

Ampl Contig 1

LOCUS 1A_1

DEFINITION

FEATURES

gene

Location/Qualifiers

complement(181..2049)

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/sscore="10.91"

/locus_tag="1A_01"

/conf="99.99"

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complement(181..2049)

/rbs_motif="AGGA"

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CDS

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gene	
CDS	
gene	

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7621	tcaaatgaat	ctgacaagag	acgattagta	tctggataat	ttccttctag	taaacgtgtg
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9361	ttcggcagtt	atgtatttga	ttcgtgcttg	gggattatca	tgtaagacct	tattaccaat
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11461 tgtccttcaa tattgactag ggcaccacca gagttaccag tgggatcctc tagagtcgac
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11581 gtcatagct

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Ampl contig 2

LOCUS 1A_2

DEFINITION

FEATURES

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gene	complement(430..1758) /rbs_motif="GGAG/GAGG" /uscore="4.62" /rscore="6.9" /sscore="7.88" /locus_tag="1A_13" /conf="100.0" /ID="1A_13" /cscore="166.07" /partial=0 /tscore="-3.65" /gc_cont="0.414" /rbs_spacer="5-10bp" /start_type="TTG" /score=174.0 /codon_start=1
CDS	complement(430..1758) /rbs_motif="GGAG/GAGG" /uscore="4.62" /rscore="6.9" /sscore="7.88" /locus_tag="1A_13" /conf="100.0" /ID="1A_13"

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/conf="82.35"
/ID="1A_14"
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/sscore="-10.51"
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/partial=0
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ORIGIN

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2521	cgtaggaagt	ggtttctaat	cgttgcttgc	gtgcgtccgt	cgaggattgt	gatgactttt
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2641	cagctcatat	tctcaggcag	ccaattccag	tcggttttta	attggaactc	atttagcttg
2701	cgactgacgg	ttgaggtaga	gacggcaagg	cgcttgga	tgctcggtcat	agactgtttt
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Amp3

LOCUS 3A

DEFINITION

FEATURES

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Location/Qualifiers

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CDS

284..1903

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gene	<pre> complement(3587..3943) /rbs_motif="GGAG/GAGG" /uscore="-1.98" /rscore="6.9" /sscore="2.53" /locus_tag="3A_07" /conf="100.0" /ID="3A_07" /cscore="41.29" /partial=0 /tscore="-3.65" /gc_cont="0.367" /rbs_spacer="5-10bp" /product="hypothetical protein" /start_type="TTG" /score=43.8 /codon_start=1 </pre>
gene	<pre> complement(3936..4037) /rbs_motif="GGAG/GAGG" /uscore="1.38" /rscore="2.73" /sscore="5.33" /locus_tag="3A_08" /conf="90.9" /ID="3A_08" /cscore="4.68" </pre>

	<pre> /partial=0 /tscore="1.21" /gc_cont="0.422" /rbs_spacer="5-10bp" /start_type="ATG" /score=10.0 /codon_start=1 complement(3936..4037) /rbs_motif="GGAG/GAGG" /uscore="1.38" /rscore="2.73" /sscore="5.33" /locus_tag="3A_08" /conf="90.9" /ID="3A_08" /cscore="4.68" /partial=0 /tscore="1.21" /gc_cont="0.422" /rbs_spacer="5-10bp" /product="hypothetical protein" /start_type="ATG" /score=10.0 /codon_start=1 </pre>
CDS	
	<pre> complement(4132..4368) /rbs_motif="None" /uscore="-3.5" /rscore="-3.49" /sscore="-4.12" /locus_tag="3A_09" /conf="79.71" /ID="3A_09" /cscore="10.07" /partial=0 /tscore="2.87" /gc_cont="0.405" /rbs_spacer="None" /start_type="ATG" /score=6.0 /codon_start=1 </pre>
gene	
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CDS	
	<pre> complement(4438..4770) /rbs_motif="AGGAG" /uscore="5.99" /rscore="11.88" </pre>
gene	

	/sscore="20.28" /locus_tag="3A_10" /conf="100.0" /ID="3A_10" /cscore="44.62" /partial=0 /tscore="3.07" /gc_cont="0.429" /rbs_spacer="5-10bp" /start_type="ATG" /score=64.9 /codon_start=1 complement(4438..4770) /rbs_motif="AGGAG" /uscore="5.99" /rscore="11.88" /sscore="20.28" /locus_tag="3A_10" /conf="100.0" /ID="3A_10" /cscore="44.62" /partial=0 /tscore="3.07" /gc_cont="0.429" /rbs_spacer="5-10bp" /product="hypothetical protein X839_01085" /start_type="ATG" /score=64.9 /codon_start=1
CDS	
	complement(4951..5823) /rbs_motif="None" /uscore="-3.3" /rscore="-3.27" /sscore="-4.15" /locus_tag="3A_11" /conf="100.0" /ID="3A_11" /cscore="84.66" /partial=0 /tscore="3.07" /gc_cont="0.431" /rbs_spacer="None" /start_type="ATG" /score=80.5 /codon_start=1
gene	
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CDS	

gene	/codon_start=1 5889..8216 /rbs_motif="None" /uscore="3.14" /rscore="-3.27" /sscore="2.94" /locus_tag="3A_12" /conf="99.99" /ID="3A_12" /cscore="394.79" /partial=0 /tscore="3.07" /gc_cont="0.427" /rbs_spacer="None" /start_type="ATG" /score=397.7
CDS	/codon_start=1 5889..8216 /rbs_motif="None" /uscore="3.14" /rscore="-3.27" /sscore="2.94" /locus_tag="3A_12" /conf="99.99" /ID="3A_12" /cscore="394.79" /partial=0 /tscore="3.07" /gc_cont="0.427" /rbs_spacer="None" /product="penicillin-binding protein 2A" /start_type="ATG" /score=397.7
gene	/codon_start=1 8426..8602 /rbs_motif="AGGAG" /uscore="0.01" /rscore="8.27" /sscore="2.63" /locus_tag="3A_13" /conf="69.09" /ID="3A_13" /cscore="0.87" /partial=0 /tscore="-4.99" /gc_cont="0.401" /rbs_spacer="5-10bp" /start_type="GTG" /score=3.5
CDS	/codon_start=1 8426..8602 /rbs_motif="AGGAG" /uscore="0.01" /rscore="8.27" /sscore="2.63" /locus_tag="3A_13" /conf="69.09" /ID="3A_13" /cscore="0.87" /partial=0 /tscore="-4.99"

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gene 8799..9338
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/rscore="7.92"
/sscore="13.41"
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gene 9637..9948
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/rscore="-3.27"
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/conf="95.19"
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/cscore="17.54"
/partial=0
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	<pre> /conf="95.19" /ID="3A_15" /cscore="17.54" /partial=0 /tscore="3.07" /gc_cont="0.442" /rbs_spacer="None" /product="phosphoesterase" /start_type="ATG" /score=13.0 /codon_start=1 </pre>
gene	<pre> complement(10080..10376) /rbs_motif="None" /uscore="-5.55" /rscore="-3.27" /sscore="-5.75" /locus_tag="3A_16" /conf="99.93" /ID="3A_16" /cscore="37.09" /partial=0 /tscore="3.07" /gc_cont="0.407" /rbs_spacer="None" /start_type="ATG" /score=31.3 /codon_start=1 </pre>
CDS	<pre> complement(10080..10376) /rbs_motif="None" /uscore="-5.55" /rscore="-3.27" /sscore="-5.75" /locus_tag="3A_16" /conf="99.93" /ID="3A_16" /cscore="37.09" /partial=0 /tscore="3.07" /gc_cont="0.407" /rbs_spacer="None" /product="haloacid dehalogenase" /start_type="ATG" /score=31.3 /codon_start=1 </pre>
gene	<pre> complement(10336..10575) /rbs_motif="None" /uscore="2.17" /rscore="-3.45" /sscore="-4.94" /locus_tag="3A_17" /conf="77.97" /ID="3A_17" /cscore="10.44" /partial=0 /tscore="-3.67" /gc_cont="0.408" /rbs_spacer="None" /start_type="GTG" /score=5.5 /codon_start=1 </pre>
CDS	<pre> complement(10336..10575) </pre>

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gene complement(10674..10910)
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/locus_tag="3A_18"
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/ID="3A_18"
/cscore="16.5"
/partial=0
/tscore="2.87"
/gc_cont="0.401"
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/score=17.0
CDS /codon_start=1
complement(10674..10910)
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/start_type="ATG"
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gene complement(10885..11343)
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/uscore="-2.29"
/rscore="-3.27"
/sscore="4.35"
/locus_tag="3A_19"
/conf="99.99"
/ID="3A_19"
/cscore="34.83"
/partial=0
/tscore="3.07"
/gc_cont="0.379"

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	<pre> /rbs_spacer="None" /start_type="ATG" /score=39.2 /codon_start=1 </pre>
CDS	<pre> complement(10885..11343) /rbs_motif="None" /uscore="-2.29" /rscore="-3.27" /sscore="4.35" /locus_tag="3A_19" /conf="99.99" /ID="3A_19" /cscore="34.83" /partial=0 /tscore="3.07" /gc_cont="0.379" /rbs_spacer="None" /product="cytochrome C" /start_type="ATG" /score=39.2 /codon_start=1 </pre>
gene	<pre> complement(11343..11651) /rbs_motif="AGxAGG/AGGxGG" /uscore="4.39" /rscore="3.21" /sscore="9.52" /locus_tag="3A_20" /conf="84.17" /ID="3A_20" /cscore="-2.25" /partial=0 /tscore="3.07" /gc_cont="0.398" /rbs_spacer="5-10bp" /start_type="ATG" /score=7.3 /codon_start=1 </pre>
CDS	<pre> complement(11343..11651) /rbs_motif="AGxAGG/AGGxGG" /uscore="4.39" /rscore="3.21" /sscore="9.52" /locus_tag="3A_20" /conf="84.17" /ID="3A_20" /cscore="-2.25" /partial=0 /tscore="3.07" /gc_cont="0.398" /rbs_spacer="5-10bp" /product="hypothetical protein Y018_01275" /start_type="ATG" /score=7.3 /codon_start=1 </pre>
gene	<pre> 11825..14326 /rbs_motif="GGAG/GAGG" /uscore="6.25" /rscore="6.9" /sscore="16.22" /locus_tag="3A_21" /conf="99.99" </pre>

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CDS	
	<pre> 14668..14895 /rbs_motif="GGA/GAG/AGG" /uscore="0.79" /rscore="0.82" /sscore="-2.91" /locus_tag="3A_22" /conf="91.12" /ID="3A_22" /cscore="13.04" /partial=0 /tscore="-3.86" /gc_cont="0.311" /rbs_spacer="5-10bp" /start_type="GTG" /score=10.1 /codon_start=1 </pre>
gene	
	<pre> 14668..14895 /rbs_motif="GGA/GAG/AGG" /uscore="0.79" /rscore="0.82" /sscore="-2.91" /locus_tag="3A_22" /conf="91.12" /ID="3A_22" /cscore="13.04" /partial=0 /tscore="-3.86" /gc_cont="0.311" /rbs_spacer="5-10bp" /product="transcriptional regulator" /start_type="GTG" /score=10.1 /codon_start=1 </pre>
CDS	
	<pre> 15025..15117 /rbs_motif="GGAG/GAGG" </pre>
gene	

	/uscore="0.37" /rscore="2.49" /sscore="3.96" /locus_tag="3A_23" /conf="89.21" /ID="3A_23" /cscore="5.22" /partial=0 /tscore="1.1" /gc_cont="0.301" /rbs_spacer="5-10bp" /start_type="ATG" /score=9.2 /codon_start=1 15025..15117 /rbs_motif="GGAG/GAGG" /uscore="0.37" /rscore="2.49" /sscore="3.96" /locus_tag="3A_23" /conf="89.21" /ID="3A_23" /cscore="5.22" /partial=0 /tscore="1.1" /gc_cont="0.301" /rbs_spacer="5-10bp" /product="hypothetical protein Y018_01295" /start_type="ATG" /score=9.2 /codon_start=1
CDS	15127..15549 /rbs_motif="GGA/GAG/AGG" /uscore="1.07" /rscore="0.91" /sscore="6.23" /locus_tag="3A_24" /conf="99.56" /ID="3A_24" /cscore="17.31" /partial=0 /tscore="3.07" /gc_cont="0.338" /rbs_spacer="5-10bp" /start_type="ATG" /score=23.5 /codon_start=1
gene	15127..15549 /rbs_motif="GGA/GAG/AGG" /uscore="1.07" /rscore="0.91" /sscore="6.23" /locus_tag="3A_24" /conf="99.56" /ID="3A_24" /cscore="17.31" /partial=0 /tscore="3.07" /gc_cont="0.338" /rbs_spacer="5-10bp" /start_type="ATG" /score=23.5 /codon_start=1
CDS	15127..15549 /rbs_motif="GGA/GAG/AGG" /uscore="1.07" /rscore="0.91" /sscore="6.23" /locus_tag="3A_24" /conf="99.56" /ID="3A_24" /cscore="17.31" /partial=0 /tscore="3.07" /gc_cont="0.338" /rbs_spacer="5-10bp" /product="acyl-CoA thioesterase"

gene	/start_type="ATG" /score=23.5 /codon_start=1 15500..16123 /rbs_motif="GGAG/GAGG" /uscore="-0.87" /rscore="6.9" /sscore="9.1" /locus_tag="3A_25" /conf="99.91" /ID="3A_25" /cscore="21.4" /partial=0 /tscore="3.07" /gc_cont="0.362" /rbs_spacer="5-10bp" /start_type="ATG" /score=30.5 /codon_start=1 15500..16123 /rbs_motif="GGAG/GAGG" /uscore="-0.87" /rscore="6.9" /sscore="9.1" /locus_tag="3A_25" /conf="99.91" /ID="3A_25" /cscore="21.4" /partial=0 /tscore="3.07" /gc_cont="0.362" /rbs_spacer="5-10bp" /product="acyl-CoA thioesterase" /start_type="ATG" /score=30.5 /codon_start=1 16553..18007 /rbs_motif="GGAGG" /uscore="4.71" /rscore="14.48" /sscore="14.89" /locus_tag="3A_26" /conf="99.99" /ID="3A_26" /cscore="260.46" /partial=0 /tscore="-3.65" /gc_cont="0.424" /rbs_spacer="5-10bp" /start_type="TTG" /score=275.4 /codon_start=1 16553..18007 /rbs_motif="GGAGG" /uscore="4.71" /rscore="14.48" /sscore="14.89" /locus_tag="3A_26" /conf="99.99" /ID="3A_26" /cscore="260.46"
CDS	
gene	
CDS	

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gene	
CDS	
gene	
CDS	

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gene	19398..20735 /rbs_motif="GGAGG" /uscore="0.57" /rscore="14.48" /sscore="18.11" /locus_tag="3A_29" /conf="99.99" /ID="3A_29" /cscore="240.78" /partial=0 /tscore="3.07" /gc_cont="0.407" /rbs_spacer="5-10bp" /start_type="ATG" /score=258.9 /codon_start=1
CDS	19398..20735 /rbs_motif="GGAGG" /uscore="0.57" /rscore="14.48" /sscore="18.11" /locus_tag="3A_29" /conf="99.99" /ID="3A_29" /cscore="240.78" /partial=0 /tscore="3.07" /gc_cont="0.407" /rbs_spacer="5-10bp" /product="aminopeptidase C" /start_type="ATG" /score=258.9 /codon_start=1
gene	20865..22193 /rbs_motif="GGAG/GAGG" /uscore="4.62" /rscore="6.9" /sscore="7.88" /locus_tag="3A_30" /conf="100.0" /ID="3A_30" /cscore="166.14" /partial=0 /tscore="-3.65" /gc_cont="0.413" /rbs_spacer="5-10bp" /start_type="TTG" /score=174.0

CDS	/codon_start=1 20865..22193 /rbs_motif="GGAG/GAGG" /uscore="4.62" /rscore="6.9" /sscore="7.88" /locus_tag="3A_30" /conf="100.0" /ID="3A_30" /cscore="166.14" /partial=0 /tscore="-3.65" /gc_cont="0.413" /rbs_spacer="5-10bp" /product="transposase" /start_type="TTG" /score=174.0
gene	/codon_start=1 complement(22269..24599) /rbs_motif="AGxAGG/AGGxGG" /uscore="2.45" /rscore="3.21" /sscore="10.0" /locus_tag="3A_31" /conf="99.99" /ID="3A_31" /cscore="400.21" /partial=0 /tscore="3.07" /gc_cont="0.395" /rbs_spacer="5-10bp" /start_type="ATG" /score=410.2
CDS	/codon_start=1 complement(22269..24599) /rbs_motif="AGxAGG/AGGxGG" /uscore="2.45" /rscore="3.21" /sscore="10.0" /locus_tag="3A_31" /conf="99.99" /ID="3A_31" /cscore="400.21" /partial=0 /tscore="3.07" /gc_cont="0.395" /rbs_spacer="5-10bp" /product="penicillin-binding protein 1A" /start_type="ATG" /score=410.2
gene	/codon_start=1 complement(24599..25108) /rbs_motif="None" /uscore="0.57" /rscore="-3.27" /sscore="-0.28" /locus_tag="3A_32" /conf="100.0" /ID="3A_32" /cscore="52.95" /partial=0

	/tscore="3.07" /gc_cont="0.38" /rbs_spacer="None" /start_type="ATG" /score=52.7 /codon_start=1 complement(24599..25108) /rbs_motif="None" /uscore="0.57" /rscore="-3.27" /sscore="-0.28" /locus_tag="3A_32" /conf="100.0" /ID="3A_32" /cscore="52.95" /partial=0 /tscore="3.07" /gc_cont="0.38" /rbs_spacer="None" /product="Holliday junction resolvase" /start_type="ATG" /score=52.7 /codon_start=1
CDS	
gene	25273..25395 /rbs_motif="GGAG/GAGG" /uscore="-3.72" /rscore="3.31" /sscore="1.07" /locus_tag="3A_33" /conf="86.94" /ID="3A_33" /cscore="7.18" /partial=0 /tscore="1.47" /gc_cont="0.333" /rbs_spacer="5-10bp" /start_type="ATG" /score=8.2 /codon_start=1
CDS	25273..25395 /rbs_motif="GGAG/GAGG" /uscore="-3.72" /rscore="3.31" /sscore="1.07" /locus_tag="3A_33" /conf="86.94" /ID="3A_33" /cscore="7.18" /partial=0 /tscore="1.47" /gc_cont="0.333" /rbs_spacer="5-10bp" /product="hypothetical protein" /start_type="ATG" /score=8.2 /codon_start=1
gene	25409..25789 /rbs_motif="GGA/GAG/AGG" /uscore="-2.94" /rscore="0.91" /sscore="2.17"

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Amp6

LOCUS

6A

DEFINITION

FEATURES

gene

Location/Qualifiers

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CDS

87..656

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CDS

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19621	agcttctttc	ctatatgtag	aaggttttca	atagtgata	atcttctaaa	gatttttgta
19681	atcaagctag	atgcaaaatg	tgatcaataa	ttcctacgag	tttacttgac	actaataaaa
19741	atgcttttgt	ctcaacaaaa	atctaaaacg	agaaggttaa	aacttatgac	aagccaaaca
19801	ccatccctct	cttttgaagt	ctttccacct	aatccagccg	taggcaataa	gaaaatcttg
19861	cttgcccttg	atgacatgaa	aggatcggca	ccccatttta	tcagtgtaac	agctagtaat
19921	aacaaatata	atatcaaaga	gacaacggtt	cctttggcag	accatattca	aatgacctg
19981	gctattccta	ctattgctca	ccttccagca	atctatttga	gcaaagaaaa	ggtagctgat
20041	actttgagag	aattagatgc	tgttggagta	aatcgatatcc	tggcacttcg	tggcgacatc
20101	attcctgggg	tcgaaccttt	aaaagacttc	agatatgcaa	ctgatttgat	tgagtttatc

20161	aaggcagaag	ctcctaactt	tgatatcatt	ggtgcttggt	atcctgaagg	tcatcctgat
20221	tcaccaaadc	aaatctctga	tattcaaaat	cttaagaaga	aagtagatgc	aggttggtca
20281	agtcttgtaa	cccaactctt	ctttgataat	gaacgcttct	acgatttcca	agataaatgt
20341	actcttgctg	gcattaatgt	gcctatctat	gctggtatta	tgcctatctt	gaatcgtaac
20401	caagccctac	gtttacttaa	gacgtgtgaa	aatatccatt	tgccacgtaa	attccgtgct
20461	atcttggtata	agtatgagca	tgattctgaa	tctctgagag	ctgccgggtct	agcttatgct
20521	gttgacccaa	tcgtggattt	ggttacgcaa	gacgttgctg	gagttcacct	ttatacgatg
20581	aataatgcag	agactgcacg	tcatatctac	gaagctactc	actccttggt	taagcatcat
20641	tcacaagtcg	gcgcactgta	attgaataat	agaaaaacca	cctatatatt	taatctatag
20701	gtgggtttctt	ggtgtagcag	cgaaagattg	taattactta	tatggggcat	tattatcatg
20761	tatcaaaaaa	gacctagagc	ttagctctaa	gtcaaaaagta	ttattcacct	acaaaagcat
20821	tgattttctgc	ttcgatgtta	gcaatctttt	tcttttagcat	ccgcttcagt	ttctccaact
20881	gttgcaatgt	aaaatttgat	ttttggttct	gtacctgaag	gacgaacggc	aaacctgaa
20941	tcatcagcca	agatgtatct	caaacgttta	cttgaggagg	ttgtcaattt	ttctacgccg
21001	tcagcagtag	tagctgtttg	ttccaagaag	tcttctgttt	tagcaatata	agtgttggtg
21061	aattgttttag	gagcattgag	acggaatttg	tccatgattt	tcttgatttc	tgagcacca
21121	tcaaacacctg	aaagcgtaac	tgaaattgtc	ttttctgaga	agtaaccata	ttgtttgtag
21181	atttcttcga	taccatctgc	caatgtcata	ccacgtgaac	ggtagtatgc	agcaatttct
21241	gcaacgataa	gaacggcttg	gatagcgtct	ttatcgcgta	caaattggtt	gatgaggtaa
21301	ccgaagcttt	cttcaaaacc	aaacatgtaa	gtgtaattgt	gttggtgttc	aaattcatga
21361	atctttttcac	cgataaatct	gaagccagtc	aagacattaa	acattgttgc	gccgtagctt
21421	tctgcaatct	tagtaactaa	ttcagttgat	acgattgatt	tacaaagggc	agcattagca
21481	gggagagtac	cagctgtttt	gtgagcttca	aggatatatt	tggcgatgat	agcaccaatt
21541	tgggttaccag	aaagggttgag	gtatgaacca	tctggttggc	ggatttcaac	gccaaagacgg
21601	tccgcgtcag	ggtcagttgc	aaccaatacg	tcggcatcta	catt	

//

Kan10

LOCUS 10K

DEFINITION

FEATURES

gene

Location/Qualifiers

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CDS

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CDS	/locus_tag="10K_03" complement(3352..3792) /rbs_motif="None" /uscore="1.42" /rscore="-3.27" /sscore="1.22" /conf="100.0" /cscore="44.7" /partial=0 /tscore="3.07" /product="hypothetical protein X841_05855" /rbs_spacer="None" /gc_cont="0.306" /start_type="ATG" /score=45.9
gene	/codon_start=1 /locus_tag="10K_03" complement(3734..4402) /rbs_motif="None" /uscore="6.14" /rscore="-3.27" /sscore="5.28" /conf="100.0" /cscore="64.59" /partial=0 /tscore="3.07" /rbs_spacer="None" /gc_cont="0.332" /start_type="ATG" /score=69.9
CDS	/locus_tag="10K_04" complement(3734..4402) /rbs_motif="None" /uscore="6.14" /rscore="-3.27" /sscore="5.28" /conf="100.0" /cscore="64.59" /partial=0 /tscore="3.07" /product="hypothetical protein" /rbs_spacer="None" /gc_cont="0.332" /start_type="ATG" /score=69.9

gene	/codon_start=1 /locus_tag="10K_04" 4585..5574 /rbs_motif="AGGAG" /uscore="3.46" /rscore="11.88" /sscore="18.4" /conf="99.99" /cscore="178.52" /partial=0 /tscore="3.07" /rbs_spacer="5-10bp" /gc_cont="0.384" /start_type="ATG" /score=196.9
CDS	/locus_tag="10K_05" 4585..5574 /rbs_motif="AGGAG" /uscore="3.46" /rscore="11.88" /sscore="18.4" /conf="99.99" /cscore="178.52" /partial=0 /tscore="3.07" /product="lipoate-protein ligase A" /rbs_spacer="5-10bp" /gc_cont="0.384" /start_type="ATG" /score=196.9
gene	/codon_start=1 /locus_tag="10K_05" complement(5571..5693) /rbs_motif="AGGA/GGAG/GAGG" /uscore="0.29" /rscore="2.01" /sscore="3.12" /conf="67.3" /cscore="0.02" /partial=0 /tscore="1.47" /rbs_spacer="11-12bp" /gc_cont="0.301" /start_type="ATG" /score=3.1
CDS	/locus_tag="10K_06" complement(5571..5693) /rbs_motif="AGGA/GGAG/GAGG" /uscore="0.29" /rscore="2.01" /sscore="3.12" /conf="67.3" /cscore="0.02" /partial=0 /tscore="1.47" /product="hypothetical protein V528_04795" /rbs_spacer="11-12bp" /gc_cont="0.301" /start_type="ATG" /score=3.1 /codon_start=1

gene	/locus_tag="10K_06" 5808..6872 /rbs_motif="None" /uscore="4.17" /rscore="-3.27" /sscore="-1.65" /conf="100.0" /cscore="77.3" /partial=0 /tscore="-3.65" /rbs_spacer="None" /gc_cont="0.385" /start_type="TTG" /score=75.7
CDS	/locus_tag="10K_07" 5808..6872 /rbs_motif="None" /uscore="4.17" /rscore="-3.27" /sscore="-1.65" /conf="100.0" /cscore="77.3" /partial=0 /tscore="-3.65" /product="site-specific tyrosine recombinase XerS" /rbs_spacer="None" /gc_cont="0.385" /start_type="TTG" /score=75.7
gene	/codon_start=1 /locus_tag="10K_07" complement(7041..9581) /rbs_motif="AGGAG" /uscore="1.01" /rscore="11.88" /sscore="15.95" /conf="99.99" /cscore="460.66" /partial=0 /tscore="3.07" /rbs_spacer="5-10bp" /gc_cont="0.404" /start_type="ATG" /score=476.6
CDS	/locus_tag="10K_08" complement(7041..9581) /rbs_motif="AGGAG" /uscore="1.01" /rscore="11.88" /sscore="15.95" /conf="99.99" /cscore="460.66" /partial=0 /tscore="3.07" /product="aminopeptidase N" /rbs_spacer="5-10bp" /gc_cont="0.404" /start_type="ATG" /score=476.6 /codon_start=1 /locus_tag="10K_08"

gene	complement(9715..10371) /rbs_motif="AGGA/GGAG/GAGG" /uscore="0.06" /rscore="4.18" /sscore="8.31" /conf="100.0" /cscore="130.3" /partial=0 /tscore="3.07" /rbs_spacer="11-12bp" /gc_cont="0.411" /start_type="ATG" /score=138.6 /locus_tag="10K_09"
CDS	complement(9715..10371) /rbs_motif="AGGA/GGAG/GAGG" /uscore="0.06" /rscore="4.18" /sscore="8.31" /conf="100.0" /cscore="130.3" /partial=0 /tscore="3.07" /product="PhoU family transcriptional regulator" /rbs_spacer="11-12bp" /gc_cont="0.411" /start_type="ATG" /score=138.6 /codon_start=1 /locus_tag="10K_09"
gene	complement(10396..11154) /rbs_motif="AGGAG" /uscore="0.37" /rscore="11.88" /sscore="16.45" /conf="100.0" /cscore="111.64" /partial=0 /tscore="3.07" /rbs_spacer="5-10bp" /gc_cont="0.41" /start_type="ATG" /score=128.1 /locus_tag="10K_10"
CDS	complement(10396..11154) /rbs_motif="AGGAG" /uscore="0.37" /rscore="11.88" /sscore="16.45" /conf="100.0" /cscore="111.64" /partial=0 /tscore="3.07" /product="phosphate ABC transporter ATP-binding protein" /rbs_spacer="5-10bp" /gc_cont="0.41" /start_type="ATG" /score=128.1 /codon_start=1 /locus_tag="10K_10"
gene	complement(11167..11970)

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CDS complement(11167..11970)
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/start_type="ATG"
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gene /locus_tag="10K_12"
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/score=150.9
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/rscure="14.48"
/sscore="17.65"
/conf="100.0"
/cscore="133.23"
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/tscore="3.07"
/product="phosphate-binding protein"
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/gc_cont="0.404"
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/score=150.9
/codon_start=1
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complement(14772..16082)
/rbs_motif="GGA/GAG/AGG"
/uscure="0.1"

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CDS	complement(14772..16082) /rbs_motif="GGA/GAG/AGG" /uscore="0.1" /rscore="0.91" /sscore="4.08" /conf="100.0" /cscore="171.68" /partial=0 /tscore="3.07" /product="23S rRNA methyltransferase" /rbs_spacer="5-10bp" /gc_cont="0.41" /start_type="ATG" /score=175.8 /codon_start=1 /locus_tag="10K_15"
gene	complement(16165..16932) /rbs_motif="AGGA" /uscore="0.77" /rscore="7.92" /sscore="6.26" /conf="100.0" /cscore="90.42" /partial=0 /tscore="-3.65" /rbs_spacer="5-10bp" /gc_cont="0.37" /start_type="TTG" /score=96.7 /locus_tag="10K_16"
CDS	complement(16165..16932) /rbs_motif="AGGA" /uscore="0.77" /rscore="7.92" /sscore="6.26" /conf="100.0" /cscore="90.42" /partial=0 /tscore="-3.65" /product="inositol monophosphatase" /rbs_spacer="5-10bp" /gc_cont="0.37" /start_type="TTG" /score=96.7 /codon_start=1 /locus_tag="10K_16"
gene	complement(16922..17203) /rbs_motif="GGA/GAG/AGG" /uscore="-0.28" /rscore="0.91"

	/sscore="4.95" /conf="99.99" /cscore="37.35" /partial=0 /tscore="3.07" /rbs_spacer="5-10bp" /gc_cont="0.404" /start_type="ATG" /score=42.3 /locus_tag="10K_17"
CDS	complement(16922..17203) /rbs_motif="GGA/GAG/AGG" /uscore="-0.28" /rscore="0.91" /sscore="4.95" /conf="99.99" /cscore="37.35" /partial=0 /tscore="3.07" /product="hypothetical protein" /rbs_spacer="5-10bp" /gc_cont="0.404" /start_type="ATG" /score=42.3 /codon_start=1 /locus_tag="10K_17"
gene	complement(17196..17609) /rbs_motif="GGA/GAG/AGG" /uscore="-5.09" /rscore="0.91" /sscore="-7.82" /conf="100.0" /cscore="53.7" /partial=0 /tscore="-3.65" /rbs_spacer="5-10bp" /gc_cont="0.353" /start_type="TTG" /score=45.9 /locus_tag="10K_18"
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gene	complement(17680..18591) /rbs_motif="None" /uscore="0.72" /rscore="-3.27" /sscore="5.08"

	/conf="100.0" /cscore="133.22" /partial=0 /tscore="3.07" /rbs_spacer="None" /gc_cont="0.404" /start_type="ATG" /score=138.3 /locus_tag="10K_19"
CDS	complement(17680..18591) /rbs_motif="None" /uscore="0.72" /rscore="-3.27" /sscore="5.08" /conf="100.0" /cscore="133.22" /partial=0 /tscore="3.07" /product="riboflavin biosynthesis protein RibF" /rbs_spacer="None" /gc_cont="0.404" /start_type="ATG" /score=138.3 /codon_start=1
gene	/locus_tag="10K_19" complement(18588..19421) /rbs_motif="GGA/GAG/AGG" /uscore="4.44" /rscore="0.91" /sscore="7.76" /conf="100.0" /cscore="123.57" /partial=0 /tscore="3.07" /rbs_spacer="5-10bp" /gc_cont="0.421" /start_type="ATG" /score=131.3
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gene	/locus_tag="10K_20" complement(19638..19943) /rbs_motif="None" /uscore="-1.81" /rscore="-3.27" /sscore="-9.38" /conf="99.87"

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CDS	<pre> complement(19638..19943) /rbs_motif="None" /uscore="-1.81" /rscore="-3.27" /sscore="-9.38" /conf="99.87" /cscore="38.15" /partial=0 /tscore="-3.65" /product="hypothetical protein, partial" /rbs_spacer="None" /gc_cont="0.399" /start_type="TTG" /score=28.8 </pre>
gene	<pre> /codon_start=1 /locus_tag="10K_21" complement(20600..20884) /rbs_motif="GGAG/GAGG" /uscore="-0.26" /rscore="6.9" /sscore="9.06" /conf="99.99" /cscore="31.03" /partial=0 /tscore="3.07" /rbs_spacer="5-10bp" /gc_cont="0.379" /start_type="ATG" /score=40.1 </pre>
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gene	<pre> /codon_start=1 /locus_tag="10K_22" complement(21150..21770) /rbs_motif="AGGAG" /uscore="-0.93" /rscore="11.88" /sscore="14.01" /conf="100.0" /cscore="109.89" </pre>

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CDS complement(21893..22387)
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31921	tgaaagggtta	atgatgggcc	aacaaactac	tgatactgat	tttaaacatt	ttatagattt
31981	tgatgataat	cttctttttt	agactaactg	aaactaaagt	tgacaatgga	cgacctgaca
32041	ttcttttttca	ttggcaccca	gaacttgaaa	tctaatacgt	ctatgaaggg	actgctcgct
32101	atcacattga	ttatgactat	tttgatagtc	aggctggaga	tatcttttcta	attcgtccta
32161	atggactcaa	ttctgtccat	cctattgcta	atcagtcgca	ccataactaac	actcttcatt
32221	ttcatttaga	tatgttagga	caatttctag	tggatcctct	tagtctccgt	tatcttcaac
32281	ccttacagaa	ttctaatttt	aagttcaaac	aatgtttaaa	accaactgat	gaggggtatt
32341	ctgaaattaa	gggaacccta	tttgcaattt	ttaagatcat	tagacaaaaa	gagagacact
32401	acgggattttt	gcttaagtcc	aaatcggagg	aactcatcta	ccttttctac	tactatcgtt
32461	tggtagagag	aaagacttct	gatgatcatt	atcgtaaaaa	tgaaaaaatt	cgggaaatca
32521	ttgatcacat	caataagcat	tatgtcgaga	cgcttactat	tgaacaattg	tccgagctca
32581	tggggtacag	taagacgcat	tttatgacca	tatttaaaca	acatacaggt	acctcttgca
32641	ctgaattttat	tattattcag	gatagactga	atgctgcttg	tgaggaactc	cgtaatagcg
32701	taaaaccagt	tttagaaatt	tctacgagcg	ttgggttttaa	caacctttca	aactttaacc
32761	gccaattttaa	gcattattat	gctcaaacac	cgagccagta	caggaagaca	catagcaaca
32821	agaaaacaaa	taagagttaa	ccattgggta	actcttatta	tttatgcaga	gaagctattt
32881	agttttttctc	tttacctttg	tgtttgccac	taagtccaaa	catcgtaagc	aacatgcca
32941	gtccaagaag	acctgcatgt	gaagctttat	cccctgttgt	tggaagttct	tcggtttggc
33001	ttggagtttc	agtaactttt	tcagtttcct	taagagtttc	gtttgaagtt	taaacgaaga
33061	agactttacc	gttaggtgtt	gttactactt	tagataccac	tggtttcggt	ttttctgaaa
33121	cttttagaagc	tacagttgag	tcaacaggat	ttactggatt	aaccgttgta	tcttctgcat
33181	tcttttttctt	gttcaaagca	gcaaatttgg	cacttgaaat	agaaatttta	cgatgaattag
33241	gattaataac	tgcgtatttc	gtaagatctg	catgctgcaa	gtaatcggca	aagactgtat
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33361	gccaagaaat	cgtttgttac	tagataataa	ggtgggatcc	tctagagtcg	acctgcaggc
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33481	tgtttcctgt	g				

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