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DEFINITION     Integrative and conjugative element ICE_1
    CDS            complement(1..1772)
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                 /note="Transposon Tn1000 resolvase, similar to AA
                 sequence:UniProtKB:P03012 protein motif:CLUSTERS:PRK13413
                 protein motif:Pfam:PF00239.15"
                 /product="Transposon Tn1000 resolvase [DDE recombinase]"
                 /"ID=B40_04892
                 /gene="tnpR"""
                 /protein_id="gnl|SC|B40_04892"
                 /codon_start=1
    fasta_record    1..61464
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    CDS            complement(2360..2587)
                 /color=7
                 /locus_tag="B40_04893"
                 /note="Helix-turn-helix domain, protein
                 motif:Pfam:PF12645.1"
                 /product="Helix-turn-helix domain [transcriptional
                 regulator]"
                 /"ID=B40_04893
                 /protein_id="gnl|SC|B40_04893"""
                 /codon_start=1
    CDS            complement(2580..3008)
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                 /locus_tag="B40_04894"
                 /note="RNA polymerase sigma factor Sigma-70 region 4,
                 protein motif:TIGRFAMs:TIGR02937 protein
                 motif:Pfam:PF08281.6"
                 /product="RNA polymerase sigma factor  Sigma-70  region 4
                 [transcriptional regulator]"
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                 /protein_id="gnl|SC|B40_04894"""
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                 /note="Hypothetical protein"
                 /product="hypothetical protein"
                 /protein_id="gnl|SC|B40_04895"
                 /codon_start=1
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CDS         complement(3492..4472)
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         /locus_tag="B40_04896"
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         Helix-turn-helix domain, similar to AA
         sequence:UniProtKB:P28816 protein motif:CLUSTERS:PRK15121
         protein motif:Cdd:COG3449 protein motif:TIGRFAMs:TIGR04094
         protein motif:Pfam:PF12833.1"
         /product="AraC family transcriptional regulator
         Helix-turn-helix domain [transcriptional regulator]"
         /"ID=B40_04896
         /protein_id="gnl|SC|B40_04896"""
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CDS         complement(4838..5029)
         /ID=B40_04897
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         /locus_tag="B40_04897"
         /note="Hypothetical protein"
         /product="hypothetical protein  DUF4177 containing
         protein"
         /protein_id="gnl|SC|B40_04897"
         /codon_start=1
CDS         complement(5100..5393)
         /color=8
         /locus_tag="B40_04898"
         /note="Predicted ester cyclase  SnoaL-like polyketide
         cyclase, protein motif:Cdd:COG5485 protein
         motif:TIGRFAMs:TIGR02096 protein motif:Pfam:PF07366.6"
         /product="Predicted ester cyclase  SnoaL-like polyketide
         cyclase [ester cyclase]"
         /"ID=B40_04898
         /protein_id="gnl|SC|B40_04898"""
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CDS         complement(5412..5510)
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         /color=1
         /locus_tag="B40_04899"
         /note="Hypothetical protein"
         /product="hypothetical protein"
         /protein_id="gnl|SC|B40_04899"
         /codon_start=1
CDS         complement(5580..6194)
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            /note="y4mF family Helix-turn-helix, protein
            motif:TIGRFAMs:TIGR03070 protein motif:Pfam:PF01381.16"
            /product="y4mF family Helix-turn-helix [transcriptional
            regulator]"
            /"ID=B40_04900
            /protein_id="gnl|SC|B40_04900"""
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CDS            complement(6218..6877)
            /color=8
            /locus_tag="B40_04901"
            /note="PAP2 superfamily, protein motif:Pfam:PF01569.15"
            /product="PAP2 superfamily [phosphatase]"
            /"ID=B40_04901
            /protein_id="gnl|SC|B40_04901"""
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CDS            complement(7160..7876)
            /color=8
            /locus_tag="B40_04902"
            /eC_number=2.1.1.157
            /note="Sarcosine/dimethylglycine N-methyltransferase,
            similar to AA sequence:UniProtKB:Q83WC3 protein
            motif:TIGRFAMs:TIGR02021 protein motif:Pfam:PF08241.6"
            /product="Sarcosine/dimethylglycine N-methyltransferase
            [methyltransferase]"
            /"ID=B40_04902
            /protein_id="gnl|SC|B40_04902"""
            /codon_start=1
CDS            complement(7998..8624)
            /color=7
            /locus_tag="B40_04903"
            /note="Potential acrAB operon repressor, similar to AA
            sequence:UniProtKB:P0ACS9 protein motif:CLUSTERS:PRK10668
            protein motif:TIGRFAMs:TIGR03968 protein
            motif:Pfam:PF00440.17"
            /product="Potential acrAB operon repressor
            [transcriptional regulator]"
            /"ID=B40_04903
            /gene="acrR"""
            /protein_id="gnl|SC|B40_04903"
            /codon_start=1
CDS            complement(8914..9054)
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          /note="Hypothetical protein"
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CDS          complement(9105..10016)
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          /locus_tag="B40_04905"
          /note="Cadmium  cobalt and zinc/H-K antiporter, similar to
          AA sequence:UniProtKB:O07084 protein
          motif:CLUSTERS:PRK09509 protein motif:Cdd:COG0053 protein
          motif:TIGRFAMs:TIGR01297 protein motif:Pfam:PF01545.15"
          /product="Cadmium  cobalt and zinc/H%28 %29-K%28 %29
          antiporter [heavy metal defense]"
          /"ID=B40_04905
          /gene="czcD"""
          /protein_id="gnl|SC|B40_04905"
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CDS          complement(10028..10471)
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          /color=8
          /locus_tag="B40_04906"
          /note="Hypothetical protein"
          /product="RibD %28riboflavin biosynthesis%29 family
          protein [pyrimidine reductase]"
          /protein_id="gnl|SC|B40_04906"
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CDS          complement(10582..10938)
          /ID=B40_04907
          /color=7
          /locus_tag="B40_04907"
          /note="Hypothetical protein"
          /product="WYL domain-containing protein [transcriptional
          regulator]"
          /protein_id="gnl|SC|B40_04907"
          /codon_start=1
CDS          complement(10962..11534)
          /color=7
          /locus_tag="B40_04908"
          /note="Helix-turn-helix domain, protein
          motif:CLUSTERS:PRK11886 protein motif:Pfam:PF08279.6"
          /product="Helix-turn-helix domain [transcriptional
          regulator]"
          /"ID=B40_04908
          /protein_id="gnl|SC|B40_04908"""
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          /codon_start=1
CDS          complement(11810..12604)
          /color=2
          /locus_tag="B40_04909"
          /eC_number=2.7.1.95
          /note="Aminoglycoside 3'-phosphotransferase, similar to AA
          sequence:UniProtKB:P0A3Y5 protein motif:Cdd:COG3231
          protein motif:Pfam:PF01636.17"
          /product="Aminoglycoside 3'-phosphotransferase [antibiotic
          resistance]"
          /"ID=B40_04909
          /gene="aphA"""
          /protein_id="gnl|SC|B40_04909"
          /codon_start=1
CDS          complement(12697..13239)
          /color=2
          /locus_tag="B40_04910"
          /note="streptothricin N-acetyltransferase Sat4, protein
          motif:CLUSTERS:PRK10975 protein motif:TIGRFAMs:TIGR01575
          protein motif:Pfam:PF00583.18"
          /product="streptothricin N-acetyltransferase Sat4
          [antibiotic resistance]"
          /"ID=B40_04910
          /gene="sat4"""
          /protein_id="gnl|SC|B40_04910"
          /codon_start=1
CDS          complement(13236..14144)
          /color=2
          /locus_tag="B40_04911"
          /eC_number=2.7.7.-
          /note="Aminoglycoside 6-adenylyl transferase Streptomycin
          adenylyl transferase, similar to AA
          sequence:UniProtKB:P17585 protein motif:Pfam:PF04439.6"
          /product="Aminoglycoside 6-adenylyltransferase
          Streptomycin adenylyltransferase [antibiotic resistance]"
          /"ID=B40_04911
          /gene="aadK"""
          /protein_id="gnl|SC|B40_04911"
          /codon_start=1
CDS          complement(14177..14785)
          /color=8
          /locus_tag="B40_04912"
          /eC_number=2.1.1.-
          /note="Uncharacterized methyltransferase ycgJ , similar to
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                AA sequence:UniProtKB:O31474 protein
                motif:CLUSTERS:PRK08317 protein motif:Cdd:COG4976 protein
                motif:TIGRFAMs:TIGR02072 protein motif:Pfam:PF08241.6"
                /product="Uncharacterized methyltransferase ycgJ
                [methyltransferase]"
                /"ID=B40_04912
                /gene="ycgJ""""
                /protein_id="gnl|SC|B40_04912"
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CDS                 complement(14769..15524)
                /ID=B40_04913
                /color=10
                /locus_tag="B40_04913"
                /note="Hypothetical protein"
                /product="Replication protein repR [replication
                initiation]"
                /gene="repR"
                /protein_id="gnl|SC|B40_04913"
                /codon_start=1
ncRNA                  15682..15812
                /ID=B40_04914
                /color=10
                /locus_tag="B40_04914"
                /product="Plasmid_RNAIII [repR repressor]"
CDS                 complement(15919..16158)
                /color=10
                /locus_tag="B40_04915"
                /note="Replication initiation protein RepA, protein
                motif:Pfam:PF01381.16"
                /product="Replication initiation protein RepA
                [replication]"
                /"ID=B40_04915
                /gene="repA""""
                /protein_id="gnl|SC|B40_04915"
                /codon_start=1
CDS                 complement(16402..16515)
                /ID=B40_04916
                /color=1
                /locus_tag="B40_04916"
                /note="Hypothetical protein"
                /product="hypothetical protein"
                /protein_id="gnl|SC|B40_04916"
                /codon_start=1
CDS                 complement(16520..17257)
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          /color=2
          /locus_tag="B40_04917"
          /eC_number=2.1.1.184
          /note="rRNA adenine N-6-methyltransferase, similar to AA
          sequence:UniProtKB:P21236 protein motif:CLUSTERS:PRK00274
          protein motif:Cdd:COG0030 protein motif:TIGRFAMs:TIGR00755
          protein motif:Pfam:PF00398.14"
          /product="rRNA adenine N-6-methyltransferase [antibiotic
          resistanc]"
          /"ID=B40_04917
          /gene="ermB"""
          /protein_id="gnl|SC|B40_04917"
          /codon_start=1
CDS          complement(17886..18251)
          /color=1
          /locus_tag="B40_04918"
          /note="Predicted outer membrane protein LPXTG cell wall
          anchor domain, protein motif:Cdd:COG4932 protein
          motif:TIGRFAMs:TIGR01167 protein motif:Pfam:PF00746.15"
          /product="Predicted outer membrane protein LPXTG cell wall
          anchor domain [membrane protein]"
          /"ID=B40_04918
          /protein_id="gnl|SC|B40_04918"""
          /codon_start=1
CDS          complement(18251..19165)
          /color=8
          /locus_tag="B40_04919"
          /note="ABC transporter permease, protein
          motif:CLUSTERS:PRK05625 protein motif:TIGRFAMs:TIGR00227
          protein motif:Pfam:PF01872.11"
          /product="ABC transporter permease [transporter]"
          /"ID=B40_04919
          /protein_id="gnl|SC|B40_04919"""
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CDS          complement(19162..19845)
          /ID=B40_04920
          /color=8
          /locus_tag="B40_04920"
          /note="Hypothetical protein"
          /product="ABC transporter permease [transporter]"
          /protein_id="gnl|SC|B40_04920"
          /codon_start=1
CDS          complement(19842..20687)
          /color=8
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          /locus_tag="B40_04921"
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          /note="ABC transporter ATP-binding protein, similar to AA
          sequence:UniProtKB:O07190 protein motif:CLUSTERS:PRK13536
          protein motif:Cdd:COG4555 protein motif:TIGRFAMs:TIGR01188
          protein motif:Pfam:PF00005.21"
          /product="ABC transporter ATP-binding protein [ATPase]"
          /"ID=B40_04921
          /protein_id="gnl|SC|B40_04921"""
          /codon_start=1
CDS         complement(20791..21378)
          /color=7
          /locus_tag="B40_04922"
          /note="tetR/arcR family transcriptional regulator, protein
          motif:CLUSTERS:PRK09975 protein motif:TIGRFAMs:TIGR03968
          protein motif:Pfam:PF00440.17"
          /product="tetR/arcR family transcriptional regulator
          [transcriptional regulator]"
          /"ID=B40_04922
          /protein_id="gnl|SC|B40_04922"""
          /codon_start=1
CDS         complement(21450..22307)
          /color=8
          /locus_tag="B40_04923"
          /note="Alpha/beta hydrolase family, protein
          motif:Cdd:COG1647 protein motif:Pfam:PF12697.1"
          /product="Alpha/beta hydrolase family [hydrolase]"
          /"ID=B40_04923
          /protein_id="gnl|SC|B40_04923"""
          /codon_start=1
CDS         complement(22520..23413)
          /color=4
          /locus_tag="B40_04924"
          /note="Conjugative transposon protein TcpC, protein
          motif:Pfam:PF12642.1"
          /product="Conjugative transposon protein TcpC [mating pair
          formation]"
          /"ID=B40_04924
          /gene="tcpC"""
          /protein_id="gnl|SC|B40_04924"
          /codon_start=1
CDS         complement(23429..24436)
          /color=4
          /locus_tag="B40_04925"
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        /note="Peptidase P60 bifunctional lytic
        transglycosylase/NlpC/P60 family protein, similar to AA
        sequence:UniProtKB:P21171 protein motif:CLUSTERS:PRK13914
        protein motif:Cdd:COG3584 protein motif:Pfam:PF00877.13"
        /product="Peptidase P60 bifunctional lytic
        transglycosylase/NlpC/P60 family protein [pepidase]"
        /"ID=B40_04925
        /protein_id="gnl|SC|B40_04925"""
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CDS       complement(24433..26565)
        /ID=B40_04926
        /color=1
        /locus_tag="B40_04926"
        /note="Hypothetical protein"
        /product="YtxH domain-containing protein  MFS transporter
        membrane protein  conjugative transposon protein"
        /protein_id="gnl|SC|B40_04926"
        /codon_start=1
CDS       complement(26565..29015)
        /color=4
        /locus_tag="B40_04927"
        /note="Type IV secretion system protein TraC  VirB4
        components, protein motif:Cdd:COG3451 protein
        motif:TIGRFAMs:TIGR02746 protein motif:Pfam:PF12846.1"
        /product="Type IV secretion system protein TraC  VirB4
        components [ATPase  mating pair formation]"
        /"ID=B40_04927
        /gene="traC"""
        /protein_id="gnl|SC|B40_04927"
        /codon_start=1
CDS       complement(29002..29391)
        /color=4
        /locus_tag="B40_04928"
        /note="TcpE family, protein motif:Pfam:PF12648.1"
        /product="TcpE family [mating pair formation]"
        /"ID=B40_04928
        /gene="tcpE"""
        /protein_id="gnl|SC|B40_04928"
        /codon_start=1
CDS       complement(29556..30059)
        /color=4
        /locus_tag="B40_04929"
        /note="Antirestriction protein ArdA, protein
        motif:Cdd:COG4734 protein motif:Pfam:PF07275.5"
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            /product="Antirestriction protein ArdA [anti-ristriction
            modification]"
            /"ID=B40_04929
            /gene="ardA"""
            /protein_id="gnl|SC|B40_04929"
            /codon_start=1
CDS            complement(30075..30572)
            /color=4
            /locus_tag="B40_04930"
            /note="Antirestriction protein ArdA, protein
            motif:Cdd:COG4734 protein motif:Pfam:PF07275.5"
            /product="Antirestriction protein ArdA [anti-ristriction
            modification]"
            /"ID=B40_04930
            /gene="ardA"""
            /protein_id="gnl|SC|B40_04930"
            /codon_start=1
CDS            complement(30855..31871)
            /ID=B40_04931
            /color=1
            /locus_tag="B40_04931"
            /note="Hypothetical protein"
            /product="hypothetical protein"
            /protein_id="gnl|SC|B40_04931"
            /codon_start=1
CDS            complement(31942..32163)
            /ID=B40_04932
            /color=1
            /locus_tag="B40_04932"
            /note="Hypothetical protein"
            /product="hypothetical protein"
            /protein_id="gnl|SC|B40_04932"
            /codon_start=1
CDS            complement(32164..32304)
            /color=1
            /locus_tag="B40_04933"
            /note="Protein of unknown function  DUF3789, protein
            motif:Pfam:PF12664.1"
            /product="Protein of unknown function  DUF3789"
            /"ID=B40_04933
            /protein_id="gnl|SC|B40_04933""""
            /codon_start=1
CDS            complement(32308..33429)
            /color=4
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               /locus_tag="B40_04934"
               /note="Putative replication initiation factor Tn916-like
               CTn1-Orf26, protein motif:Pfam:PF02486.13"
               /product="Putative replication initiation factor
               Tn916-like  CTn1-Orf26  Replication initiation factor
               domain-containing protein [relaxase]"
               /"ID=B40_04934
               /protein_id="gnl|SC|B40_04934""""
               /codon_start=1
     CDS          complement(33709..35103)
               /color=4
               /locus_tag="B40_04935"
               /note="DNA translocase FtsK DNA segregation ATPase
               FtsK/SpoIIIE and related proteins, similar to AA
               sequence:UniProtKB:P64165 protein motif:Cdd:COG1674
               protein motif:TIGRFAMs:TIGR03924 protein
               motif:Pfam:PF01580.12"
               /product="DNA translocase FtsK DNA segregation ATPase
               FtsK/SpoIIIE and related proteins [ATPase coupling
               protein]"
               /"ID=B40_04935
               /gene="ftsK""""
               /protein_id="gnl|SC|B40_04935"
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     CDS          complement(35214..35780)
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               /color=1
               /locus_tag="B40_04936"
               /note="Hypothetical protein"
               /product="YcxB family protein [transmembrane protein]"
               /protein_id="gnl|SC|B40_04936"
               /codon_start=1
     CDS          complement(35777..36319)
               /color=1
               /locus_tag="B40_04937"
               /note="Protein of unknown function  DUF3795, protein
               motif:Pfam:PF12675.1"
               /product="Protein of unknown function  DUF3795"
               /"ID=B40_04937
               /protein_id="gnl|SC|B40_04937""""
               /codon_start=1
     CDS          complement(36380..36817)
               /ID=B40_04938
               /color=1
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          /locus_tag="B40_04938"
          /note="Hypothetical protein"
          /product="hypothetical protein"
          /protein_id="gnl|SC|B40_04938"
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CDS         complement(36882..37202)
          /color=7
          /locus_tag="B40_04939"
          /note="Regulator of competence-specific genes TfoX
          N-terminal domain, protein motif:Cdd:COG3070 protein
          motif:Pfam:PF04993.7"
          /product="Regulator of competence-specific genes TfoX
          N-terminal domain [transcriptional regulator]"
          /"ID=B40_04939
          /protein_id="gnl|SC|B40_04939""""
          /codon_start=1
CDS         37448..37732
          /ID=B40_04940
          /color=9
          /locus_tag="B40_04940"
          /note="Hypothetical protein"
          /product="Transposase [DDE recombinase]"
          /protein_id="gnl|SC|B40_04940"
          /codon_start=1
CDS         37729..38643
          /color=9
          /locus_tag="B40_04941"
          /note="IS3 family transposase, protein
          motif:Pfam:PF00665.20"
          /product="IS3 family transposase [DDE recombinase]"
          /"ID=B40_04941
          /protein_id="gnl|SC|B40_04941""""
          /codon_start=1
CDS         complement(38662..39009)
          /color=1
          /locus_tag="B40_04942"
          /note="Protein of unknown function  DUF3788, protein
          motif:Pfam:PF12663.1"
          /product="Protein of unknown function  DUF3788"
          /"ID=B40_04942
          /protein_id="gnl|SC|B40_04942""""
          /codon_start=1
CDS         complement(39073..39531)
          /color=8
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          /locus_tag="B40_04943"
          /note="Glyoxalase, protein motif:CLUSTERS:PRK04101 protein
          motif:Pfam:PF12681.1"
          /product="Glyoxalase [glyoxalase]"
          /"ID=B40_04943
          /protein_id="gnl|SC|B40_04943"""
          /codon_start=1
CDS         complement(39627..40013)
          /color=1
          /locus_tag="B40_04944"
          /note="Protein of unknown function  DUF961, protein
          motif:Pfam:PF06125.5"
          /product="Protein of unknown function  DUF961"
          /"ID=B40_04944
          /protein_id="gnl|SC|B40_04944"""
          /codon_start=1
CDS         complement(40027..40350)
          /color=1
          /locus_tag="B40_04945"
          /note="Protein of unknown function  DUF961, protein
          motif:Pfam:PF06125.5"
          /product="Protein of unknown function  DUF961"
          /"ID=B40_04945
          /protein_id="gnl|SC|B40_04945"""
          /codon_start=1
CDS         complement(40557..43607)
          /color=1
          /locus_tag="B40_04946"
          /note="Predicted outer membrane protein LPXTG cell wall
          anchor domain, protein motif:Cdd:COG4932 protein
          motif:Pfam:PF05738.7"
          /product="Predicted outer membrane protein LPXTG cell wall
          anchor domain [membrane protein]"
          /"ID=B40_04946
          /protein_id="gnl|SC|B40_04946"""
          /codon_start=1
CDS         complement(43851..44219)
          /ID=B40_04947
          /color=1
          /locus_tag="B40_04947"
          /note="Hypothetical protein"
          /product="hypothetical protein"
          /protein_id="gnl|SC|B40_04947"
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CDS        complement(44462..45010)
         /ID=B40_04948
         /color=1
         /locus_tag="B40_04948"
         /note="Hypothetical protein"
         /product="hypothetical protein"
         /protein_id="gnl|SC|B40_04948"
         /codon_start=1
CDS        complement(44997..45311)
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         /color=1
         /locus_tag="B40_04949"
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            /product="Glutamyl-tRNA amidotransferase subunit A
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            /protein_id="gnl|SC|D90_02948"
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            components, protein motif:CLUSTERS:PRK13897protein
            motif:Cdd:COG3505protein motif:TIGRFAMs:TIGR02767protein
            motif:Pfam:PF02534.8"
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            components [coupling protein]"
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          /product="LtrC-like late transcriptional regulators
          protein [transcriptional regulator]"
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          /locus_tag="D90_02953"
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          motif:Pfam:PF03432.8"
          /product="Relaxase/Mobilisation nuclease domain
          [relaxase]"
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          protein motif:Pfam:PF05713.5"
          /product="Bacterial mobilisation relaxosome protein MobC
          [relaxosome]"
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         protein motif:Pfam:PF12957.1"
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         motif:Pfam:PF00176.17"
         /product="N-6 DNA methylase [methyltransferase]"
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          protein motif:Cdd:COG4932protein motif:Pfam:PF05738.7"
          /product="Cys-Gln thioester bond-forming surface protein"
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          /product="Prokaryotic membrane lipoprotein lipid
          attachment site profile"
          /protein_id="gnl|SC|D90_02965"
          /codon_start=1
CDS          complement(49561..50505)
          /color=10
          /locus_tag="D90_02966"
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          sequence:UniProtKB:P0CAV8protein
          motif:CLUSTERS:PRK13832protein
          motif:TIGRFAMs:TIGR00180protein motif:Pfam:PF02195.12"
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          proteinParB-like nuclease domain [partitioning system]"
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          /gene="parB"
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          sequence:UniProtKB:P37522protein
          motif:CLUSTERS:PRK13869protein motif:Cdd:COG2894protein
          motif:TIGRFAMs:TIGR03453protein motif:Pfam:PF01656.17"
          /product="CobQ/CobB/MinD/ParA nucleotide binding domain
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          /protein_id="gnl|SC|D90_02967""""
          /gene="parA"
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CDS          51893..52417
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          /locus_tag="D90_02968"
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          oxidoreductase ywqN Flavodoxin family protein, similar to
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           motif:Cdd:COG0431protein motif:Pfam:PF03358.9"
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           /protein_id="gnl|SC|D90_02968""""
           /gene="ywqN"
           /codon_start=1
CDS           53433..56477
           /color=8
           /locus_tag="D90_02969"
           /note="Sortase B-anchored collagen-binding adhesin LPXTG
           cell wall anchor domain-containing protein, protein
           motif:Cdd:COG4932protein motif:Pfam:PF05738.7"
           /product="Sortase B-anchored collagen-binding adhesin
           LPXTG cell wall anchor domain-containing protein
           [virulence]"
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           /protein_id="gnl|SC|D90_02969""""
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           /note="YdcP family protein DUF961 domain-containing
           protein, protein motif:Pfam:PF06125.5"
           /product="YdcP family protein DUF961 domain-containing
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           /"ID=D90_02971
           /protein_id="gnl|SC|D90_02971""""
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CDS           57052..57435
           /color=1
           /locus_tag="D90_02972"
           /note="YdcP family protein DUF961 domain-containing
           protein, protein motif:Pfam:PF06125.5"
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          /color=7
          /locus_tag="D90_02973"
          /note="Helix-turn-helix transcriptional regulator ImmR,
          similar to AA sequence:UniProtKB:P96631protein
          motif:CLUSTERS:PRK09706protein motif:Cdd:COG1426protein
          motif:TIGRFAMs:TIGR03070protein motif:Pfam:PF12844.1"
          /product="Helix-turn-helix transcriptional regulator ImmR
          [transcriptional regulator]"
          /"ID=D90_02973
          /protein_id="gnl|SC|D90_02973""""
          /gene="immR"
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CDS          58026..58352
          /ID=D90_02974
          /color=1
          /locus_tag="D90_02974"
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          /product="hypothetical protein"
          /protein_id="gnl|SC|D90_02974"
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CDS          58453..59847
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          /locus_tag="D90_02975"
          /note="DNA translocase FtsKDNA segregation ATPase
          FtsK/SpoIIIE and related proteins, similar to AA
          sequence:UniProtKB:P64165protein motif:Cdd:COG1674protein
          motif:TIGRFAMs:TIGR03924protein motif:Pfam:PF01580.12"
          /product="DNA translocase FtsKDNA segregation ATPase
          FtsK/SpoIIIE and related proteins [ATPase coupling
          protein]"
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          /protein_id="gnl|SC|D90_02975""""
          /gene="ftsK"
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CDS          60031..61227
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          /note="XRE family transcriptional regulator Replication
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            motif:TIGRFAMs:TIGR03070protein motif:Pfam:PF02486.13"
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            /color=1
            /locus_tag="D90_02977"
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            conjugative transposon protein Tn916-like CTn1-Orf25,
            protein motif:Pfam:PF12664.1"
            /product="DUF3789 domain-containing protein Putative
            conjugative transposon protein Tn916-like CTn1-Orf25"
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            /protein_id="gnl|SC|D90_02977"""
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            /color=4
            /locus_tag="D90_02978"
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            /product="Conjugation related protein"
            /protein_id="gnl|SC|D90_02978"
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CDS            61800..62576
            /color=7
            /locus_tag="D90_02979"
            /note="Helix-turn-helix transcriptional regulator immR,
            similar to AA sequence:UniProtKB:P96631protein
            motif:CLUSTERS:PRK09706protein
            motif:TIGRFAMs:TIGR03070protein motif:Pfam:PF12844.1"
            /product="Helix-turn-helix transcriptional regulator immR
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            /protein_id="gnl|SC|D90_02979"""
            /gene="immR"
            /codon_start=1
CDS            62876..63379
            /color=4
            /locus_tag="D90_02980"
            /note="Antirestriction protein ArdA, protein
            motif:Pfam:PF07275.5"
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CDS          63397..63900
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          /locus_tag="D90_02981"
          /note="Antirestriction protein ArdA , protein
          motif:Cdd:COG4734protein motif:Pfam:PF07275.5"
          /product="Antirestriction protein ArdA [anti-resitriction
          modification]"
          /"ID=D90_02981
          /gene="ardA"""
          /protein_id="gnl|SC|D90_02981"
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CDS          64018..64416
          /color=4
          /locus_tag="D90_02982"
          /note="TcpE family, protein motif:Pfam:PF12648.1"
          /product="TcpE family [mating pair formation]"
          /"ID=D90_02982
          /gene="tcpE"""
          /protein_id="gnl|SC|D90_02982"
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CDS          64394..66844
          /color=4
          /locus_tag="D90_02983"
          /note="Type IV secretion system protein TraC VirB4
          components, protein motif:Cdd:COG3451protein
          motif:TIGRFAMs:TIGR02746protein motif:Pfam:PF12846.1"
          /product="Type IV secretion system protein TraC VirB4
          components [ATPase mating pair formation]"
          /"ID=D90_02983
          /gene="traC"""
          /protein_id="gnl|SC|D90_02983"
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CDS          66844..69039
          /color=4
          /locus_tag="D90_02984"
          /note="Conjugative transposon protein Tn916 orf15-like MFS
          transporter YtxH domain-containing protein, protein
          motif:Cdd:COG0349"
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          /note="Endopepidase NLPC/P60, similar to AA
          sequence:UniProtKB:P21171protein
          motif:CLUSTERS:PRK13914protein motif:Cdd:COG3584protein
          motif:Pfam:PF00877.13"
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          /protein_id="gnl|SC|D90_02985""""
          /codon_start=1
CDS          70059..70970
          /color=4
          /locus_tag="D90_02986"
          /note="Conjugative transposon protein TcpC, protein
          motif:Pfam:PF12642.1"
          /product="Conjugative transposon protein TcpC [mating pair
          formation]"
          /"ID=D90_02986
          /gene="tcpC""""
          /protein_id="gnl|SC|D90_02986"
          /codon_start=1
CDS          71091..71468
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          /locus_tag="D90_02987"
          /note="GntR family transcriptional regulator
          Helix-turn-helix domain-containing protein, similar to AA
          sequence:UniProtKB:O34817protein
          motif:CLUSTERS:PRK09990protein motif:Cdd:COG1802protein
          motif:TIGRFAMs:TIGR02325protein motif:Pfam:PF00392.15"
          /product="GntR family transcriptional regulator
          Helix-turn-helix domain-containing protein
          [transcriptional regulator]"
          /"ID=D90_02987
          /protein_id="gnl|SC|D90_02987""""
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          /locus_tag="D90_02988"
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          protein motif:Cdd:COG4555 protein
          motif:TIGRFAMs:TIGR01188protein motif:Pfam:PF00005.21"
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          [transporter]"
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CDS          72329..72973
          /ID=D90_02989
          /color=8
          /locus_tag="D90_02989"
          /note="ABC-2 transporter permease"
          /product="ABC-2 transporter permease [transporter]"
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          /color=1
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          /product="DNA-binding protein"
          /protein_id="gnl|SC|D90_02990"
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CDS          73382..73570
          /ID=D90_02991
          /color=4
          /locus_tag="D90_02991"
          /note="Cystein-rich KTR conjugal transfer protein"
          /product="Cystein-rich KTR conjugal transfer protein"
          /protein_id="gnl|SC|D90_02991"
          /codon_start=1
CDS          complement(73678..74037)
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          /locus_tag="D90_02992"
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          motif:TIGRFAMs:TIGR00270protein motif:Pfam:PF12844.1"
          /product="helix-turn-helix transcriptional regulator
          [transcriptional regulator]"
          /"ID=D90_02992
          /protein_id="gnl|SC|D90_02992"""
          /codon_start=1
CDS          74209..74418
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            /locus_tag="D90_02993"
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            Repressor, protein motif:Pfam:PF07764.5"
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            Repressor [transcriptional regulator]"
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CDS            74435..74707
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            /locus_tag="D90_02994"
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            system antitoxin, similar to AA
            sequence:UniProtKB:Q57231protein motif:Pfam:PF08998.5"
            /product="Plasmid epsilon-zeta postsegregational killing
            system antitoxin [toxin-antitoxin]"
            /"ID=D90_02994
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CDS            74919..75338
            /color=8
            /locus_tag="D90_02995"
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            system Zeta toxin AAA family ATPase, protein
            motif:Pfam:PF06414.6"
            /product="Plasmid epsilon-zeta postsegregational killing
            system Zeta toxin AAA family ATPase [toxin-antitoxin]"
            /"ID=D90_02995
            /protein_id="gnl|SC|D90_02995""""
            /codon_start=1
CDS            75385..76122
            /color=2
            /locus_tag="D90_02996"
            /eC_number=2.1.1.184
            /note="23S rRNA adenine(2058)-N-methyltransferase ErmB,
            similar to AA sequence:UniProtKB:P21236protein
            motif:CLUSTERS:PRK14896protein motif:Cdd:COG0030protein
            motif:TIGRFAMs:TIGR00755 protein motif:Pfam:PF00398.14"
            /product="23S rRNA
            %28adenine%282058%29-N%286%29%29-methyltransferase
            Erm%28B%29 [antibiotic resistance]"
            /"ID=D90_02996
            /protein_id="gnl|SC|D90_02996""""
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          /gene="erm"
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CDS         76127..76258
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          /product="hypothetical protein"
          /protein_id="gnl|SC|D90_02997"
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CDS         76655..77533
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          /locus_tag="D90_02998"
          /note="ParA family protein CobQ/CobB/MinD/ParA nucleotide
          binding domain, similar to AA
          sequence:UniProtKB:P37522protein motif:Cdd:COG4963protein
          motif:TIGRFAMs:TIGR03453protein motif:Pfam:PF01656.17"
          /product="ParA family protein CobQ/CobB/MinD/ParA
          nucleotide binding domain [partitioning system]"
          /"ID=D90_02998
          /protein_id="gnl|SC|D90_02998"""
          /gene="parA"
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CDS         77981..78397
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          /locus_tag="D90_02999"
          /note="RNA polymerase sigma factor Sigma-70 region 4,
          protein motif:Cdd:COG2739protein
          motif:TIGRFAMs:TIGR02937protein motif:Pfam:PF08281.6"
          /product="RNA polymerase sigma factor Sigma-70 region 4
          [transcriptional regulator]"
          /"ID=D90_02999
          /protein_id="gnl|SC|D90_02999"""
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CDS         78404..78652
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          /locus_tag="D90_03000"
          /note="helix-turn-helix domain-containing protein, protein
          motif:Pfam:PF12645.1"
          /product="helix-turn-helix domain-containing protein
          [transcriptional regulator]"
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          /protein_id="gnl|SC|D90_03000"""
          /codon_start=1
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                     [excisionase]"
                     /"ID=D90_03001
                     /protein_id="gnl|SC|D90_03001"""
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     CDS             79323..80768
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                     /note="Tyrosine recombinase, protein
                     motif:CLUSTERS:PRK00236protein motif:Cdd:COG4973protein
                     motif:TIGRFAMs:TIGR02224protein motif:Pfam:PF00589.16"
                     /product="Tyrosine recombinase [recombinase]"
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80461 gcctacgcca tttaagtacg ggttataaac tcaaaatgac aaacggagat gttaagtccg
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   80521 tacaaggcga tactggtcac gcagaagcag aaatggttac agatgtatat tcagaaatca
   80581 ttgacgagga cagacgtttc aatgcacaaa aaatggataa agaattttat tctacgctta
   80641 atgatgatac agacaatcca aagcaagata ccgacttaac cgatagtgat atggcgttat
   80701 tggaactgat taaatcttta tcgccagaaa tgaaagagca atttttaaag caggcacttc
   80761 aaagatagaa tttcaaaagt gttagcaaat tccaaaaaaa ccagcgattt ttcttcaaaa
   80821 ataaaaaagt gttagcaagc ctatttcctt aaaagtctta aaaaaatatc gaataaaaaa
   80881 tgacagattg aaaacaattc gtattcagcg taaatagaaa gccataaata aagaaacgct
   80941 gaaaaccttg taaaataagg ctttcagcgg agtttgtggc gtcccagaca
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DEFINITION     Integrative and mobilisable element IME_1
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                motif:CLUSTERS:PRK11823 protein motif:Pfam:PF09250.5"
                /product="Replication initiation protein RepA
                [replication]"
                /"ID=B40_02172
                /gene="repA""""
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    CDS             2779..3141
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CDS         3110..3460
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          [replication]"
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          /gene="repA"
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CDS         3532..4704
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          /locus_tag="B40_02175"
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          similar to AA sequence:UniProtKB:P77994 protein
          motif:CLUSTERS:PRK05901 protein motif:TIGRFAMs:TIGR02393
          protein motif:Pfam:PF04542.8"
          /product="RNA polymerase sigma factor  Sigma-70 region 2
          [transcriptional regulator]"
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          /protein_id="gnl|SC|B40_02175"""
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CDS         5132..5782
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          /color=1
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          /product="hypothetical protein"
          /protein_id="gnl|SC|B40_02176"
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CDS         5932..6417
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          /locus_tag="B40_02177"
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          /product="helix-turn-helix [transcriptional regulator]"
          /protein_id="gnl|SC|B40_02177"
          /codon_start=1
CDS         complement(6735..7280)
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        /locus_tag="B40_02178"
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        /product="Uma2 family endonuclease [restriction
        modification]"
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CDS       7994..8269
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        /product="Putative phage-type endonuclease [restriction
        modification]"
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CDS       8379..8852
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        /product="hypothetical protein"
        /protein_id="gnl|SC|B40_02182"
        /codon_start=1
CDS       9653..9832
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        /color=1
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          /product="hypothetical protein"
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          /product="hypothetical protein"
          /protein_id="gnl|SC|B40_02184"
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          /locus_tag="B40_02185"
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          /product="hypothetical protein"
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CDS          10594..10881
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          /color=9
          /locus_tag="B40_02186"
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          /product="Tyrosine-type recombinase [recombinase]"
          /protein_id="gnl|SC|B40_02186"
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CDS          11079..12212
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          /color=7
          /locus_tag="B40_02187"
          /note="Helix-turn-helix domain  DNA-binding protein
          conjugative transposon protein"
          /product="Helix-turn-helix domain  DNA-binding protein
          conjugative transposon protein [transcriptional
          regulator]"
          /protein_id="gnl|SC|B40_02187"
          /codon_start=1
CDS          12230..12442
          /ID=B40_02188
          /color=1
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                /DUF5348=transposon
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                /product="hypothetical protein  DUF5348 containing protein
                conugative transposon protein"
                /protein_id="gnl|SC|B40_02188"
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CDS                12486..12962
                /color=1
                /locus_tag="B40_02189"
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                protein  conjugative transposon protein, protein
                motif:Pfam:PF12687.1"
                /product="PcfB family protein  DUF3801 domain-containing
                protein  conjugative transposon protein"
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CDS                12959..14506
                /color=4
                /locus_tag="B40_02190"
                /note="Type IV secretory systeim protein TraG  VirD4
                components, protein motif:CLUSTERS:PRK13876 protein
                motif:Cdd:COG3505 protein motif:TIGRFAMs:TIGR02759 protein
                motif:Pfam:PF02534.8"
                /product="Type IV secretory systeim protein TraG  VirD4
                components [coupling protein]"
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                /gene="traG"
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                /product="Transposon-encoded TnpV family protein"
                /protein_id="gnl|SC|B40_02191"
                /gene="tnpV"
                /codon_start=1
CDS                14985..15176
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          /product="hypothetical protein"
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CDS         complement(15196..16239)
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          /color=1
          /locus_tag="B40_02193"
          /note="hypothetical protein"
          /product="hypothetical protein"
          /protein_id="gnl|SC|B40_02193"
          /codon_start=1
CDS         16571..16795
          /color=7
          /locus_tag="B40_02194"
          /note="Helix-turn-helix domain-containing protein
          Excisionase family DNA-binding domain, protein
          motif:Pfam:PF12728.1"
          /product="Helix-turn-helix domain-containing protein
          Excisionase family DNA-binding domain [transcriptional
          regulator]"
          /"ID=B40_02194
          /protein_id="gnl|SC|B40_02194"""
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CDS         16911..17117
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          /locus_tag="B40_02195"
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          /product="hypothetical protein"
          /protein_id="gnl|SC|B40_02195"
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CDS         17178..18686
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          /color=1
          /locus_tag="B40_02196"
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          /product="SRRM2 %28serine/arginine repetitive matrix
          protein 2%29"
          /protein_id="gnl|SC|B40_02196"
          /codon_start=1
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CDS         18702..19388
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          /locus_tag="B40_02197"
          /note="DNA primase, similar to AA
          sequence:UniProtKB:P0ABS5 protein motif:CLUSTERS:PRK05667
          protein motif:Cdd:COG0358 protein motif:TIGRFAMs:TIGR01391
          protein motif:Pfam:PF01807.14"
          /product="DNA primase [RNA polymerase]"
          /"ID=B40_02197
          /protein_id="gnl|SC|B40_02197""""
          /codon_start=1
CDS         19348..20706
          /color=8
          /locus_tag="B40_02198"
          /note="Virulence-associated protein E, protein
          motif:Cdd:COG5545 protein motif:Pfam:PF05272.5"
          /product="Virulence-associated protein E [virulence]"
          /"ID=B40_02198
          /protein_id="gnl|SC|B40_02198""""
          /codon_start=1
CDS         20974..21201
          /ID=B40_02199
          /color=1
          /locus_tag="B40_02199"
          /note="hypothetical protein"
          /product="hypothetical protein"
          /protein_id="gnl|SC|B40_02199"
          /codon_start=1
CDS         21214..22863
          /ID=B40_02200
          /color=9
          /locus_tag="B40_02200"
          /note="protein motif:Pfam:PF00239.15"
          /product="Serine recombinase [recombinase]"
          /protein_id="gnl|SC|B40_02200"
          /codon_start=1
CDS         complement(22934..23854)
          /color=7
          /locus_tag="B40_02201"
          /note="AraC family transcriptional regulator
          helix-turn-helix domain, protein motif:CLUSTERS:PRK10572
          protein motif:Cdd:COG2169 protein motif:TIGRFAMs:TIGR04094
          protein motif:Pfam:PF12833.1"
          /product="AraC family transcriptional regulator
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            helix-turn-helix domain [transcriptional regulator]"
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            /protein_id="gnl|SC|B40_02201"""
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CDS            24070..25083
            /color=8
            /locus_tag="B40_02202"
            /note="ABC transporter substrate-binding protein yclQ,
            similar to AA sequence:UniProtKB:P94421 protein
            motif:CLUSTERS:PRK10957 protein motif:Cdd:COG4594 protein
            motif:Pfam:PF01497.12"
            /product="ABC transporter substrate-binding protein yclQ
            [transporter]"
            /"ID=B40_02202
            /protein_id="gnl|SC|B40_02202"""
            /gene="yclQ"
            /codon_start=1
CDS            25049..26122
            /color=8
            /locus_tag="B40_02203"
            /note="Iron-uptake system permease protein FeuB  iron ABC
            transporter permease, similar to AA
            sequence:UniProtKB:P40410 protein motif:CLUSTERS:PRK10577
            protein motif:Cdd:COG0609 protein motif:TIGRFAMs:TIGR03869
            protein motif:Pfam:PF01032.12"
            /product="Iron-uptake system permease protein FeuB  iron
            ABC transporter permease [transporter]"
            /"ID=B40_02203
            /protein_id="gnl|SC|B40_02203"""
            /gene="feuB"
            /codon_start=1
CDS            26119..27114
            /color=8
            /locus_tag="B40_02204"
            /note="Iron-uptake system permease protein FeuC  iron ABC
            transporter permease, similar to AA
            sequence:UniProtKB:P40411 protein motif:CLUSTERS:PRK10577
            protein motif:Cdd:COG0609 protein motif:TIGRFAMs:TIGR03869
            protein motif:Pfam:PF01032.12"
            /product="Iron-uptake system permease protein FeuC  iron
            ABC transporter permease [transporter]"
            /"ID=B40_02204
            /protein_id="gnl|SC|B40_02204"""
            /gene="feuC"
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          /codon_start=1
CDS         27128..27940
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          /locus_tag="B40_02205"
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          protein, similar to AA sequence:UniProtKB:O32188 protein
          motif:CLUSTERS:PRK11231 protein motif:Cdd:COG4604 protein
          motif:TIGRFAMs:TIGR03873 protein motif:Pfam:PF00005.21"
          /product="Iron dicitrate  ABC transporter ATP-binding
          protein [transporter]"
          /"ID=B40_02205
          /protein_id="gnl|SC|B40_02205""""
          /codon_start=1
CDS         28083..29861
          /color=8
          /locus_tag="B40_02206"
          /eC_number=3.6.3.-
          /note="Iron import ATP-binding/permease protein IrtA,
          similar to AA sequence:UniProtKB:P63391 protein
          motif:CLUSTERS:PRK13657 protein motif:Cdd:COG2274 protein
          motif:TIGRFAMs:TIGR02204 protein motif:Pfam:PF00005.21"
          /product="Iron import ATP-binding/permease protein IrtA
          [transporter]"
          /"ID=B40_02206
          /protein_id="gnl|SC|B40_02206""""
          /gene="irtA"
          /codon_start=1
CDS         29858..31606
          /color=8
          /locus_tag="B40_02207"
          /note="Putative multidrug export ATP-binding/permease
          protein SAV1866, similar to AA sequence:UniProtKB:Q99T13
          protein motif:CLUSTERS:PRK13657 protein motif:Cdd:COG2274
          protein motif:TIGRFAMs:TIGR02203 protein
          motif:Pfam:PF00664.17"
          /product="Putative multidrug export ATP-binding/permease
          protein SAV1866 [transporter]"
          /"ID=B40_02207
          /protein_id="gnl|SC|B40_02207""""
          /codon_start=1
CDS         32071..32439
          /color=8
          /locus_tag="B40_02208"
          /note="MN-binding protein  fumarate reductase flavoprotein
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          subunit, protein motif:Cdd:COG4659 protein
          motif:TIGRFAMs:TIGR01947 protein motif:Pfam:PF04205.8"
          /product="FMN-binding protein  fumarate reductase
          flavoprotein subunit"
          /"ID=B40_02208
          /protein_id="gnl|SC|B40_02208"""
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CDS            32795..33034
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          /color=4
          /locus_tag="B40_02209"
          /note="TraM recognition domain-containing protein  type IV
          secretory system conjugative DNA transfer family protein"
          /product="TraM recognition domain-containing protein  type
          IV secretory system conjugative DNA transfer family
          protein [relaxosome]"
          /protein_id="gnl|SC|B40_02209"
          /codon_start=1
CDS            33099..33239
          /color=1
          /locus_tag="B40_02210"
          /note="Maff2 family protein, protein motif:Pfam:PF12750.1"
          /product="Maff2 family protein"
          /"ID=B40_02210
          /protein_id="gnl|SC|B40_02210"""
          /codon_start=1
CDS            33389..34429
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          /locus_tag="B40_02211"
          /note="Transcriptional repressor DicA  helix-turn-helix,
          protein motif:CLUSTERS:PRK09706 protein motif:Cdd:COG3800
          protein motif:TIGRFAMs:TIGR03070 protein
          motif:Pfam:PF12844.1"
          /product="Transcriptional repressor DicA  helix-turn-helix
          [transcriptional regulator]"
          /"ID=B40_02211
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CDS            34596..35039
          /color=7
          /locus_tag="B40_02212"
          /note="RNA polymerase sigma factor  Sigma-70  region 4,
          protein motif:CLUSTERS:PRK11924 protein
          motif:TIGRFAMs:TIGR02937 protein motif:Pfam:PF08281.6"
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          /product="RNA polymerase sigma factor  Sigma-70  region 4
          [transcriptional regulator]"
          /"ID=B40_02212
          /protein_id="gnl|SC|B40_02212"""
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CDS          35032..35232
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          motif:Pfam:PF12645.1"
          /product="helix-turn-helix domain-containing protein
          [transcriptional regulator]"
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          /protein_id="gnl|SC|B40_02213"""
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CDS          35288..35659
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          /color=1
          /locus_tag="B40_02214"
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          /product="hypothetical protein"
          /protein_id="gnl|SC|B40_02214"
          /codon_start=1
CDS          36276..36671
          /ID=B40_02215
          /color=4
          /locus_tag="B40_02215"
          /note="plasmid mobilization relaxosome protein MobC"
          /product="Plasmid mobilization relaxosome protein MobC
          [relaxosome]"
          /protein_id="gnl|SC|B40_02215"
          /gene="mobC"
          /codon_start=1
CDS          36634..38265
          /color=4
          /locus_tag="B40_02216"
          /note="Relaxase/Mobilisation nuclease domain , protein
          motif:Pfam:PF03432.8"
          /product="Relaxase/Mobilisation nuclease domain
          [relaxase]"
          /"ID=B40_02216
          /protein_id="gnl|SC|B40_02216"""
          /codon_start=1
CDS          38450..38662
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                /codon_start=1
CDS                 38652..39395
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                /locus_tag="B40_02218"
                /note="phage replisome organizer N-terminal region,
                protein motif:TIGRFAMs:TIGR01714 protein
                motif:Pfam:PF09681.4"
                /product="phage replisome organizer N-terminal region
                [replication]"
                /"ID=B40_02218
                /protein_id="gnl|SC|B40_02218"""
                /codon_start=1
CDS                 39392..40249
                /color=10
                /locus_tag="B40_02219"
                /note="Primosomal protein DnaI  ATP binding protein,
                similar to AA sequence:UniProtKB:P06567 protein
                motif:CLUSTERS:PRK08116 protein motif:Cdd:COG1484 protein
                motif:Pfam:PF01695.11"
                /product="Primosomal protein DnaI  ATP binding protein
                [replication]"
                /"ID=B40_02219
                /protein_id="gnl|SC|B40_02219"""
                /gene="dnaI"
                /codon_start=1
CDS                 40246..40434
                /ID=B40_02220
                /color=9
                /locus_tag="B40_02220"
                /note="transposon-encoded protein:"
                /product="Transposon-encoded protein TnpW"
                /protein_id="gnl|SC|B40_02220"
                /gene="tnpW"
                /codon_start=1
CDS                 40546..40746
                /ID=B40_02221
                /color=9
                /locus_tag="B40_02221"
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          /note="Serine recombinase TnpX"
          /product="Serine recombinase TnpX [recombinase]"
          /protein_id="gnl|SC|B40_02221"
          /gene="tnpX"
          /codon_start=1
CDS         complement(40739..42412)
          /color=9
          /locus_tag="B40_02222"
          /note="Serine recombinase, protein motif:Pfam:PF00239.15"
          /product="Serine recombinase [recombinase]"
          /"ID=B40_02222
          /protein_id="gnl|SC|B40_02222""""
          /codon_start=1
CDS         complement(42490..42663)
          /ID=B40_02223
          /color=9
          /locus_tag="B40_02223"
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          /product="Transposon-encoded protein TnpW"
          /protein_id="gnl|SC|B40_02223"
          /gene="tnpW"
          /codon_start=1
CDS         complement(43122..43364)
          /color=7
          /locus_tag="B40_02224"
          /note="helix-turn-helix domain-containing protein, protein
          motif:Pfam:PF12645.1"
          /product="helix-turn-helix domain-containing protein
          [transcriptional regulator]"
          /"ID=B40_02224
          /protein_id="gnl|SC|B40_02224""""
          /codon_start=1
CDS         complement(43348..43785)
          /color=7
          /locus_tag="B40_02225"
          /note="RNA polymerase sigma factor  Sigma-70  region 4,
          protein motif:CLUSTERS:PRK11924 protein
          motif:TIGRFAMs:TIGR02937 protein motif:Pfam:PF08281.6"
          /product="RNA polymerase sigma factor  Sigma-70  region 4
          [transcriptional regulator]"
          /"ID=B40_02225
          /protein_id="gnl|SC|B40_02225""""
          /codon_start=1
CDS         complement(44259..45242)
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        /color=8
        /locus_tag="B40_02226"
        /eC_number=2.1.1.192
        /note="23S rRNA adenine 2503 methyl transferase RlmN,
        similar to AA sequence:UniProtKB:Q7A600 protein
        motif:CLUSTERS:PRK14469 protein motif:TIGRFAMs:TIGR00048
        protein motif:Pfam:PF04055.15"
        /product="23S rRNA
        %28adenine%282503%29-C%282%29%29-methyltransferase RlmN
        [methyltransferase]"
        /"ID=B40_02226
        /protein_id="gnl|SC|B40_02226"""
        /gene="rlmN"
        /codon_start=1
CDS       45843..46199
        /color=7
        /locus_tag="B40_02227"
        /note="helix-turn-helix, protein motif:CLUSTERS:PRK08154
        protein motif:Cdd:COG3800 protein motif:Pfam:PF12844.1"
        /product="helix-turn-helix [transcriptional regulator]"
        /"ID=B40_02227
        /protein_id="gnl|SC|B40_02227"""
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CDS       46401..46730
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        /note="Plasmid mobilization relaxosome protein MobC,
        protein motif:Pfam:PF05713.5"
        /product="Plasmid mobilization relaxosome protein MobC
        [relaxosome]"
        /"ID=B40_02228
        /protein_id="gnl|SC|B40_02228"""
        /gene="mobC"
        /codon_start=1
CDS       46691..48025
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        /note="Relaxase/Mobilisation nuclease domain, protein
        motif:Pfam:PF03432.8"
        /product="Relaxase/Mobilisation nuclease domain
        [relaxase]"
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CDS         complement(48227..48436)
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        TTRAP"
        /protein_id="gnl|SC|B40_02230"
        /codon_start=1
CDS         complement(48441..51788)
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        /note="Antirestriction protein ArdA, protein
        motif:Pfam:PF07275.5"
        /product="Antirestriction protein ArdA [anti-ristriction
        modification]"
        /"ID=B40_02231
        /protein_id="gnl|SC|B40_02231""""
        /gene="ardA"
        /codon_start=1
CDS         complement(51914..52282)
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        /note="conjugal transfer protein Cysteine-rich VLP"
        /product="conjugal transfer protein  Cysteine-rich VLP"
        /protein_id="gnl|SC|B40_02232"
        /codon_start=1
CDS         complement(52279..54354)
        /color=10
        /locus_tag="B40_02233"
        /eC_number=5.99.1.2
        /note="Type IA DNA topoisomerase, similar to AA
        sequence:UniProtKB:P14294 protein motif:CLUSTERS:PRK07726
        protein motif:Cdd:COG0550 protein motif:TIGRFAMs:TIGR01056
        protein motif:Pfam:PF01131.14"
        /product="Type IA DNA topoisomerase [topoisomerase]"
        /"ID=B40_02233
        /protein_id="gnl|SC|B40_02233""""
        /codon_start=1
CDS         complement(54351..55100)
        /color=1
        /locus_tag="B40_02234"
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          /protein_id="gnl|SC|B40_02234"""
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          /locus_tag="B40_02235"
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          /note="phosphoadenosine phosphosulfate reductase, protein
          motif:CLUSTERS:PRK13794 protein motif:Cdd:COG5270"
          /product="phosphoadenosine phosphosulfate reductase
          [reductase]"
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          /eC_number=3.4.19.11
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          endopeptidase CwlS , similar to AA
          sequence:UniProtKB:O31852 protein motif:CLUSTERS:PRK13914
          protein motif:Cdd:COG3584 protein motif:TIGRFAMs:TIGR02594
          protein motif:Pfam:PF00877.13"
          /product="D-gamma-glutamyl-meso-diaminopimelic acid
          endopeptidase CwlS [pepidase]"
          /"ID=B40_02237
          /protein_id="gnl|SC|B40_02237"""
          /gene="cwlS"
          /codon_start=1
CDS         complement(58066..59022)
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          /locus_tag="B40_02238"
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          /note="Adenine specific DNA methyltransferase, similar to
          AA sequence:UniProtKB:P09358 protein
          motif:CLUSTERS:PRK11524 protein motif:Cdd:COG2189 protein
          motif:Pfam:PF01555.12"
          /product="Adenine specific DNA methyltransferase
          [methyltransferase]"
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          /protein_id="gnl|SC|B40_02238"""
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CDS          complement(59019..61415)
          /color=4
          /note="Type IV secretory system protein TraC  VirB4
          components  AAA domain, protein motif:Cdd:COG3451 protein
          motif:TIGRFAMs:TIGR02746 protein
          motif:Pfam:PF12846.1locus_tag=B40_02239product=Conjugal"
          /product="Type IV secretory system protein TraC  VirB4
          components  AAA domain [ATPase  mating pair formation]"
          /"ID=B40_02239
          /gene="traC"""
          /protein_id="gnl|SC|B40_02239"
          /codon_start=1
CDS          complement(61375..61767)
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          /locus_tag="B40_02240"
          /note="PrgI family protein  Type IV secretion system,
          protein motif:Pfam:PF12666.1"
          /product="PrgI family protein  Type IV secretion system"
          /"ID=B40_02240
          /protein_id="gnl|SC|B40_02240"""
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CDS          complement(61769..62317)
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          /note="Transcriptional activator  adenine-specific DNA
          methyltransferase, protein motif:Cdd:COG4725 protein
          motif:Pfam:PF05063.8"
          /product="Transcriptional activator  adenine-specific DNA
          methyltransferase [methyltransferase]"
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          /protein_id="gnl|SC|B40_02241"""
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CDS          complement(62328..63191)
          /ID=B40_02242
          /color=1
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                    conjugative transposon protein"
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                    /note="Serine recombinase, protein motif:Pfam:PF07508.7"
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                    /color=9
                    /locus_tag="B40_02244"
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                    /product="Transposon-encoded protein TnpW"
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                    /gene="tnpW"
                    /codon_start=1
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                    similar to AA sequence:UniProtKB:P06567 protein
                    motif:CLUSTERS:PRK08116 protein motif:Cdd:COG1484 protein
                    motif:Pfam:PF01695.11"
                    /product="Primosomal protein DnaI  ATP binding protein
                    [replication]"
                    /"ID=B40_02245
                    /protein_id="gnl|SC|B40_02245""""
                    /gene="dnaI"
                    /codon_start=1
     CDS              complement(66192..66950)
                    /color=10
                    /locus_tag="B40_02246"
                    /note="phage replisome organizer protein, protein
                    motif:TIGRFAMs:TIGR01714 protein motif:Pfam:PF09681.4"
                    /product="phage replisome organizer protein [replication]"
                    /"ID=B40_02246
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          /note="Relaxase/Mobilisation nuclease domain:protein
          motif:Pfam:PF03432.8"
          /product="Relaxase/Mobilisation nuclease domain
          [relaxase]"
          /protein_id="gnl|SC|B40_02247"
          /codon_start=1
CDS          complement(68912..69310)
          /ID=B40_02248
          /color=4
          /locus_tag="B40_02248"
          /note="Plasmid mobilization relaxosome protein MobC"
          /product="Plasmid mobilization relaxosome protein MobC
          [relaxosome]"
          /protein_id="gnl|SC|B40_02248"
          /gene="mobC"
          /codon_start=1
CDS          complement(69844..70047)
          /color=7
          /locus_tag="B40_02249"
          /note="helix-turn-helix domain-containing protein, protein
          motif:Pfam:PF12645.1"
          /product="helix-turn-helix domain-containing protein
          [transcriptional regulator]"
          /"ID=B40_02249
          /protein_id="gnl|SC|B40_02249""""
          /codon_start=1
CDS          70742..72661
          /color=2
          /locus_tag="B40_02250"
          /note="Tetracycline resistance protein tetM from
          transposon Tn916, similar to AA sequence:UniProtKB:P21598
          protein motif:CLUSTERS:PRK13351 protein motif:Cdd:COG0050
          protein motif:TIGRFAMs:TIGR00484 protein
          motif:Pfam:PF00009.21"
          /product="Tetracycline resistance protein tetM from
          transposon Tn916 [antibiotic resistance]"
          /"ID=B40_02250
          /protein_id="gnl|SC|B40_02250""""
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          /gene="tetM"
          /codon_start=1
CDS          72713..73951
          /color=2
          /locus_tag="B40_02251"
          /note="tetracycline efflux MFS transporter Tet40, protein
          motif:CLUSTERS:PRK10054 protein motif:TIGRFAMs:TIGR00880
          protein motif:Pfam:PF07690.10"
          /product="tetracycline efflux MFS transporter Tet40
          [antibiotic resistance]"
          /"ID=B40_02251
          /protein_id="gnl|SC|B40_02251""""
          /gene="tet40"
          /codon_start=1
CDS          complement(74094..74234)
          /color=1
          /locus_tag="B40_02252"
          /note="Maff2 family protein  membrane protein  conjugal
          transfer protein, protein motif:Pfam:PF12750.1"
          /product="Maff2 family protein  membrane protein  conjugal
          transfer protein"
          /"ID=B40_02252
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CDS          complement(74302..75051)
          /color=4
          /locus_tag="B40_02253"
          /note="type IV secretion system protein TraG  VirD4
          components, protein motif:CLUSTERS:PRK13850 protein
          motif:Cdd:COG3505 protein motif:TIGRFAMs:TIGR02759 protein
          motif:Pfam:PF12696.1"
          /product="type IV secretion system protein TraG  VirD4
          components [coupling protein]"
          /"ID=B40_02253
          /protein_id="gnl|SC|B40_02253""""
          /gene="traG"
          /codon_start=1
CDS          complement(75228..75593)
          /ID=B40_02254
          /color=1
          /locus_tag="B40_02254"
          /note="hypothetical protein"
          /product="hypothetical protein"
          /protein_id="gnl|SC|B40_02254"
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CDS          complement(75672..75863)
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          /note="transposon-encoded protein TnpW"
          /product="Transposon-encoded protein TnpW"
          /protein_id="gnl|SC|B40_02255"
          /gene="tnpW"
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          /codon_start=1
CDS          complement(75907..76770)
          /color=10
          /locus_tag="B40_02256"
          /note="DNA replication protein dnaC  ATP binding protein,
          similar to AA sequence:UniProtKB:P0AEF0 protein
          motif:CLUSTERS:PRK08116 protein motif:Cdd:COG1484 protein
          motif:TIGRFAMs:TIGR00362 protein motif:Pfam:PF01695.11"
          /product="DNA replication protein dnaC  ATP binding
          protein [replication]"
          /"ID=B40_02256
          /protein_id="gnl|SC|B40_02256""""
          /gene="dnaC"
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CDS          complement(76767..77519)
          /color=10
          /locus_tag="B40_02257"
          /note="phage replisome organizer  putative  N-terminal
          region, protein motif:TIGRFAMs:TIGR01714 protein
          motif:Pfam:PF09681.4"
          /product="phage replisome organizer  putative  N-terminal
          region [replication]"
          /"ID=B40_02257
          /protein_id="gnl|SC|B40_02257""""
          /codon_start=1
CDS          complement(77633..78031)
          /ID=B40_02258
          /color=1
          /locus_tag="B40_02258"
          /note="Cysteine-rich VLP domain-containing protein"
          /product="Cysteine-rich VLP domain-containing protein"
          /protein_id="gnl|SC|B40_02258"
          /codon_start=1
CDS          complement(78012..78188)
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          /ID=B40_02259
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          /locus_tag="B40_02259"
          /note="hypothetical protein"
          /product="hypothetical protein"
          /protein_id="gnl|SC|B40_02259"
          /codon_start=1
CDS         complement(78288..79838)
          /color=4
          /locus_tag="B40_02260"
          /note="Plasmid mobilization system relaxase  MobA/MobL
          family, similar to AA sequence:UniProtKB:P07112 protein
          motif:CLUSTERS:PRK13889 protein motif:TIGRFAMs:TIGR02768
          protein motif:Pfam:PF03389.9"
          /product="DNA strand transferase  Plasmid mobilization
          system relaxase  MobA/MobL family [relaxase]"
          /"ID=B40_02260
          /protein_id="gnl|SC|B40_02260""""
          /gene="mobA"
          /codon_start=1
CDS         complement(79921..80217)
          /color=1
          /locus_tag="B40_02261"
          /note="Protein of unknown function  DUF3847, protein
          motif:Pfam:PF12958.1"
          /product="Protein of unknown function  DUF3847"
          /"ID=B40_02261
          /protein_id="gnl|SC|B40_02261""""
          /codon_start=1
CDS         complement(80157..80696)
          /color=7
          /locus_tag="B40_02262"
          /note="RNA polymerase sigma factor  Sigma-70  region 4,
          protein motif:TIGRFAMs:TIGR02937"
          /product="RNA polymerase sigma factor  Sigma-70  region 4
          [transcriptional regulator]"
          /"ID=B40_02262
          /protein_id="gnl|SC|B40_02262""""
          /codon_start=1
CDS         complement(80693..81154)
          /color=7
          /locus_tag="B40_02263"
          /note="RNA polymerase sigma factor  Sigma-70  region 4,
          protein motif:TIGRFAMs:TIGR02937 protein
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          motif:Pfam:PF08281.6"
          /product="RNA polymerase sigma factor  Sigma-70  region 4
          [transcriptional regulator]"
          /"ID=B40_02263
          /protein_id="gnl|SC|B40_02263"""
          /codon_start=1
CDS          complement(81165..81617)
          /color=7
          /locus_tag="B40_02264"
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          motif:CLUSTERS:PRK11924 protein motif:TIGRFAMs:TIGR02937"
          /product="RNA polymerase sigma factor  Sigma-24
          [transcriptional regulator]"
          /"ID=B40_02264
          /protein_id="gnl|SC|B40_02264"""
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CDS          complement(81721..82134)
          /color=7
          /locus_tag="B40_02265"
          /note="RNA polymerase sigma factor  Sigma-70  region 4,
          protein motif:TIGRFAMs:TIGR02937 protein
          motif:Pfam:PF08281.6"
          /product="RNA polymerase sigma factor  Sigma-70  region 4
          [transcriptional regulator]"
          /"ID=B40_02265
          /protein_id="gnl|SC|B40_02265"""
          /codon_start=1
CDS          complement(82624..84279)
          /color=8
          /locus_tag="B40_02266"
          /note="ABC-F family ATP-binding cassette domain-containing
          protein, similar to AA sequence:UniProtKB:P63389 protein
          motif:CLUSTERS:PRK11819 protein motif:Cdd:COG4555 protein
          motif:TIGRFAMs:TIGR03719 protein motif:Pfam:PF00005.21"
          /product="ABC-F family ATP-binding cassette
          domain-containing protein [transporter]"
          /"ID=B40_02266
          /protein_id="gnl|SC|B40_02266"""
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CDS          complement(84598..84951)
          /ID=B40_02267
          /color=9
          /locus_tag="B40_02267"
          /note="transposon-encoded TnpV family protein"
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             /product="Transposon-encoded TnpV family protein"
             /protein_id="gnl|SC|B40_02267"
             /gene="tnpV"
             /codon_start=1
CDS             complement(84978..86858)
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             /locus_tag="B40_02268"
             /note="Serine recombinase, protein motif:Pfam:PF07508.7"
             /product="Serine recombinase [recombinase]"
             /"ID=B40_02268
             /protein_id="gnl|SC|B40_02268"""
             /codon_start=1
CDS             complement(86932..87906)
             /color=4
             /locus_tag="B40_02269"
             /note="type IV secretion system protein TraG  VirD4
             components, protein motif:CLUSTERS:PRK13876 protein
             motif:Cdd:COG3505 protein motif:Pfam:PF02534.8"
             /product="type IV secretion system protein TraG  VirD4
             components [coupling protein]"
             /"ID=B40_02269
             /protein_id="gnl|SC|B40_02269"""
             /gene="traG"
             /codon_start=1
CDS             complement(87903..88376)
             /color=1
             /locus_tag="B40_02270"
             /note="uncharacterised PcfB family protein, protein
             motif:Pfam:PF12687.1"
             /product="uncharacterised PcfB family protein"
             /"ID=B40_02270
             /protein_id="gnl|SC|B40_02270"""
             /codon_start=1
CDS             complement(88413..89357)
             /ID=B40_02271
             /color=7
             /locus_tag="B40_02271"
             /note="helix-turn-helix domain-containing protein"
             /product="helix-turn-helix domain-containing protein
             [transcriptional regulator]"
             /protein_id="gnl|SC|B40_02271"
             /codon_start=1
CDS             complement(89486..89704)
             /ID=B40_02272
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           /locus_tag="B40_02272"
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           /product="hypothetical protein"
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CDS           89908..91311
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           /note="Serine recombinase, protein motif:Pfam:PF07508.7"
           /product="Serine recombinase [recombinase]"
           /"ID=B40_02273
           /protein_id="gnl|SC|B40_02273"""
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CDS           91570..92433
           /ID=B40_02274
           /color=1
           /locus_tag="B40_02274"
           /note="hypothetical protein  membrane protein  putative
           conjugal transfer protein TrbL/VirB6"
           /product="hypothetical protein  membrane protein  putative
           conjugal transfer protein TrbL/VirB6"
           /protein_id="gnl|SC|B40_02274"
           /codon_start=1
CDS           92743..93972
           /color=9
           /locus_tag="B40_02275"
           /note="IS91 family transposase, protein
           motif:Pfam:PF04986.7"
           /product="IS91 family transposase [DDE recombinase]"
           /"ID=B40_02275
           /protein_id="gnl|SC|B40_02275"""
           /codon_start=1
CDS           94026..94211
           /ID=B40_02276
           /color=1
           /locus_tag="B40_02276"
           /note="hypothetical protein"
           /product="hypothetical protein"
           /protein_id="gnl|SC|B40_02276"
           /codon_start=1
CDS           94168..94635
           /ID=B40_02277
           /color=1
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            /locus_tag="B40_02277"
            /note="hypothetical protein"
            /product="hypothetical protein"
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            /ID=B40_02278
            /color=4
            /note="protein motif:Cdd:COG3451 protein
            motif:TIGRFAMs:TIGR02746 protein
            motif:Pfam:PF12846.1locus_tag=B40_02278product=Conjugal"
            /product="Type IV secretory system protein TraC  VirB4
            components  AAA domain [ATPase  mating pair formation]"
            /gene="traC"
            /protein_id="gnl|SC|B40_02278"
            /codon_start=1
CDS            97385..98623
            /ID=B40_02279
            /color=4
            /locus_tag="B40_02279"
            /note="NlpC/P60 family protein"
            /product="NlpC/P60 family protein [pepidase]"
            /protein_id="gnl|SC|B40_02279"
            /codon_start=1
CDS            98636..99331
            /color=4
            /locus_tag="B40_02280"
            /note="NlpC/P60 family protein, similar to AA
            sequence:UniProtKB:P21171 protein motif:CLUSTERS:PRK13914
            protein motif:Cdd:COG3584 protein motif:Pfam:PF00877.13"
            /product="NlpC/P60 family protein [pepidase]"
            /"ID=B40_02280
            /protein_id="gnl|SC|B40_02280"""
            /codon_start=1
CDS            99355..99618
            /ID=B40_02281
            /color=1
            /locus_tag="B40_02281"
            /note="hypothetical protein DUF4315 containing protein
            conjugative transposon"
            /product="hypothetical protein  DUF4315 containing protein
            conjugative transposon protein"
            /protein_id="gnl|SC|B40_02281"
            /codon_start=1
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CDS         99608..100375
          /ID=B40_02282
          /color=1
          /locus_tag="B40_02282"
          /note="hypothetical protein"
          /product="hypothetical protein  DUF4366 containing protein
          cell surface protein"
          /protein_id="gnl|SC|B40_02282"
          /codon_start=1
CDS         100372..102462
          /color=10
          /locus_tag="B40_02283"
          /eC_number=5.99.1.2
          /note="DNA topoisomerase III, similar to AA
          sequence:UniProtKB:P14294 protein motif:CLUSTERS:PRK07726
          protein motif:Cdd:COG0550 protein motif:TIGRFAMs:TIGR01056
          protein motif:Pfam:PF01131.14"
          /product="DNA topoisomerase III [replication]"
          /"ID=B40_02283
          /protein_id="gnl|SC|B40_02283""""
          /codon_start=1
CDS         102672..102827
          /ID=B40_02284
          /color=1
          /locus_tag="B40_02284"
          /note="hypothetical protein"
          /product="hypothetical protein"
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          protein motif:Pfam:PF12847.1"
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          protein motif:TIGRFAMs:TIGR00180 protein
          motif:Pfam:PF02195.12"
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          motif:CLUSTERS:PRK13869 protein motif:Cdd:COG2894 protein
          motif:TIGRFAMs:TIGR03453 protein motif:Pfam:PF01656.17"
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          /gene="parA"
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          motif:Cdd:COG3464 protein motif:Pfam:PF01610.11"
          /product="ISL3 family transposase [DDE recombinase]"
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          protein motif:Pfam:PF07505.5"
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                     motif:Cdd:COG3311 protein motif:TIGRFAMs:TIGR01764 protein
                     motif:Pfam:PF12728.1"
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                     motif:TIGRFAMs:TIGR01764 protein motif:Pfam:PF12728.1"
                     /product="DNA binding domain  excisionase family
                     Helix-turn-helix domain [excisionase]"
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              protein motif:CLUSTERS:PRK09907 protein
              motif:Pfam:PF02452.11"
              /product="Type II toxin-antitoxin system PemK/MazF family
              toxin MazF [toxin-antitoxin]"
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              /protein_id="gnl|SC|C83_00316""""
              /gene="mazF"
              /codon_start=1
CDS             complement(49697..49912)
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              /note="Antitoxin PezA  XRE family HTH domain
              [toxin-antitoxin], similar to AA sequence:UniProtKB:Q97QZ2
              protein motif:CLUSTERS:PRK08154 protein motif:Cdd:COG3800
              protein motif:TIGRFAMs:TIGR03070 protein
              motif:Pfam:PF12844.1"
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CDS             complement(50264..50827)
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              [transcriptional regulator]"
              /product="Phage transcriptional regulator  ArpU family
              [transcriptional regulator]"
              /protein_id="gnl|SC|C83_00318"
              /codon_start=1
CDS             51114..51563
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              /locus_tag="C83_00319"
              /note="helix-turn-helix HTH transcriptional regulator
              containing a XRE family HTH domain [transcriptional
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            regulator], protein motif:CLUSTERS:PRK09706 protein
            motif:Pfam:PF12844.1"
            /product="helix-turn-helix %28HTH%29 transcriptional
            regulator containing a XRE family HTH domain
            [transcriptional regulator]"
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CDS            51615..52169
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            sequence:UniProtKB:Q01609 protein motif:Cdd:COG4925
            protein motif:Pfam:PF12695.1"
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            /protein_id="gnl|SC|C83_00321"
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            motif:Pfam:PF02627.1"
            /product="4-carboxymuconolactone decarboxylase
            [carboxy-lyase]"
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            /protein_id="gnl|SC|C83_00322"
            /gene="pcaC"
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CDS          complement(53951..54052)
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          /product="carboxymuconolactone decarboxylase family
          protein [carboxyl-lyase]"
          /protein_id="gnl|SC|C83_00323"
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CDS          complement(54056..54595)
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          similar to AA sequence:UniProtKB:Q188R7 protein
          motif:CLUSTERS:PRK03767 protein motif:Cdd:COG0431 protein
          motif:TIGRFAMs:TIGR03567 protein motif:Pfam:PF03358.9"
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          /protein_id="gnl|SC|C83_00324"
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CDS          54702..55139
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          /locus_tag="C83_00325"
          /note="HTH-type transcriptional regulator AdhR  response
          to aldehyde stress [transcriptional regulator], similar to
          AA sequence:UniProtKB:O06008 protein
          motif:CLUSTERS:PRK09514 protein motif:Cdd:COG4978 protein
          motif:TIGRFAMs:TIGR02043 protein motif:Pfam:PF00376.17"
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          /gene="adhR"
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CDS               complement(57909..58256)
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                motif:CLUSTERS:PRK10250 protein motif:Cdd:COG2315 protein
                motif:Pfam:PF04237.7"
                /product="MmcQ/YjbR family DNA-binding protein"
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                /eC_number=3.1.21.3
                /note="Type 1 restriction endonuclease subunit R, similar
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                motif:TIGRFAMs:TIGR00348 protein motif:Pfam:PF11867.2"
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                /gene="hsdR"
                /codon_start=1
CDS               complement(61471..62652)
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                /note="Type I restriction enzyme EcoKI  subunit S
                [restriction modification], protein
                motif:CLUSTERS:PRK09737 protein motif:Cdd:COG1708 protein
                motif:Pfam:PF01420.13"
                /product="Type I restriction enzyme EcoKI  subunit S
                [restriction modification]"
                /"ID=C83_00330
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          /eC_number=2.1.1.72
          /note="Type I restriction enzyme EcoKI  subunit M, similar
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          protein motif:TIGRFAMs:TIGR00497 protein
          motif:Pfam:PF02384.10"
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          [restriction modification]"
          /"ID=C83_00331
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          /gene="hsdM"
          /codon_start=1
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          regulator], protein motif:Cdd:COG3655 protein
          motif:Pfam:PF01381.16"
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          containing a XRE family HTH domain [transcriptional
          regulator]"
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          /protein_id="gnl|SC|C83_00332"
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          motif:Pfam:PF00239.15"
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          /protein_id="gnl|SC|C83_00333"
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CDS         complement(67212..67454)
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         /note="helix-turn-helix domain-containing protein
         [transcriptional regulator], protein motif:Pfam:PF12645.1"
         /product="helix-turn-helix domain-containing protein
         [transcriptional regulator]"
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CDS         complement(67438..67875)
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         /locus_tag="C83_00336"
         /note="RNA polymerase sigma factor  Sigma-70  region 4,
         protein motif:CLUSTERS:PRK11924 protein
         motif:TIGRFAMs:TIGR02937 protein motif:Pfam:PF08281.6"
         /product="RNA polymerase sigma factor  Sigma-70  region 4"
         /"ID=C83_00336
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         /protein_id="gnl|SC|C83_00336"
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         /eC_number=2.1.1.192
         /note="23S rRNA adenine-C-methyltransferase RlmN, similar
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         motif:CLUSTERS:PRK14469 protein motif:TIGRFAMs:TIGR00048
         protein motif:Pfam:PF04055.15"
         /product="23S rRNA
         %28adenine%282503%29-C%282%29%29-methyltransferase RlmN
         [methyltransferase]"
         /"ID=C83_00337
         /protein_id="gnl|SC|C83_00337"""
         /gene="rlmN"
         /codon_start=1
CDS         69583..70830
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            protein motif:Pfam:PF01610.11"
            /product="ISL3 family transposase"
            /"ID=C83_00338
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            /protein_id="gnl|SC|C83_00338"
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CDS            complement(70861..72081)
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            /locus_tag="C83_00339"
            /note="Macrolide efflux protein A  Major Facilitator
            Superfamily [antibiotic resistance], similar to AA
            sequence:UniProtKB:P64783 protein motif:CLUSTERS:PRK10489
            protein motif:Cdd:COG2814 protein motif:TIGRFAMs:TIGR00900
            protein motif:Pfam:PF07690.10"
            /product="Macrolide efflux protein A  Major Facilitator
            Superfamily [antibiotic resistance]"
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            /gene="mefA"
            /protein_id="gnl|SC|C83_00339"
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CDS            complement(73086..73352)
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            /locus_tag="C83_00340"
            /note="Conjugatice transposon membrane protein"
            /product="Conjugatice transposon membrane protein"
            /protein_id="gnl|SC|C83_00340"
            /codon_start=1
CDS            complement(73426..73641)
            /color=4
            /locus_tag="C83_00341"
            /note="Conjugal transfer protein  Maff2 family, protein
            motif:Pfam:PF12750.1"
            /product="Conjugal transfer protein  Maff2 family"
            /"ID=C83_00341
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            /protein_id="gnl|SC|C83_00341"
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CDS            complement(73709..75109)
            /color=4
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          /note="Type IV secretion system protein TraG  VirD4
          component [coupling protein], protein
          motif:CLUSTERS:PRK13850 protein motif:Cdd:COG3505 protein
          motif:TIGRFAMs:TIGR02759 protein motif:Pfam:PF02534.8"
          /product="Type IV secretion system protein TraG  VirD4
          component [coupling protein]"
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          /gene="traG"
          /protein_id="gnl|SC|C83_00342"
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CDS          complement(75288..77189)
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          /note="Replication initiation protein RepA [replication],
          protein motif:CLUSTERS:PRK11823 protein motif:Cdd:COG0358
          protein motif:TIGRFAMs:TIGR02237"
          /product="Replication initiation protein RepA
          [replication]"
          /"ID=C83_00343
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          /gene="repA"
          /protein_id="gnl|SC|C83_00343"
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CDS          complement(77205..78593)
          /color=4
          /locus_tag="C83_00344"
          /note="MobA/MobL family protein  DNA strand transferase
          MobA [relaxase], similar to AA sequence:UniProtKB:P07112
          protein motif:CLUSTERS:PRK13889 protein
          motif:TIGRFAMs:TIGR02768 protein motif:Pfam:PF03389.9"
          /product="MobA/MobL family protein  DNA strand transferase
          MobA [relaxase]"
          /"ID=C83_00344
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          /protein_id="gnl|SC|C83_00344"
          /gene="mobA"
          /codon_start=1
CDS          complement(78945..79250)
          /color=8
          /locus_tag="C83_00345"
          /note="DUF3847 domain-containing protein  AAA family
          ATPase, protein motif:Pfam:PF12958.1"
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          ATPase"
          /"ID=C83_00345
          /"
          /protein_id="gnl|SC|C83_00345"
          /codon_start=1
CDS          complement(79372..80205)
          /color=8
          /locus_tag="C83_00346"
          /eC_number=2.1.1.187
          /note="23S rRNA methyltransferase
          guanine-N-methyltransferase , similar to AA
          sequence:UniProtKB:P36999 protein motif:CLUSTERS:PRK11088
          protein motif:TIGRFAMs:TIGR02072 protein
          motif:Pfam:PF08241.6"
          /product="23S rRNA methyltransferase
          %28guanine%28745%29-N%281%29%29-methyltransferase
          [methyltransferase]"
          /"ID=C83_00346
          /protein_id="gnl|SC|C83_00346""""
          /gene="rlmA"
          /codon_start=1
CDS          complement(80391..80687)
          /ID=C83_00347
          /color=8
          /locus_tag="C83_00347"
          /note="Molecular chaperone"
          /product="Molecular chaperone"
          /protein_id="gnl|SC|C83_00347"
          /codon_start=1
CDS          complement(80822..81013)
          /ID=C83_00348
          /color=9
          /locus_tag="C83_00348"
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          /product="Transposon-encoded protein TnpW"
          /gene="tnpW"
          /protein_id="gnl|SC|C83_00348"
          /codon_start=1
CDS          complement(81092..81943)
          /ID=C83_00349
          /color=9
          /locus_tag="C83_00349"
          /note="Site-specific recombinase  DUF4368
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                     domain-containing protein [recombinase]"
                     /product="Site-specific recombinase  DUF4368
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                     motif:Pfam:PF07508.7"
                     /product="Serine recombinase [recombinase]"
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                     /protein_id="gnl|SC|C83_00350"
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                     /ID=C83_00351
                     /color=4
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                     /note="Type IV secretion system protein TraG  VirD4
                     component [coupling protein]"
                     /product="Type IV secretion system protein TraG  VirD4
                     component [coupling protein]"
                     /protein_id="gnl|SC|C83_00351"
                     /gene="traG"
                     /codon_start=1
     CDS                complement(83293..83766)
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                     /locus_tag="C83_00352"
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                     protein, protein motif:Pfam:PF12687.1"
                     /product="PcfB family protein  DUF3801 domain-containing
                     protein"
                     /"ID=C83_00352
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                     /protein_id="gnl|SC|C83_00352"
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          motif:Pfam:PF12846.1"
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21721 tttattgatg gaagactggc gattcctgtt gactaatgta tttaatgaag ccgcatctgc
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22141 tatatgctta tctccaacat catttgccgt tttttcaata gattctgcaa gtttttttatt
22201 tcctctatca gttatcttct taagatatgt tttcaaatac cgcatgtact tttctcctat
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22681 gcatagcaga cattaatatt tgactttgta taatgctttc catcatccaa atgacgttcg
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23101 ttaaagctct ttacaattcg gatctctcca gtatttgatt cctgccactt ttcattaatc
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   23401 aatttcatac tgcacccct ataatacttt agtgttttta ttcaatttta ctacaaaaca
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   24301 acggcatatt acccagatac aaagaaattt gaagatgatt taaagactcg aagaaagagg
   24361 tgatggatat gtgtatgtat tgtaaaaata gtacaactgt caatagcaca acaacacacg
   24421 tcgtaaatta taaaaattgt attattgtaa ttaaaaatgt tccatgcctt gaatgtgatc
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   24541 tggcgaaaaa attaatgcag gaaattgcag ttatcgatta tccacaggtg gcttaataat
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          motif:CLUSTERS:PRK13721 protein motif:Cdd:COG3451 protein
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          motif:Pfam:PF03374.8"
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          /product="lysozyme  Glycoside hydrolase family protein
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          protein motif:TIGRFAMs:TIGR00900 protein
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          motif:CLUSTERS:PRK10975 protein motif:TIGRFAMs:TIGR01575
          protein motif:Pfam:PF00583.18"
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      481 aaacaggcag agcagggaaa ggtcaaaagc tatgtgcagg atattgccct tgcggtgctg
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      661 caggcaggag aaaaggcttg taaaatcagg gataacaagc tggaaaaata ctacaatatg
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    3601 tgacagaagt tcactcatgc ggttcacccc ctttctctac ctgtctgggg gcggtagcgt
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          motif:TIGRFAMs:TIGR02253 protein motif:Pfam:PF00702.1"
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          protein motif:Pfam:PF00501.22"
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          protein motif:Pfam:PF09364.4"
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