"

/db\_xref="UniProtKB/Swiss-Prot:P03747"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

primer\_bind complement(26611..26636)

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F24-RP"

misc\_feature 26633..29953

/note="Geneious type: Concatenated sequence"

/standard\_name="PaqCI-12-F9"

misc\_feature 26633..26636

/note="Geneious type: ligation"

/standard\_name="Ligation"

primer\_bind 26633..26656

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F25-FP"

regulatory 27274

/regulatory\_class="promoter"

/note="T7 promoter phi13"

/standard\_name="T7 promoter phi13 regulatory"

misc\_structure 27281

/note="possible RNase III site R13"

/standard\_name="possible RNase III site R13 misc

structure"

CDS 27307..27723

/note="unnamed protein product; gene 13, internal virion

protein"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24431.1"

/db\_xref="InterPro:IPR020335"

/db\_xref="UniProtKB/Swiss-Prot:P03723"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

CDS 27728..28318

/note="unnamed protein product; gene 14, internal virion

protein"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24432.1"

/db\_xref="UniProtKB/Swiss-Prot:P03724"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

CDS 28325..30568

/note="unnamed protein product; gene 15, internal virion

protein"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24433.1"

/db\_xref="UniProtKB/Swiss-Prot:P03725"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

primer\_bind complement(29933..29953)

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F27-RP"

misc\_feature 29950..33267

/note="Geneious type: Concatenated sequence"

/standard\_name="PaqCI-12-F10"

misc\_feature 29950..29953

/note="Geneious type: ligation"

/standard\_name="Ligation"

primer\_bind 29950..29971

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F28-FP"

CDS 30595..34551

/note="unnamed protein product; gene 16, internal virion

protein"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24434.1"

/db\_xref="GOA:P03726"

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/db\_xref="UniProtKB/Swiss-Prot:P03726"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

primer\_bind complement(33245..33267)

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F30-RP"

misc\_feature 33264..36587

/note="Geneious type: Concatenated sequence"

/standard\_name="PaqCI-12-F11"

misc\_feature 33264..33267

/note="Geneious type: ligation"

/standard\_name="Ligation"

primer\_bind 33264..33285

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F31-FP"

regulatory 34566

/regulatory\_class="promoter"

/note="T7 promoter phi17"

/standard\_name="T7 promoter phi17 regulatory"

CDS 34624..36285

/note="unnamed protein product; gene 17, tail fiber

protein"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24435.1"

/db\_xref="InterPro:IPR005604"

/db\_xref="InterPro:IPR022246"

/db\_xref="UniProtKB/Swiss-Prot:P03748"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

CDS 36344..36547

/note="unnamed protein product; gene 17.5, lysis protein

[17]"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24436.1"

/db\_xref="GOA:P03802"

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/db\_xref="UniProtKB/Swiss-Prot:P03802"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

primer\_bind complement(36549..36587)

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F33-RP"

CDS 36553..36822

/note="unnamed protein product; gene 18, DNA maturation

protein"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24437.1"

/db\_xref="GOA:P03693"

/db\_xref="UniProtKB/Swiss-Prot:P03693"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

misc\_feature 36584..39420

/note="Geneious type: Concatenated sequence"

/standard\_name="PaqCI-12-F12"

misc\_feature 36584..36587

/note="Geneious type: ligation"

/standard\_name="Ligation"

primer\_bind 36584..36610

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F34-FP"

regulatory 36836

/regulatory\_class="promoter"

/note="E. coli promoter E[6]"

/standard\_name="E. coli promoter E[6] regulatory"

misc\_structure 36856

/note="RNase III site R18.5"

/standard\_name="RNase III site R18.5 misc structure"

CDS 36917..37348

/note="unnamed protein product; gene 18.5, homologous to

lambda Rz lysis protein [10]"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24438.1"

/db\_xref="GOA:P03803"

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/db\_xref="UniProtKB/Swiss-Prot:P03803"

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

CDS 37032..37283

/note="unnamed protein product; gene 18.7"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24439.1"

/db\_xref="InterPro:IPR020130"

/db\_xref="UniProtKB/Swiss-Prot:P03788"

/standard\_name="unnamed protein product; gene 18.7 CDS"

CDS 37370..39130

/note="unnamed protein product; gene 19, DNA maturation

protein"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24440.1"

/db\_xref="GOA:P03694"

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/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="CDS"

CDS 38016..38273

/note="unnamed protein product; gene 19.2"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24441.1"

/db\_xref="InterPro:IPR020148"

/db\_xref="UniProtKB/Swiss-Prot:P03789"

/standard\_name="unnamed protein product; gene 19.2 CDS"

CDS 38553..38726

/note="unnamed protein product; gene 19.3"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24442.1"

/db\_xref="UniProtKB/Swiss-Prot:P03790"

/standard\_name="unnamed protein product; gene 19.3 CDS"

regulatory 39229

/regulatory\_class="promoter"

/note="T7 promoter phiOR"

/standard\_name="T7 promoter phiOR regulatory"

primer\_bind complement(39389..39420)

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F36-RP"

CDS 39389..39538

/note="unnamed protein product; gene 19.5"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA24443.1"

/db\_xref="UniProtKB/Swiss-Prot:P03804"

/standard\_name="unnamed protein product; gene 19.5 CDS"

misc\_feature 39417..3946

/note="Geneious type: Concatenated sequence"

/standard\_name="PaqCI-12-F1"

misc\_feature 39417..39420

/note="Geneious type: ligation"

/standard\_name="Ligation"

primer\_bind 39417..39443

/note="Derived using Geneious Prime 2023.0.4 'Annotate

from Database' based on nucleotide similarity"

/standard\_name="F1-FP"

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