Xylophilus ampelinus strain CECT 7646 Ga0244619_101, whole genome shotgun sequence

GenBank: QJTC01000001.1

FASTA Graphics

Go to:

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LOCUS       QJTC01000001          320051 bp    DNA     linear   BCT 12-JUN-
2018
DEFINITION  Xylophilus ampelinus strain CECT 7646 Ga0244619_101, whole
genome
            shotgun sequence.
ACCESSION   QJTC01000001 QJTC01000000
VERSION     QJTC01000001.1
DBLINK      BioProject: PRJNA463320
            BioSample: SAMN09074800
KEYWORDS    WGS.
SOURCE      Xylophilus ampelinus
  ORGANISM  Xylophilus ampelinus
            Bacteria; Pseudomonadati; Pseudomonadota; Betaproteobacteria;
            Burkholderiales; Xylophilus.
REFERENCE   1  (bases 1 to 320051)
  AUTHORS   Whitman,W.
  TITLE     Genomic Encyclopedia of Type Strains, Phase III (KMG-III): the
            genomes of soil and plant-associated and newly described type
            strains
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 320051)
  AUTHORS   Whitman,W., Huntemann,M., Clum,A., Pillay,M., Palaniappan,K.,
            Varghese,N., Mikhailova,N., Stamatis,D., Reddy,T., Daum,C.,
            Shapiro,N., Ivanova,N., Kyrpides,N. and Woyke,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUN-2018) Prokaryotic Super Group, DOE Joint
Genome
            Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     ##Genome-Assembly-Data-START##
            Assembly Method        :: SPAdes v. 3.10.1
            Expected Final Version :: No
            Genome Coverage        :: 290.0x
            Sequencing Technology  :: Illumina HiSeq
            ##Genome-Assembly-Data-END##
FEATURES             Location/Qualifiers
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RAGLVLRSVGESPESAHALGYPVRRIRLAAAVAGGALCGLAGAYISTVYTPLWVEGMV

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CDS 66213..67265
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IWSALDVLKAERIDHGVQAIHDPALMRRLAQDRIALTVCPLSNQKLCVFPDLADHNLG

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CDS 68847..70964
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CDS 71164..71700
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CDS 73050..73454
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gene 73458..73781

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CDS 73458..73781

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gene 73843..74361

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CDS 73843..74361

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/protein_id="PYE79741.1"

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CDS 76339..76677
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gene 76677..77420
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CDS 76677..77420
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CDS complement(88131..88772)
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RGVVNLLAADRLMQSPRLYATLLLWLLSELFEQLPEIGDPDKPKLVFFFDEAHLLFDG

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AVRATAQTMRQKPGLDIEAAITELQVGEALVSLLDAQGRPSVTDRAFVLPPASLLRPI

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CDS 127359..128084
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gene 132392..133012
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KRTRESLAHMLCEPCAVCQGKGSVKTARSVTYDILREILREARQFHPREFRVVASPKV
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CDS complement(134736..136607)
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PGEVVAFVGPSGSGKTTLANLLPRFVLPTAGSVSLQGHDVADWHLPALRAQFAMVSQD

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CDS 136819..138072
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CDS 138117..138653
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ARRASGFDMEVRYHNRHALTDVDYPYAASLKELAEWADFLVIASAGGADTQGLVSAEI

LDALGPQGYLVNISRGTVVDEAALVDALAHNRIAGAGLDVFAREPQVPAALAALDNVV
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     CDS             complement(147573..147728)
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     CDS             complement(147718..147873)
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     CDS             complement(148109..148483)
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system"
/protein_id="PYE79815.1"

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CDS 150528..150917
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CDS 154203..154778
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CDS 154781..155779
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sulfotransferase (PAPS reductase)/FAD synthetase"
/protein_id="PYE79821.1"

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protein"
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gene complement(160113..160331)
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CDS complement(160113..160331)
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gene 161441..162127
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CDS 162124..162357
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gene 164416..165780
/locus_tag="DFQ15_101150"
CDS 164416..165780
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gene 166241..167179
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EIQTIVKGEAVYHTGTAFADVWGKDAVLAFTTPASMQEMGSPSYGYTYQLNEGPEVEE
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CDS 167477..167779
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CDS 167776..168222
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CDS 168298..169056
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gene 169175..172885
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gene 173286..175199
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CDS 192065..193468
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CDS complement(234096..234800)
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CDS complement(234790..236943)
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     CDS             complement(237745..239451)
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SALRTPNFMLPGCFHNHGNYIISLGNLTRWLAEQAEGLGVEIFPGFPAAEVLYDEDGS
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transporter"
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CDS 244720..245877
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/protein_id="PYE79904.1"

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LLPGLDAPWFFRTFVSQEKADSGRLEKQAAIAFDDIWPQVTKLNLYDPLTLLAALPGT
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gene complement(246148..248319)
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CDS complement(246148..248319)
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CDS 248398..248859
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gene 249020..249913
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CDS 249020..249913
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protein"

/protein_id="PYE79907.1"

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CDS 249910..250572
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protein"
/protein_id="PYE79908.1"

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CDS 250625..251440
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binding
protein"
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CDS complement(254125..254499)
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gene complement(254496..255602)
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CDS complement(254496..255602)
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GLKISEFREFANRIATNVLDDQEEIPVKLRSTLDLLRDPTIINQAELAWRLGLAFAGF

NFVVMALAISNVNPRAGRSGNLVFALFAFVVYYNLLNLAQSWMVGGKLNFVGVIVLLH
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gene 256722..258212
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CDS 256722..258212
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gene 258247..258678
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CDS 258247..258678
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/protein_id="PYE79917.1"

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gene 258682..259110
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CDS 258682..259110
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gene 259226..260356
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CDS 259226..260356
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