

LOCUS JAQZAU010000001 5193 bp dna linear ENV 17-MAR-2023
 DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_10007, whole genome
 shotgun sequence.
 ACCESSION JAQZAU010000001 JAQZAU010000000
 VERSION JAQZAU010000001.1
 DBLINK BioProject: PRJNA929258
 BioSample: SAMN33142973
 KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
 REFERENCE 1 (bases 1 to 5193)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 5193)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
 ##Genome-Assembly-Data-END##
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VERSION    JAQZAU010000003.1
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SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 54148)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 54148)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission

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JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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gene 3494..3799
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CDS 3494..3799
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100 , identity 100 , evalue 2.23e-62 , alnlength 101 ,
Bacteria , Proteobacteria , WP_051062205.1 MULTISPECIES:
transposase [unclassified Wolbachia]"
/cog="COG3547 COG3547 303 Transposase and inactivated
derivatives"
/pfam="Transposase_20"
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/translation="MPELGRLNREIACLVGVAPKTSESGRKVGKAQIKGGRFYARKA
LYMSALVAMRHNRMKAFYQRLVDSGKAAKVALVAVMRKIIIVCLNAMIKNNNFYLDLS"
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, identity 100 , evalue 2.23e-62 , alnlength 101 ,
Bacteria , Proteobacteria , WP_051062205.1 MULTISPECIES:
transposase [unclassified Wolbachia]"
gene 3875..5248
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CDS 3875..5248
/locus_tag="wEsol_00026"
/codon_start=1
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100 , identity 100 , evalue 0.0 , alnlength 457 ,
Bacteria , Proteobacteria , WP_015589121.1 MULTISPECIES:
dihydrolipoyl dehydrogenase [unclassified Wolbachia]"
/cog="Lpd COG1249 454 Pyruvate/2-oxoglutarate
dehydrogenase complex, dihydrolipoamide dehydrogenase
(E3) component, and related enzymes"
/pfam="FAD_binding_3 Thi4 HI0933_like Pyr_redox_2 GIDA
DAO FAD_oxidored FAD_binding_2 Pyr_redox_3 NAD_binding_8
K_oxygenase 2-Hacid_dh_C Pyr_redox_FAD_binding_3 3HCDH_N
NAD_binding_8 HI0933_like Pyr_redox_3 DAO NAD_binding_9
Pyr_redox_dim"
/tigr="TIGR01350 lipoamide_DH 461 dihydrolipoyl
dehydrogenase"

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NAQHAMTPERLPKSLIIIGSGAIGIEFASFYSTLGVDVTIIEIKSTILPLEDKDISDL
AQEIFTKQGIKIYTNSSVKALTKSKDSAQVLLSSGESKEFDKIVIVAVGIQANIENIGL
ENTKIKLSPSGFIETNEWYETSESNVYAIGDVAGPPCLAHKASHEAVICIEKIAGKNA
HALKKECIPNCTYSH PQIASIGLTEEQAIKGGYDIKIGKFHSNFNGKSVALSETEGLV
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gene complement(5254..5646)
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CDS complement(5254..5646)
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100 , identity 100 , evalue 1.14e-80 , alnlength 130 ,
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hypothetical protein [Wolbachia]"
/translation="MIVELKMPKSN SKKEPNEKNKPQE QREGRSGGFLELLKNI IKIL
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gene 5716..6747
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CDS 5716..6747
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/fullproduct="qcoverage 100 , hcoverage 100 , similarity
99.7 , identity 99.7 , evalue 3.75e-239 , alnlength 343 ,
Bacteria , Proteobacteria , WP_015589119.1 MULTISPECIES:
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beta-N-acetylglucosaminyltransferase [Wolbachia]"
/cog="MurG COG0707 357 UDP-N-acetylglucosamine:LPS
N-acetylglucosamine transferase"
/pfam="Glyco_transf_28 Glyco_trans_4_4 Glyco_trans_1_3
Glyco_tran_28_C"
/tigr="TIGR01133 murG 353
undecaprenyldiphospho-muramoylpentapeptide
beta-N-acetylglucosaminyltransferase"
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beta-N-acetylglucosaminyltransferase"
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STEKILNILVIAGSQGANFFDDVVS RVICDLPIKMKKKIRVTQQCTKKNVNKVKSLYK
SEKIDCEELSEFFDDMENRLANAHLVISRAGATSIAEITLARRSAIYIPYPYSKDNHQF
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beta-N-acetylglucosaminyltransferase [Wolbachia]"
gene complement(6732..7661)
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CDS complement(6732..7661)
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100 , identity 100 , evalue 2.21e-223 , alnlength 309 ,
Bacteria , Proteobacteria , WP_015589118.1 MULTISPECIES:
glutathione synthase [Wolbachia]"
/cog="RimK COG0189 318 Glutathione synthase/Ribosomal
protein S6 modification enzyme (glutaminy transferase)"
/pfam="GSH-S_N GSH-S_ATP ATPgrasp_YheCD RimK"
/tigr="TIGR01380 glut_syn 312 glutathione synthase"
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/translation="MKIAFQMDENINFETDTTFVLIKEAQRRKHEVFVYAPNNLALKL
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VIRIQDENSIQVVVDLMIAYECPVIAQSFCKNIDKDKRILLLYGQPIGVMKRIPKIS
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Bacteria , Proteobacteria , WP_015589118.1 MULTISPECIES:
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gene complement(7722..8318)
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CDS complement(7722..8318)
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100 , identity 100 , evalue 1.02e-125 , alnlength 198 ,
Bacteria , Proteobacteria , WP_006279461.1 MULTISPECIES:
BON domain-containing protein [Wolbachia]"
/cog="OsmY COG2823 196 Predicted periplasmic or secreted
lipoprotein"
/pfam="BON BON"
/product="BON domain-containing protein"
/translation="MRLITSFLLAIFLITQSGCTTLIIGGVVATATATAITMQDKSLG
NIIDDTMVIRINKGLLKHGLFSSIKVKVSEGRVLLIGSVDTPEKQLTAEKIAWQQKE
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, identity 100 , evalue 1.02e-125 , alnlength 198 ,
Bacteria , Proteobacteria , WP_006279461.1 MULTISPECIES:
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gene 8465..8623
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CDS 8465..8623
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/codon_start=1
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Wolbachia]"
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isomerase (trigger factor)"
          /pfam="Trigger_N FKBP_C Trigger_C"
          /tigr="TIGR00115 tig 410 trigger factor"
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EFIDSIKTKFPNFASVDDASYQAKDGDKLIIDFEGRIRNKLQGGSSKDFAVNLGSGT
FINGFEDQLTGMKKGETKNFKLKFENYQAIISLAGQEADFSVRVNEIQIAKDFENDDE
IAKSIGFKDYSLLINHAKKMIGDQCTEMRNLLIKKELFDYLDANYSFDLPTDIVKQEQ
QRMEGELGAQNDSRKEAEKRVKLAMLFMKFSAEHKISLTQNDVLSVIVNQYVSKDVQF
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similarity 100 , identity 100 , evaluate 7.48e-311 ,
alnlength 444 , Bacteria , Proteobacteria ,
WP_015589117.1 MULTISPECIES: trigger factor [unclassified
Wolbachia]"
gene      10045..10671
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CDS       10045..10671
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100 , identity 100 , evaluate 9.15e-143 , alnlength 208 ,
Bacteria , Proteobacteria , WP_006280254.1 MULTISPECIES:
ATP-dependent Clp endopeptidase proteolytic subunit ClpP
[Wolbachia]"
          /cog="ClpP COG0740 200 Protease subunit of ATP-dependent
Clp proteases"
          /pfam="CLP_protease Pfam-B_306"
          /tigr="TIGR00493 clpP 192 ATP-dependent Clp
endopeptidase, proteolytic subunit ClpP"
          /product="ATP-dependent Clp
endopeptidase proteolytic subunit ClpP"
          /translation="MTLPIVVEQTSRGERAYDIYSRLVKERIIFVTGPIEDNMA SVI
VAQLLFLESENPDKDICYINSPGGVVTAGLSIYDTMQYINPDVSTLCIGQAASMGSL
LLAAGTKGKRYSLPHSRIMIHQPSGGYHGQATDIEIHANEILRVKKLNQIYEKHTGN
SLKKIEGMMERDKFMDPEEARKIGLIDRVIAERTDIEIENIKVKQKVG"
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, identity 100 , evaluate 9.15e-143 , alnlength 208 ,
Bacteria , Proteobacteria , WP_006280254.1 MULTISPECIES:
ATP-dependent Clp endopeptidase proteolytic subunit ClpP
[Wolbachia]"
gene      10671..11948
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CDS       10671..11948
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ATP-dependent Clp protease ATP-binding subunit ClpX
[Wolbachia]"
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subunit"
/pfam="zf-C4_ClpX MCM PhoH DEAD Sigma54_activat T2SE
RuvB_N AAA_2 IstB_IS21 AAA_22 Mg_chelatase AAA_14 AAA_5
AAA_AAA_17 ClpB_D2-small"
/tigr="TIGR00382 clpX 414 ATP-dependent Clp protease,
ATP-binding subunit ClpX"
/product="ATP-dependent Clp
protease ATP-binding subunit ClpX"
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EGTVAYVPPQGGRKHPQQEFIQVDTSNILFICGGA FEGLDKIIEARKKGT SVGFGADI
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, identity 100 , evalue 1.86e-301 , alnlength 425 ,
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[Wolbachia]"
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CDS 11964..14417
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/codon_start=1
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100 , identity 100 , evalue 0.0 , alnlength 817 ,
Bacteria , Proteobacteria , WP_141456951.1 MULTISPECIES:
endopeptidase La [unclassified Wolbachia]"
/cog="Lon COG0466 782 ATP-dependent Lon protease,
bacterial type"
/pfam="LON IstB_IS21 AAA_PrkA RuvB_N AAA_16 AAA_25 AAA_14
AAA_22 AAA_17 AAA_AAA_5 RNA_helicase AAA_24 AAA_3 AAA_2
Lon_C ChlI"
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VAINSIDQIKEVDQLVDTVASHLNIKVSDKQSILEAYDPEERLKKAFAFIEREMSILN
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QEAREKAITDLKRYKKMNPISPEATVISSYLHWLLELPWGKYKDAKINLNAAKKILDE
NHYGIEKVKDRIIEFLAVLKRVKEIKGPILCLVGPVGKTS LAKSMARAVGRDFVRI
ALGGVRDESEIRGHRKTYIGSMPGKIIQHMKKANSCNPLFLLDEIDKMGSDSRGDPAS
ALLEVLDTEHNKHFTDHYLEVEFDLSSVMFVATANSNLNPLPHLRDRMEI IQLSGYTED
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AVKEILTDKNKKISVGVDNLQDYLGVRYKTFGIAENESLVGIVTGLAYTETGGDILMI
ESVLIPGKGEIKYTGKLGEVMQESIKAAYSYIRSNCLFFGIKPEKFQNNDIHLHVPEG
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Proteobacteria , WP_141456951.1 MULTISPECIES:
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gene complement(14414..14521)
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CDS complement(14414..14521)
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similarity 96.4 , identity 89.3 , evalue 5.63e-10 ,
alnlength 28 , Bacteria , Proteobacteria , RLT59764.1 ABC
transporter ATP-binding domain protein [Wolbachia
endosymbiont of Drosophila ananassae]"
gene 14701..15996
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CDS 14701..15996
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99.8 , identity 99.8 , evalue 3.12e-287 , alnlength 431 ,
Bacteria , Proteobacteria , WP_141456953.1 MULTISPECIES:
sodium:proton antiporter [unclassified Wolbachia]"
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/pfam="CitMHS Na_H antiporter DUF1686 Na_H antiporter"
/tigr="TIGR00931 antiport_nhaC 454 Na+/H+ antiporter
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GAMFGDNLSIISDTTIASVMSQKADIKKKLKLNAKVALIASIFTIIILFYSSSNSAAI
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KGFMSMHEIMLLSLMVGGLSGLVGKNSKELADKLSSWVMIQRGGQKTAQLFIAKIVSI
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, identity 99.8 , evalue 3.12e-287 , alnlength 431 ,
Bacteria , Proteobacteria , WP_141456953.1 MULTISPECIES:
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gene 15989..17281
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CDS 15989..17281
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100 , identity 100 , evalue 1.66e-302 , alnlength 430 ,
Bacteria , Proteobacteria , WP_015589113.1 cbb3-type
cytochrome c oxidase subunit I [Wolbachia endosymbiont of
Drosophila simulans]"
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PSAQYIFDNALVIHVNL SILVWMCSIISLLFIINLQNTNSWFNFSWVLSTLSMLLMFI
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Bacteria , Proteobacteria , WP_015589113.1 cbb3-type
cytochrome c oxidase subunit I [Wolbachia endosymbiont of
Drosophila simulans]"
gene 18567..20306
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CDS 18567..20306
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Bacteria , Proteobacteria , WP_010962506.1 MULTISPECIES:
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[Wolbachia]"
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exonuclease"
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VVISLNNGIGKASCRSILGVDIGAAVLSAKFINLIIIEGGGHSMAAGFSIKEDKINDLH
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Proteobacteria , WP_010962506.1 MULTISPECIES:
single-stranded-DNA-specific exonuclease RecJ
[Wolbachia]"
gene complement(21133..21939)
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CDS complement(21133..21939)
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Bacteria , Proteobacteria , WP_015589111.1 MULTISPECIES:
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gene 22117..22407
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CDS 22117..22407
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/cog="GroS COG0234 96 Co-chaperonin GroES (HSP10)"
/pfam="Cpn10"
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Bacteria , Proteobacteria , WP_007549140.1 MULTISPECIES:
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CDS 22508..24157
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100 , identity 100 , evalue 0.0 , alnlength 549 ,
Bacteria , Proteobacteria , WP_141456977.1 MULTISPECIES:
chaperonin GroEL [unclassified Wolbachia]"
/cog="GroL COG0459 524 Chaperonin GroEL (HSP60 family)"
/pfam="Cpn60_TCP1"
/tigr="TIGR02348 GroEL 526 chaperonin GroL"
/product="chaperonin GroEL"
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APEITKDG YKVMKG I KPEKPLNAVIASIFAQSCSQCNDKVG DGTTC SILTSNMIMEA
SKSIAAGNDRVGIKNGIQKAKDVILKEITSMSTISLEKIDEVAQVAIISANGDKDIG
NSIADSVKKVGKEGVITVEESKGSKELEVELTTGMQFDRGYLSPYFITNNEKMIVELD
NPYLLITEKKLNIIQPLLPIL E AIVKSGKPLV IIAEDIEGEALSTLVINKLRGGLKVA
AVKAPGFGDRRKEMLEDIATLTGAKYVIKDELGIKMEDLTLDLGTAKNVKITKDNTT
VVSSENSDS SVKARIEQIKSQIETSTSDYDKEKLRLERLAKLSGGVAVLVGGATEVEV
KERRDRVEDALHATRAAIEEGIVPGGGVALLYASSVLDKLGASDEEQIGINI IKKVL
SAPIRRLVKNAGLES A VIIDYLIKQNDKELIYNVEAMNYANAFTAGVIDPAKVVR IAF
ETAVSVASVLITTESMIVDVPSKENASSPMGAGEMSGMGGF"
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Proteobacteria , WP_141456977.1 MULTISPECIES: chaperonin
GroEL [unclassified Wolbachia]"
gene complement(24711..27836)
/locus_tag="wEsol_00043"
CDS complement(24711..27836)
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/codon_start=1
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/pfam="AsmA_2 DUF3971 AsmA_2 AsmA_1"
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99.9 , identity 99.9 , evalue 0.0 , alnlength 1041 ,
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AsmA-like C-terminal domain-containing protein
[unclassified Wolbachia]"
/translation="MLKKITVLFVSALLFILCFFIFLKPLEININYNVNFYVKKHISKI
FVGSSVNVENISVVWQKGSKDPYLVITDLAIANPNFTIKVPELFFVHFKLSSLFKGNIK
FSQVLADNVRVYIKREEINVNPQNSLDLLDNHYLSNNRLPSVSFQRTLESRKKETSS
QATWMTGKKDIGMTGKKDTGMTGKNFKMTTESSAKNLLKTIREFFFDLNADSKIEFTNI
AINKGTEDEFFIDKLYIGKGEDFNVLDIHVNTKDEKGFLLDLSITIKNRNLLNLYGT
FYDLKLGLLSEFSTLVKSYNLDKNIGFKGSFSVKINKKDEIVDGNIVLNTENYLNKN
LALTNNVNLTYSNGLISVKNFHFKLNDTYLSLIGKMNFGTSHALLRINISKFAAKDL
CTYIPDSVVNSKFKSWYCDNIDGDLNTIVSFNGKINNLDVDDLSDIVIVADIENGSV
KFDEDFEQVKELKGDLLIKNNLEITVNSAKFQNFNTVNGGDIEMKSLNKEDSVLTING
KAVSDAYGLYEPPIRFKLDDVVKVERDKVSGMAKSVFNFRIFNLNADDKKVDFSANFHS
EIDNLAVYNASLGKYDIKLSFGSDFIDLNGSGMVNNTQLLFDLKSSNRNESFAWNLTG
DLPAQIFNFDSGYVSANLESVINQDKTGYVNGDIDLSEFESHSSYLGWKNRFEDHNKI
LFSTRKLGAGELLVDKLDIVGNDLDIKFSGRVENGNYLNSSSFKLDPDNDFSIEIESG
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YLSPPQRESGEHYGTLSISNFYIKDAPLLTTLLSMSSLPGIVNAIKNEGVYFYKCNAPF
SYKDGITIEIESWLEGAELGISTGGKLDIRNYKFQVAGQVIPAYSINKSLLKIPIIGK
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, identity 99.9 , evalue 0.0 , alnlength 1041 , Bacteria
, Proteobacteria , WP_015589123.1 MULTISPECIES: AsmA-like
C-terminal domain-containing protein [unclassified
Wolbachia]"
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CDS complement(27829..28266)
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/transl_table=11
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100 , identity 100 , evalue 9.71e-105 , alnlength 145 ,
Bacteria , Proteobacteria , WP_015589124.1 MULTISPECIES:
ribonuclease HI [unclassified Wolbachia]"
/cog="RnhA COG0328 154 Ribonuclease HI"
/pfam="RNase_H"
/product="ribonuclease HI"
/translation="MSKKEVTIYTDGACSGNPGAGGWAAIILFQDYRKDIYGREENTT
NNKMELTAVINGLKVLFKFCNINLYTDSLYVKHGITEWINKWKMNWGKTSNKKSVKNM
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Bacteria , Proteobacteria , WP_015589124.1 MULTISPECIES:
ribonuclease HI [unclassified Wolbachia]"
gene complement(28443..29330)
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CDS complement(28443..29330)
/locus_tag="wEsol_00045"
/codon_start=1
/transl_table=11
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100 , identity 100 , evalue 2.00e-203 , alnlength 295 ,
Bacteria , Proteobacteria , WP_015589125.1 MULTISPECIES:

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heme o synthase [unclassified Wolbachia]"
/cog="CyoE COG0109 304 Polyprenyltransferase (cytochrome
oxidase assembly factor)"
/pfam="UbiA"
/tigr="TIGR01473 cyoE_ctaB 281 protoheme IX
farnesyltransferase"
/product="heme o synthase"
/translation="MYTSVLLNVESTILDWFRLKPRIMYLVVFTAVAGMVAAPGGMH
PFLALISLICVALGSGSAGAINMWYDRDIDLLMERTKNRPIPSGRVSAESALEFGITL
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AAVTNSVSWESFILFLVIFMWTPPHFWALSLNKSEYVKASIPMFNIVYGPKKTRKYI
LIYSVLLVLTSLPALFLKKALLYLSMATFEGCVFIWYAISILRFKNHSSQKKMFSYS
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gene complement(29332..30882)
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CDS complement(29332..30882)
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/codon_start=1
/transl_table=11
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100 , identity 100 , evalule 0.0 , alnlength 516 ,
Bacteria , Proteobacteria , WP_015589126.1 MULTISPECIES:
cytochrome c oxidase subunit I [unclassified Wolbachia]"
/cog="CyoB COG0843 566 Heme/copper-type cytochrome/quinol
oxidases, subunit 1"
/pfam="Pfam-B_15059 COX1 Pfam-B_523"
/tigr="TIGR02891 CtaD_CoxA 504 cytochrome c oxidase,
subunit I"
/product="cytochrome c oxidase subunit I"
/translation="MSDVPKGIKRWLFSTNHKDIGTLYIIFSILAGIIGGLLSVIIRT
QLMHINILNNNYQLYNVMVTGHALIMVFFMIMPALMGFGNWFVPLMIGAPDMAFPRM
NNLSFWLLVSSFILLILSVFIGEGPGTGWTLYPPLSQVM SHPSAGVDIAILALHVAGM
SSIVGAINFIVTIFNMRAKGMSLTCKMPLFVWSVLLTAFMLIVALPVLGAIITMLLTDR
NIGTSFFDPAGGGDPVLFQHLFWFFGHPEVYVYIIFPAFGIISQVVSTFSHRPVFGYIG
MVYAMIGIAVFGFMVWAHMFMTVGLSADAAFFSTTTIFIGVITGVKVFWSWIATMWGG
AIEFKTPMLFALGFIFMFVGGGITGIILSHGGIDKLLHDTYYVVAHFHYVMSLAALFG
AFAGFYWIGKMSGKQYNERLGQIHFWLTFISTNITFLPQHFLGLAGMPRRIPDYPDA
FIPWNYISSIGSYMFSVSMFFVFIVIHLEFKWGGKAGDNPWKGD TLEWTVSSPPPFHT
FEKPPVVK"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalule 0.0 , alnlength 516 , Bacteria ,
Proteobacteria , WP_015589126.1 MULTISPECIES: cytochrome
c oxidase subunit I [unclassified Wolbachia]"
gene complement(30898..31662)
/locus_tag="wEsol_00047"
CDS complement(30898..31662)
/locus_tag="wEsol_00047"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalule 4.16e-180 , alnlength 254 ,
Bacteria , Proteobacteria , WP_015589127.1 MULTISPECIES:
cytochrome c oxidase subunit II [unclassified Wolbachia]"
/cog="CyoA COG1622 247 Heme/copper-type cytochrome/quinol
oxidases, subunit 2"
/pfam="COX2_TM Polysacc_synt COX2"

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/tigr="TIGR02866 CoxB 202 cytochrome c oxidase, subunit
II"
/product="cytochrome c oxidase subunit II"
/translation="MVKLFALLIIFYSNISVASAPTSWQFGFPAPATEVMEAVVRSHS
FVMLVMVTIMLFVWALLAYIAFRFRKSKVTNISKTTTHSVPLEIIFVFIPTIIVGILAF
ENAKLLKLQEEIPKADITLKVIGHQWYWSYQYPEYQGVSFDSYIKGKEDFIEGDLKLF
SVDNNIVLPVNANVRLQVTAGDVIHSWGVPAFGVKIDAIPGRLNEAWFNIKKPGVYYG
QCYELCGQGHGFMPIVVEAVSKEDFNKWIENRKLVS"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 4.16e-180 , alnlength 254 ,
Bacteria , Proteobacteria , WP_015589127.1 MULTISPECIES:
cytochrome c oxidase subunit II [unclassified Wolbachia]"
gene complement(33189..33353)
/locus_tag="wEsol_00048"
CDS complement(33189..33353)
/locus_tag="wEsol_00048"
/codon_start=1
/transl_table=11
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100 , identity 100 , evalue 2.06e-28 , alnlength 54 ,
Bacteria , Proteobacteria , WP_167482801.1 hypothetical
protein [Wolbachia endosymbiont of Carposina sasakii]"
/cog="Tra5 COG2801 232 Transposase and inactivated
derivatives"
/pfam="rve"
/product="hypothetical protein"
/translation="MSSSINKQLVMDSLMDVNRKPKAKNLLHSDQGSQYTLQGYQY
LLSIKNIDES"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 2.06e-28 , alnlength 54 ,
Bacteria , Proteobacteria , WP_167482801.1 hypothetical
protein [Wolbachia endosymbiont of Carposina sasakii]"
gene complement(33894..34076)
/locus_tag="wEsol_00049"
CDS complement(33894..34076)
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similarity 100 , identity 100 , evalue 7.96e-26 ,
alnlength 51 , Bacteria , Proteobacteria , WP_210446103.1
transposase, partial [Wolbachia endosymbiont of
Drosophila melanogaster]"
/cog="COG2963 COG2963 116 Transposase and inactivated
derivatives"
/pfam="HTH_Tnp_1 HTH_23 HTH_28"
/product="transposase, partial"
/translation="MAREYTAEFKLEAVKLANEQRKVGQPVAKVARDLGIRDSVLGKW
MKKYNEKSQRQMHFQM"
/besthit="qcoverage 85 , hcoverage 89.4736842105263 ,
similarity 100 , identity 100 , evalue 7.96e-26 ,
alnlength 51 , Bacteria , Proteobacteria , WP_210446103.1
transposase, partial [Wolbachia endosymbiont of
Drosophila melanogaster]"
gene complement(34095..34202)
/locus_tag="wEsol_00050"
CDS complement(34095..34202)
/locus_tag="wEsol_00050"
/codon_start=1
/transl_table=11

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/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evaluate 1.13e-13 , alnlength 35 ,
Bacteria , Proteobacteria , AAS14033.1 hypothetical
protein WD_0297 [Wolbachia endosymbiont of Drosophila
melanogaster]"
/translation="MNNKNKSKDRKKEIEFRIDLTQKKWREKKEFFRVK"
/product="hypothetical protein"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evaluate 1.13e-13 , alnlength 35 ,
Bacteria , Proteobacteria , AAS14033.1 hypothetical
protein WD_0297 [Wolbachia endosymbiont of Drosophila
melanogaster]"
gene complement(34399..34566)
/locus_tag="wEsol_00051"
CDS complement(34399..34566)
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/codon_start=1
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/translation="MKKMSPIDGFRMLLRTLDVLFSTFINPSIKRLKRLANGCYEFGA
VGDIKDTLFGV"
gene 35188..36435
/locus_tag="wEsol_00052"
CDS 35188..36435
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/codon_start=1
/transl_table=11
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/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evaluate 7.62e-314 , alnlength 415 ,
Bacteria , Proteobacteria , WP_155968744.1 group II
intron reverse transcriptase/maturase [Wolbachia
pipientis]"
/translation="MNKTKSFDIPKQLIWKAYKQVSKNRGAAGVDEVSITKFEENLKD
NLYKLWNRMSSGSYFPESVKAVAIPKDTGGQRTL CVPSVFDRIGQTAATMYLEPLVEP
EFHEDSYGYRPNKSALDAVSTACKRCWRSDWTIDLDISGFFDNL DHVLALQTIKKHTD
CKWVILYVERWMKAPIQLADGSKVVRNKGVPQGGSVSPIISNIFMHAFDMWMRQNY P
TIPFERYVDDAMVHCKTQKQAKFIKDKIEERLAEFKLKLHPEKTQIVYCKDDNRRDEF
PIQSFDLFGYTFRPRLAKNNKIGNYFVSFLPAISNKAKKKINQTIRSWKIRRQTYTTL
EKISKKINPIVRGWYQYYGRFYKSEMYPSLRNVEWHLVGWVRAKYKKLRNHRRLAKQF
LAKVRKRSPNIFYHWTGLGLSGK"
/product="group II intron reverse transcriptase/maturase"
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, identity 100 , evaluate 7.62e-314 , alnlength 415 ,
Bacteria , Proteobacteria , WP_155968744.1 group II
intron reverse transcriptase/maturase [Wolbachia
pipientis]"
gene 36455..36649
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CDS 36455..36649
/locus_tag="wEsol_00053"
/codon_start=1
/transl_table=11
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100 , identity 100 , evaluate 1.64e-36 , alnlength 64 ,
Bacteria , Proteobacteria , WP_213863496.1 hypothetical
protein [Wolbachia endosymbiont of Ceratitidis capitata]"
/translation="MRGLRTVLRETGGEAPPVYSPSGFPIVL SKFLGARNDYSLKRIL
ATEKNEDIFIRKKRGKNREN"
/product="hypothetical protein"

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          36828..37892
CDS       /locus_tag="wEsol_00054"
          36828..37892
          /locus_tag="wEsol_00054"
          /codon_start=1
          /transl_table=11
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          Pfam-B_1714 Ank Ank_3 Ank_5 Ank_4 Pfam-B_10896 Ank_5
          Ank_4 Ank Ank_3 Ank_2 Ank Ank_3 Ank_5"
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          SFASQQGYLDIVNTLIANGADLSTKTDKLNTPHLAAENGHLDIVNVFIEKGLDVNAV
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          DIVKVLLEAGANVNAKTDDKITPLHLASQNGFLELVDILLKAKSNVNAKDYENLTPLH
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          evalue 1.59e-39 , alnlength 330 , Bacteria ,
          Proteobacteria , WP_179947094.1 ankyrin repeat
          domain-containing protein, partial [Wolbachia
          endosymbiont of Bemisia tabaci]"
gene      37852..39429
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CDS       37852..39429
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          /transl_table=11
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          Ank_3 Ank Ank_2 Ank_4 Ank_5 Pfam-B_10896 Ank Ank_3 Ank_4
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          Pfam-B_10896 Ank_4 Ank Ank_3 Ank_5 Ank_4 Ank_3 Ank Ank_5
          Ank Ank_4 Ank_3 Ank_2 Ank Ank_4 Ank_2 Ank_5 Ank Ank_3
          Ank_4 Shigella_OspC Pfam-B_1714 Ank_5 Ank Ank_3 Ank_2
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          HTNWTPLHFAAEKGYDQIATVLLKHGADVNVKENQNKGTALHLAAQYGHKPVVKTLLI
          NGADVNAKMDKNATPLHLGAQIGNLDIVRSLLMSGAYFNARAEGGRYVPLHFAERRG
          NPEVIKLLKLVEKLFKAIEDNNYLGIESSIRDGAIIDSKNVGDGRTPHLYAVNNGHIKV
          VNILLTNGANVSQVTNKGNTPLHTATSKCYKEIVEVLLQHISRDKLNDFVNAKTTSSG
          TTSLLHVAAGGSLEVVKSLKHAIFYNIKNKEGKAPLDLSRDQNTNLLKLVEELFEN
          AKNGNVEIISKLKAIKPDERVAVTNARDDQGKSLVQVAVINKHSNLASRLLEILKSPD
          QSLQDVSVENRVKSLKL"
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          97.3837209302326 , similarity 86.9 , identity 85.4 ,
          evalue 2.41e-126 , alnlength 335 , Bacteria ,
          Proteobacteria , WP_179947054.1 ankyrin repeat
          domain-containing protein, partial [Wolbachia
          endosymbiont of Bemisia tabaci]"
gene      39965..40726

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CDS

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39965..40726
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95.3 , identity 92.5 , evalue 8.45e-159 , alnlength 253 ,
Bacteria , Proteobacteria , WP_197907410.1 NTP
transferase domain-containing protein [Wolbachia
endosymbiont of Kradibia gibbosae]"
/cog="GlmU COG1207 460 N-acetylglucosamine-1-phosphate
uridyltransferase (contains nucleotidyltransferase and
I-patch acetyltransferase domains)"
/pfam="IspD NTP_transf_3 NTP_transferase"
/tigr="TIGR01173 glmU 452 UDP-N-acetylglucosamine
diphosphorylase/glucosamine-1-phosphate
N-acetyltransferase"
/product="NTP transferase domain-containing protein"
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QDIVLIQYGDTPFISSDTVMKMTDCLKCNKNLVLGFGNSQDKQYGRLLVDDNDNVQK
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, identity 92.5 , evalue 8.45e-159 , alnlength 253 ,
Bacteria , Proteobacteria , WP_197907410.1 NTP
transferase domain-containing protein [Wolbachia
endosymbiont of Kradibia gibbosae]"

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gene

40858..41817

CDS

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99.7 , identity 99.4 , evalue 1.40e-231 , alnlength 319 ,
Bacteria , Proteobacteria , WP_015588901.1 MULTISPECIES:
NAD(P)-dependent oxidoreductase [unclassified Wolbachia]"
/cog="WcaG COG0451 314 Nucleoside-diphosphate-sugar
epimerases"
/pfam="RmlD_sub_bind Epimerase NAD_binding_10
Polysacc_synt_2_3Beta_HSD NAD_binding_4 NAD_binding_4
Polysacc_synt_2 Epimerase_Csub"
/tigr="TIGR01179 gale 332 UDP-glucose 4-epimerase"
/product="NAD(P)-dependent oxidoreductase"
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DIMPLAKCTGVIHLAAISRVIHGELYPKLCQKVNVDGTIQFLEFCKSLPNKPWFIYA
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LLDHSSRVIPALCINALKGDPRIEGKECVDFDFTYLLDDVIEGIYLTVKYLQNEKSSLP
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HSLEVGLSKFIKSLQNNQTQEYPNNIDMVIYENIKSYSWLPSLL"
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, identity 99.4 , evalue 1.40e-231 , alnlength 319 ,
Bacteria , Proteobacteria , WP_015588901.1 MULTISPECIES:
NAD(P)-dependent oxidoreductase [unclassified Wolbachia]"

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gene

41774..44101

CDS

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41774..44101
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Fer4_14 DUF4008"
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
99.5 , identity 97.4 , evalue 0.0 , alnlength 775 ,
Bacteria , Proteobacteria , WP_226079611.1
glycosyltransferase [Wolbachia endosymbiont of Tribolium
confusum]"
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Cardiocondyla obscurior]"
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VERSION    JAQZAU010000004.1
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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REFERENCE  1 (bases 1 to 3526)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 3526)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT     ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method     :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
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ORIGIN

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VERSION    JAQZAU010000005.1
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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REFERENCE  1 (bases 1 to 1489)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 1489)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage     :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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gene 962..>1489
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CDS 962..>1489
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 /codon_start=1
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 /translation="MQQAELSNLLKSVLSAKIISDDSLIYTPLTYAILCKNSKAIEEI
 LKVS KGNDILKDILNATTTIKYLDGRRATVTPLACAILCGDSIAIEEILKVSKEKDIL

NTTATIKYPDSQKVITYTPLTYAMFWKDSKAIKEILVAAKGNSTLLKDILNTTTTMMKYL
DREVITYTPLAYVILRR"
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similarity 69.5 , identity 68.3 , evaluate 7.05e-07 ,
alnlength 164 , Bacteria , Proteobacteria ,
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pipientis]"

ORIGIN

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1 ggttggtccgg aaactagtaa attcaagcat attccctctt taacataacc ctactcatag
61 ctaggtatat gaaattctca gtggatgttg tgagtaaadc atactccttc gatagccttc
121 tattcctatt aaccaagca aaagtccttt ctacaacca tcttcttggt tgtactttaa
181 acccttggtc tcttggtgtg agtagctcag gtggcgtatc tttgtgcacc caaaatctac
241 atggaggcct ttaacaatt tcaatatcta tgcataatc ttcctttatg tgattcttta
301 aatttcttcc ttggtatccc atgtcagccc acattttttt aacttttagta tattttgttc
361 tcatattggt taatgctatt ttaataccat ctctatcatt ttcgtttagca ggcgctacgt
421 aacaacctag tataaaaccc tgagtgtctg taattatatg cctttttcta ccctttactt
481 ttttacttcc atcatagcct ttgatccccc cttttctgta gtctttacag attgactatc
541 tactatacag gcactcggct gctcattcct tcctattttt cttctactat attttgtaat
601 ttcataatcc attttctcaa aaattccctg cttcttccat tgcctgaact gctcatacac
661 agtcttccat agcggaaaat catttggttaa ataccgccat tgacaccctg tacgcaatac
721 acagaaaatt gcttctaata tttctctttt gctatacttt ggcggccttc ctcttttctt
781 gtatgatact ctgaagtgtt tttctattct tgcccattcc ctttcgctta gatctgttgg
841 atactttttt ctcatcttta ccccgacta aaatttcaga tattatagcc ttttacttat
901 ttccggacaa cctcttactc atgctatatt ttgcgagaat agtcaagctg taaaggatat
961 tttgcaacaa gccgaattaa gcaacctttt aaagagtgtt cttagtgcaa aaataattag
1021 tgatgattca ttaatttaca caccacttac ttatgccata ttatgtaaaa atagcaaagc
1081 tattgaagaa attttaaaag tctctaaagg aaacgatatt ctgaaagata ttcttaacgc
1141 aacaacaact ataaaatatc tagatggctg gagagcaact gttacaccac ttgcttgtgc
1201 tatactatgt ggagatagta tagctattga agaaatttta aaagtctcta aggagaaaga
1261 tattcttaac acaacagcaa ctataaaata tccagatagc cagaaagtga cttacacacc
1321 acttacttat gctatgttct ggaaggatag caaagctatt aaagaaattc tagtagcagc
1381 taaagggaac agtactcttc tgaaagatat tcttaacaca acaacaacta tgaaatatct
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LOCUS JAQZAU010000006 911 bp dna linear ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_12340, whole genome
shotgun sequence.
ACCESSION JAQZAU010000006 JAQZAU010000000
VERSION JAQZAU010000006.1
DBLINK BioProject: PRJNA929258
BioSample: SAMN33142973
KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE Wolbachia pipientis (insect metagenome)
ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE 1 (bases 1 to 911)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL International Journal Molecular Sciences
REFERENCE 2 (bases 1 to 911)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full

Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##

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                        /mol_type="genomic DNA"
                        /submitter_seqid="contig_12340"
                        /isolate="wEsol"
                        /isolation_source="galls on Solidago altissima"
                        /host="Eurosta solidaginis MN-2018-EFC"
                        /db_xref="taxon:955"
                        /environmental_sample
                        /country="USA: Cowling Arboretum, Carleton College,
                        Northfield, MN"
                        /lat_lon="44.48 N 93.13 W"
                        /altitude="280 m"
                        /collection_date="2018-11"
                        /metagenome_source="insect metagenome"
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                        RNRRLSKEYDLLHNIH"
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                        /locus_tag="wEsol_00082"
     CDS                complement(204..362)
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                        EAL57896.1 transposase, IS5 family, OrfB, partial
                        [Wolbachia endosymbiont of Drosophila ananassae]"
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                        , similarity 100 , identity 100 , evaluate 3.71e-22 ,
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alnlength 45 , Bacteria , Proteobacteria , EAL58108.1
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 CDS complement(607..852)
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 80.3921568627451 , similarity 100 , identity 100 , evaluate
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 WP_038198919.1 transposase, partial [Wolbachia
 pipientis]"
 gene 834..>911
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ORIGIN

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121 tcctattaac ccaagcaaaa gtccttttcta caacccatct tcttggtgtg actttaaaacc
181 cttgttctct tgttggtagt agctcaggtg tgcgtatctt tgtgcaccca aaatctacat
241 ggaggccttt taacaatttc aatatctatg tcatattctt cttttatgtg attctttaa
301 tttcttcctt ggtatcccat gtcagcccac atttttttaa ctttagtata ttttgttctc
361 atattgttta atgctatttt aataccatct ctatcatttt cgtttagcagc gcctacgtaa
421 caacctagta taaaaccctg agtgtctgta attatatgcc tttttctacc ctttactttt
481 ttacttccat catagccttt gatccccctt tttctgtagt ctttacagat tgactatcta
541 ctatacaggc actcggctgc tcattccttc ctatttttct tctactatat tttgtaattt
601 cataattcat tttctcaaaa attccctgct tcttccattg cctgaactgc tcatacacag
661 tcttccatag cggaaaatca tttggtaaat accgccattg acaccctgta cgcaatacat
721 agaaaattgc tctaataattt ctcttttgct atactttggc ggccttcctc ctttcttgta
781 tgatactctg aagtgttttt ctattcttgc ccattccctt tcgcttagat ctgttgata
841 cttttttctc atctttaccc cgtactaaaa ttccagatat tatagccttt tacttatttc
901 cggacaactc t

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LOCUS JAQZAU010000007 1277 bp dna linear ENV 17-MAR-2023
 DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_12505, whole genome
 shotgun sequence.
 ACCESSION JAQZAU010000007 JAQZAU010000000
 VERSION JAQZAU010000007.1
 DBLINK BioProject: PRJNA929258
 BioSample: SAMN33142973
 KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
 REFERENCE 1 (bases 1 to 1277)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 1277)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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 /isolation_source="galls on Solidago altissima"
 /host="Eurosta solidaginis MN-2018-EFC"
 /db_xref="taxon:955"
 /environmental_sample
 /country="USA: Cowling Arboretum, Carleton College,
 Northfield, MN"
 /lat_lon="44.48 N 93.13 W"
 /altitude="280 m"
 /collection_date="2018-11"
 /metagenome_source="insect metagenome"
 /note="metagenomic"
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 CDS <1..110
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 CDS complement(111..275)
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 /cog="Tra5 COG2801 232 Transposase and inactivated
 derivatives"
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 EIFYNKQRHY"
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 , identity 100 , evalue 2.14e-30 , alnlength 54 ,
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 gene complement(272..442)

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         /product="hypothetical protein"
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         alnlength 49 , Bacteria , Proteobacteria , MBA8756266.1
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CDS      complement(873..1052)
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gene     complement(1182..>1277)
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CDS      complement(1182..>1277)
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         /codon_start=1
         /transl_table=11
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ORIGIN

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121 cgttgtttgt tataaaaaat ttctatgtat tcaaatattg cagttctagt ttgttgagca
181 gagtgtttgt aagtatcaat aagtatttct cttttcaatg agctaaagaa gctttctgca
241 acagaattgt cgtaacaaca gcctttatta ctcatctata ttctttacag ctaagagata
301 ttgataccct tagcaaagta tattgtgaac cttgatcact atgtaatagt agatttttgg
361 caggtttacg cttgttaacg tccattaata aagagttcat aaccaattgt ttattttattg
421 catcatacgt cattactacc atacgtggag catatataga cttaaagccaa atcatagcca
481 tcaagaaaaa ccctccttag gtttttagatg tagataataa aaccataact ttattttattt
541 ggttgatcga aacaataaaag tattttgtgat ctagtagatt gggagtctac agacatctat
601 tatctgtttg ttgtttttta aaattttaaa cttttcttct cagtatagtc cctgatgttc
661 attttctgca tataataactt tgcaccgttt tcaaatattg atgcaacttt tacccaaagc
721 tcaattcagc atgaatttta gggagctcca tatctacatt taaatagctt ggatatattt
781 tttgaatata tgctaataata cgtcttttat ttgctgattc ctactgcttt atttttctgt
841 ggtccactta gagtagccac tagcagaaaa tcctacataa ttctgtact tatagcagtt
901 actaatatat aataaaaaata ttttaactct tttttgtac tggccgaggg ctttctttta
961 taaatgtctc tttcccttgt tatctcttgc ttgttaaatt gtaacctctc tttgtcgtaa
1021 ggagccatgt taccatctac ctggaaatgc atctgctgcc gacttttttt tccgttgtgt
1081 ttctttatcc attttcctaa taaaccacc tttattccta aatcttcttg ctatttttgt
1141 aattgtttgt gacctgcctt ttctttgtca tgttgtccag tttaacagct tccaatttga
1201 attctgcgcg tatattctct taccatttct aatcctccaa aattttattt acccaaaaaa
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LOCUS      JAQZAU010000008          5990 bp    dna        linear    ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_12536, whole genome
            shotgun sequence.

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ACCESSION JAQZAU010000008 JAQZAU010000000
 VERSION JAQZAU010000008.1
 DBLINK BioProject: PRJNA929258
 BioSample: SAMN33142973
 KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
 REFERENCE 1 (bases 1 to 5990)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 5990)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
 ##Genome-Assembly-Data-END##
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 /isolation_source="galls on Solidago altissima"
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 /db_xref="taxon:955"
 /environmental_sample
 /country="USA: Cowling Arboretum, Carleton College,
 Northfield, MN"
 /lat_lon="44.48 N 93.13 W"
 /altitude="280 m"
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 /metagenome_source="insect metagenome"
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 CDS complement(<1..256)
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 Drosophila suzukii]"
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 /product="IS5 family transposase, partial"
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 transposase, partial [Wolbachia endosymbiont of
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gene 339..1859
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CDS 339..1859
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 100 , identity 100 , evaluate 0.0 , alnlength 506 ,
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 HlyD family type I secretion periplasmic adaptor subunit
 [Wolbachia]"
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 Pfam-B_12304 HlyD_3"
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 membrane fusion protein, HlyD family"
 /product="HlyD family type I
 secretion periplasmic adaptor subunit"
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 AEDSLARTIIKSPQDGIVTDIRYHTEGGVVIQSGVPIMSVVPSDDDLIIDAKIQTRNIE
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 type I secretion periplasmic adaptor subunit [Wolbachia]"

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CDS 2002..2244
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 [Wolbachia pipientis]"
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 derivatives"
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 [Wolbachia pipientis]"

gene 2318..2698
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CDS 2318..2698

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[Wolbachia endosymbiont of Drosophila incompta]"
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derivatives"
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ORIGIN

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BioSample: SAMN33142973

KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.

SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 1297)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 1297)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University, 1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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FEATURES Location/Qualifiers

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ORIGIN

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DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_14176, whole genome

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shotgun sequence.

ACCESSION JAQZAU010000010 JAQZAU010000000

VERSION JAQZAU010000010.1

DBLINK BioProject: PRJNA929258
BioSample: SAMN33142973

KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.

SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 1378)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 1378)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##

FEATURES Location/Qualifiers

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ORIGIN

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ORIGIN

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VERSION     JAQZAU010000012.1
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            BioSample: SAMN33142973
KEYWORDS    WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE      Wolbachia pipientis (insect metagenome)
  ORGANISM  Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
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REFERENCE   1  (bases 1 to 11379)
  AUTHORS   Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE     Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL   International Journal Molecular Sciences
REFERENCE   2  (bases 1 to 11379)
  AUTHORS   Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT     ##Genome-Assembly-Data-START##
            Assembly Date           :: JUN-2019
            Assembly Method          :: FLYE v. 06-2019
            Genome Representation     :: Full
            Expected Final Version    :: Yes
            Genome Coverage           :: 100.0x
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ORIGIN

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VERSION    JAQZAU010000013.1
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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REFERENCE  1 (bases 1 to 5775)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 5775)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
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VERSION    JAQZAU010000014.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 1413)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia

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endosymbiont of *Eurosta solidaginis* to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 1413)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University, 1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
 ##Genome-Assembly-Data-END##

FEATURES

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 /environmental_sample
 /country="USA: Cowling Arboretum, Carleton College, Northfield, MN"
 /lat_lon="44.48 N 93.13 W"
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 /collection_date="2018-11"
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ORIGIN

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961 tataaathtt aaaththttg ataathttgaa ttacgtaaaa atctatgcaa agtggataca
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 DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_15818, whole genome
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 VERSION JAQZAU010000015.1
 DBLINK BioProject: PRJNA929258
 BioSample: SAMN33142973
 KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
 REFERENCE 1 (bases 1 to 2282)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 2282)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University, 1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##

Assembly Date :: JUN-2019

Assembly Method :: FLYE v. 06-2019

Genome Representation :: Full

Expected Final Version :: Yes

Genome Coverage :: 100.0x

Sequencing Technology :: Illumina HiSeq; PacBio Sequel

##Genome-Assembly-Data-END##

FEATURES

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/lat_lon="44.48 N 93.13 W"

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VERSION    JAQZAU010000016.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 1465)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 1465)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage    :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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LOCUS JAQZAU010000017 10077 bp dna linear ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_17836, whole genome
shotgun sequence.
ACCESSION JAQZAU010000017 JAQZAU010000000
VERSION JAQZAU010000017.1
DBLINK BioProject: PRJNA929258
BioSample: SAMN33142973
KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE Wolbachia pipientis (insect metagenome)
ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE 1 (bases 1 to 10077)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL International Journal Molecular Sciences
REFERENCE 2 (bases 1 to 10077)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel

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ORIGIN

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2101 acttcagagt atcatacaag aaaggaggaa ggccgcaaaa gtatagcaaa agagaaatat
2161 tagaagcaat tttctatgta ttgcgtacag ggtgtcaatg gcggtattta ccaaatgatt
2221 ttccgctatg gaagactgtg tatgagcagt tcaggcaatg gaagaagcag ggaatttttg
2281 agaaaatgaa ttatgaaatt acaaaatata gtagaagaaa aataggaagg aatgagcagc
2341 cgagtgcctg tatagtagat agtcaatctg taaagactac agaaaagggg ggatcaaagg
2401 ctatgatgga agtaaaaaag taaagggtag aaaaaggcat ataattacag aactcaggg

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/transl_table=11
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CDS       complement(215..376)
          /locus_tag="wEsol_00162"
          /codon_start=1
          /transl_table=11
          /fullproduct="qcoverage 100 , hcoverage 100 , similarity
98.1 , identity 98.1 , evalue 4.57e-27 , alnlength 53 ,
Bacteria , Proteobacteria , WP_153801315.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
          /cog="Tra5 COG2801 232 Transposase and inactivated
derivatives"
          /pfam="rve"
          /product="hypothetical protein"
          /translation="MSSSINKQLVMDSLMAVNKRKPAKNLLHSDQGSQYTAQGYQY
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Bacteria , Proteobacteria , WP_153801315.1 MULTISPECIES:
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CDS       complement(816..1100)
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          /transl_table=11
          /fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 9.86e-56 , alnlength 94 ,
Bacteria , Proteobacteria , WP_039964423.1 transposase
[Wolbachia endosymbiont of Drosophila simulans]"
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derivatives"
          /pfam="HTH_Tnp_1 HTH_23 HTH_28 Pfam-B_9422"
          /product="transposase"
          /translation="MAREYTAEFKLEAVKLTNEQRKVGQPVAKVARDLGIRDSVLGKW
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[Wolbachia endosymbiont of Drosophila simulans]"
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          /transl_table=11
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100 , identity 100 , evalue 2.53e-32 , alnlength 56 ,
Bacteria , Proteobacteria , WP_197907316.1 hypothetical
protein [Wolbachia endosymbiont of Kradibia gibbosae]"
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, identity 100 , evalue 2.53e-32 , alnlength 56 ,

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gene Bacteria , Proteobacteria , WP_197907316.1 hypothetical protein [Wolbachia endosymbiont of Kradibia gibbosae]"
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CDS complement(1369..1701)
 /locus_tag="wEsol_00165"
 /codon_start=1
 /transl_table=11
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 /translation="MYKSHIRLDKLGKPCRVLCELYAKLCAILIFHGIVGCTEVKKN
 TELSLTKAFIELKRRVRELFLVLTKINSLKAFLKKLITWSRFSLKDKRRRARVSTLT
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 /besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 8.36e-69 , alnlength 110 , Bacteria , Proteobacteria , POG52374.1 hypothetical protein BJU59_00535 [Wolbachia sp. wRi_2]"

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CDS complement(1836..>1932)
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 /codon_start=1
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 /translation="LENEVLLGKEAKIRVRIICQKLTEYGQKKES"
 /product="transposase, IS4 family"
 /besthit="qcoverage 100 , hcoverage 81.5789473684211 , similarity 83.9 , identity 80.6 , evalue 2.59e-07 , alnlength 31 , Bacteria , Proteobacteria , KLT23187.1 transposase, IS4 family [Wolbachia endosymbiont of Armadillidium vulgare str. wVulC]"

ORIGIN

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1  gtgtggaatg ttttttacaa aaagaatgat gcatcaaatt gttctggaat gcaatagtta
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121 ctgttttagag tgccgagagg tgtctattgg taactccctt ttagagaaac tgaagaagct
181 ttctgcaaca gaattgtcgt aacaacagcc tttattactc atctatatcc tttacagcta
241 agagatatgg atacccttgc gcagtatatt gtgaaccttg atcactatgt aatagtagat
301 ttttggcagg tttacgcttg ttaacggcca ttaataaaga gtccataacc aattggttat
361 ttattgaact gctcattaac taccatgcgt gaatatagat cgattattgt tgccaaatat
421 agccatcctt ctttggtttt tatataagta atcccatact ttatttggtt gatcgacaat
481 aaagtttttg tctaataatat tgggagctac tgtccggttg ttgtttctta attttaaatt
541 ttctttctca tatagcctga ataccatttt tctgcataat actttgcaat gtttttaagt
601 tgcaactttt acccaaagcc ttaatttcag catgaatttt aggagctcca tatctacatt
661 tagaagcttg atatattttt tgaatatctg ctaataaactc tttatttgct gattctctac
721 tgcttatttt tcttggtggtc cacttatagt agccactagc agaaaatcct acataattcc
781 tgtactttat agcagttact atataaaaaa atatatttact ctttttgact ggccagggct
841 ttttttaaaa tgtctctttc tcttgttact tttgctaact ctttctgtaa atcaaatctc
901 tctttgtcat aagggtgctac atctggaaat gcatttgccg ctgacttttt ttcgttatat
961 ttcttcatcc attttcctaa tacactatcc cttattccta gatctcttgc tacttttgca
1021 actgggttgac ctacctttct ttgttcattt gtcagcttaa cagcttccaa tttgaattct
1081 gccgtatatt ctcttgccat ttctaatact ccaaaatttt attttaccca aaaaaactcc
1141 tttctttctc tccacttttt ctgggtaagg tcaaatgctc catcccttcc tggttaatggt
1201 ctgccttccc ttattgatga cagtatatat gcttccagtt ctttgtaatc taccaaaccg

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1261 gtagttctgt ttactacttt ctgactcatt gtcaaacctc catttttttta tatcaattta
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1381 gagcaaattt agagagggtta aagtggatac tctagccctt ctacgtttgt cttttaatga
1441 aaatcgcgac caagttatag tgagtttttt aagaaatgct tttaaactat taatttttgg
1501 taatactaaa aataactctc taacccgcct ttttagctca ataaatgcct ttgttaagct
1561 aagttctgta ttctttttca cttctgtgca accaactatg ccgtgaaata taagaattgc
1621 gcacaattta gcatatagtt cacataatac tctgcatggc tttcctttta gcttatcaag
1681 cctgatatgg cttttataca atttaaataa tttgccacct tactctgtaa atcgttaata
1741 cttgctcagc actaatttta ttttctggaa cattagttat accagttcaa caatttttga
1801 tttccttttag aggatcctgc gatcttgcta atctattagc tttccttctt ctggccatat
1861 tcagttagtt tctgacatat aattcttact ctaatttttg cttcttttcc taacaatacc
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LOCUS      JAQZAU010000020          972 bp    dna        linear    ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_18651, whole genome
            shotgun sequence.
ACCESSION  JAQZAU010000020  JAQZAU010000000
VERSION    JAQZAU010000020.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 972)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 972)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage     :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
            ##Genome-Assembly-Data-END##
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                                /mol_type="genomic DNA"
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                                /isolate="wEsol"
                                /isolation_source="galls on Solidago altissima"
                                /host="Eurosta solidaginis MN-2018-EFC"
                                /db_xref="taxon:955"
                                /environmental_sample
                                /country="USA: Cowling Arboretum, Carleton College,
                                Northfield, MN"
                                /lat_lon="44.48 N 93.13 W"
                                /altitude="280 m"
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CDS           <1..102
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              /translation="EYNKFRKRGKFFIISPEDIEKQWYENGPKIPGEQ"

ORIGIN
1 gaatataaca aattcagaaa aagaggaaaa tttttcatta tatcacccga agacatagaa
61 aagtggtagc agaatgggtcc aaaaatacca ggggaacaat aattttatc atcaagtttt
121 aatttttgtg tgcacatact aactgtgtat agactcggct gaggcaaaac agagttgagt
181 ttaatagcag gataccttga gcacatgcgg aaaaatttta gcagttaatc agctattaca
241 atcatcaaga agtttaagaa actccaatat agatcaatga ttgcagaaaa taatatggaa
301 gacatcaaat tagctataga aagtacagcg aattagtatt atacaacaca ctcttggtca
361 tagcaaagaa aatagcgaga taaagatcgc agcttgaaga gaacaaaaat tgcattgaatg
421 ttgaatacaa acagcaaaaa agcccagcgg taaaatccag taaacggcta tgatcactat
481 ggagcttggtg atttgctaaa agaagtcgat tttcagtata ggtatcataa agattatcta
541 tatgcagata ggacaataat ggacagagag aaaagctcta taagctgatg ataactacta
601 tggattataaa aacgaaaaat tacctccgaa aacaacgcag cagagcagac acaagttagc
661 acataaatgg ctatgacaaa ttctgcaagt caagctcata aagtcatatg atgagatagg
721 tataaagaag tggaaaaaca aaagagatga gttatggaaa aagatttaaat agaaggttta
781 attcttgcac gatttcaaaa aagaatttga tttagttttt taggaacaaa tctgaaatga
841 atcgtgagag ggaatgctac tcaaattgtga tttgcttaac caaattttac ggaaataggc
901 atggactaat ttggatagac ttcataatgt attgtgcgtt acctactatc gaagagagat
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LOCUS       JAQZAU010000021                2594 bp    dna        linear    ENV 17-MAR-2023
DEFINITION  MAG: Wolbachia pipientis isolate wEsol contig_19356, whole genome
            shotgun sequence.
ACCESSION   JAQZAU010000021  JAQZAU010000000
VERSION     JAQZAU010000021.1
DBLINK      BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS    WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE      Wolbachia pipientis (insect metagenome)
  ORGANISM  Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE   1  (bases 1 to 2594)
  AUTHORS   Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE     Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL   International Journal Molecular Sciences
REFERENCE   2  (bases 1 to 2594)
  AUTHORS   Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT     ##Genome-Assembly-Data-START##
            Assembly Date           :: JUN-2019
            Assembly Method          :: FLYE v. 06-2019
            Genome Representation    :: Full
            Expected Final Version   :: Yes
            Genome Coverage          :: 100.0x
            Sequencing Technology    :: Illumina HiSeq; PacBio Sequel
            ##Genome-Assembly-Data-END##
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                     /organism="Wolbachia pipientis"

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/host="Eurosta solidaginis MN-2018-EFC"
/db_xref="taxon:955"
/environmental_sample
/country="USA: Cowling Arboretum, Carleton College,
Northfield, MN"
/lat_lon="44.48 N 93.13 W"
/altitude="280 m"
/collection_date="2018-11"
/metagenome_source="insect metagenome"
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CDS
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similarity 100 , identity 100 , evaluate 5.72e-51 ,
alnlength 86 , Bacteria , Proteobacteria , WP_174516735.1
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Cardiocondyla obscurior]"
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/transl_table=11
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[unclassified Wolbachia]"

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121 aaattagtaa agggaatgtc tacagggttcg aaagaagata aatggcttga cagtccaact
181 ggaccatttg cttgtggtat aggaaaattc actcctggag ctgaagattt tagctatagg
241 caaaatttaa tgtaggata agtctttttt tatgggtaaa aatatttttag agtttaccca
301 gtttcttcta ttgttttttc aacttgtagc tactatcaat tcatatctac ttaactaaaa
361 cgctaatttt agaactcaat ataattttca attaaaggta gatagaatat ataagaaata
421 acaccaccaa caattgaatt acattcccaa ttcccagggt cccaaatcag taattggaaa
481 ttaggaatct gaatcctgcg tgagagctag cttttccacc tgcgttccca aaagcgttcc
541 tagaaatcat gtgtctaaag tcagccagta tagcggattc tagcttccca aaacccttat
601 atattatata tatataatag taataaataa taatagataa aataatataa gctaataata
661 aaacatacaa atctaaatgc attcaacttt taactaagtc tgacccaaaa aatagtgtta
721 aaatgttcac aaaacagaac gtagaaaagc aaatagcctt caatgtcgtt ttttaagcga
781 tctagtatct taaggtaaaa taataccaac tacacctaag taacgcttgt aacacccttt
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1021 tatggaaata taacgacttt tatctaaaac tcctaaggga atattgtgag tcttttgatg
1081 aaaaaatctc tataaacagg ttatagatga aggtcaagga aaaaagtttg aagttactgc
1141 catagaagaa gaaacagaag ctcgtaaaat ttgattgctg cttaaaatgg agacaaagag
1201 caaaatttat tgtctccaac agaaaaactt cttttgtagt agtcaaaaaa agcagagata
1261 tagggctttc tgaaggaggg ggacaatttt tcacccccct tgaaattaaa accaaaaaga
1321 tacagtttta catagcacat tttcattgta aaaaagagct atcagcccat ttcaattgtc
1381 tccattgcaa caccattctt aaaaacgcct tagaaggcta ttatagcggt actgatgatc
1441 tagataggga gatactgttt tatcaaaaac tcatgtaacc tcttctagat tcaaataatc
1501 agttgtttcc aaaatggaaa gatctcaaat agcgaagaag ctggttgtaaa agacatagct
1561 ggtttttaggc tctttttaat ttcttagctg ccttaaaatt attttaactt ttttttagaa
1621 aatcccggaa aaagtgggtg gaaatccgga gtataggggc attgagtgtg gataacacaa
1681 aagtcggcaa acaaacagag tagagaagag aagattgaag aaagcaaaaag aaatttaggc
1741 ttttggttaag ttacgtaatt gagaatttgt attttttttag atgaggtaaa aactttgttt
1801 taaggctaga tgcaacttta gggtaaaaaa atactacat taccaaagaa cgcataata
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1921 ctagtgagtt tagcacgttt tttacgcttt gcaaagaaaa attaaaaaaa agtgaacagt
1981 ttttgtaaaa tcggtgaata tatataacaa agctgggta agttgggtata ttggagggtct
2041 tatggaaata caacgacttt tatctaaaac tcctgaacaa ttgagggaat attgtgagtc
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2341 taaaagttta aaacagttgg atgagttaga tgaattatta ccacagatgt atggagaact
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2461 cttcttgccg gataacattg atactttcaa gcttctagaa aaagctgaac atgggttctat
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LOCUS      JAQZAU010000022      1088 bp      dna      linear      ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_19940, whole genome
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ACCESSION  JAQZAU010000022 JAQZAU010000000
VERSION    JAQZAU010000022.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 1088)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 1088)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage     :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
            ##Genome-Assembly-Data-END##

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FEATURES	Location/Qualifiers
source	1..1088 /organism="Wolbachia pipientis" /mol_type="genomic DNA" /submitter_seqid="contig_19940" /isolate="wEsol" /isolation_source="galls on Solidago altissima" /host="Eurosta solidaginis MN-2018-EFC" /db_xref="taxon:955" /environmental_sample /country="USA: Cowling Arboretum, Carleton College, Northfield, MN" /lat_lon="44.48 N 93.13 W" /altitude="280 m" /collection_date="2018-11" /metagenome_source="insect metagenome" /note="metagenomic"
gene	complement(<1..89) /locus_tag="wEsol_00170"
CDS	complement(<1..89) /locus_tag="wEsol_00170" /codon_start=1 /transl_table=11 /product="hypothetical protein" /translation="MPFKPRYFTYFSMAFFLLLSIRYLCSGNW"
gene	83..265 /locus_tag="wEsol_00171"
CDS	83..265 /locus_tag="wEsol_00171" /codon_start=1 /transl_table=11 /fullproduct="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 1.53e-28 , alnlength 60 , Bacteria , Proteobacteria , EAL57766.1 hypothetical protein WwAna0375 [Wolbachia endosymbiont of Drosophila ananassae]" /translation="MALRSKLLDEKVVESAKEMLKKVRNNAYVAKKLNAVIAAKKHSTAVAKICCISRKALTA" /product="hypothetical protein" /besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 1.53e-28 , alnlength 60 , Bacteria , Proteobacteria , EAL57766.1 hypothetical protein WwAna0375 [Wolbachia endosymbiont of Drosophila ananassae]"
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 , identity 100 , evalue 6.33e-43 , alnlength 74 ,
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ORIGIN

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181 aaatgctgta attgcagcaa aaaagcacag tataacagcc gtagcaaaga tatgctgcat
241 ttcaagaaag gcacttactg catgacctaa aatttggcag agaagaaaaa ttatttgctc
301 cgcctcaacg ccgtagaaaa actatattga atcaaagtca acgtgaacaa gttgaggtgt
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421 ttggtttgaa tatcagcaaa tctacagtac accgtaatat gcaaagaatg aaatttcat
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601 tcgcggtttg gcacacattc aaagattgga cacgggtggt ttaaaaaagg cattaggaca
661 caggttaagg taaaactagg taggcaaaat ttttatctct atagtgcagt taatcccaga
721 aatggagaaa gttctagctc aaacgtcaat actgattgta tgaatatatt ccttgagcag
781 atgtcacaat atttaggaac aagggaggca tttcttatca tggattgtgc tagttggcat
841 aagtcaaaaa atttaaaagt acctaaaaat atcgacatta tatacctacc accatactca
901 cctgacctca atcctgttga gaggttttgg ttatatataa aacagaacat tttgcgtaac
961 aaaatctacg acacaattgc tttgcttgag agcgctttgt gcaaatttat tacctctctt
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LOCUS JAQZAU010000023 937 bp dna linear ENV 17-MAR-2023
 DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_20599, whole genome
 shotgun sequence.
 ACCESSION JAQZAU010000023 JAQZAU010000000
 VERSION JAQZAU010000023.1
 DBLINK BioProject: PRJNA929258
 BioSample: SAMN33142973
 KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
 REFERENCE 1 (bases 1 to 937)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 937)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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 /submitter_seqid="contig_20599"
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 /isolation_source="galls on Solidago altissima"
 /host="Eurosta solidaginis MN-2018-EFC"
 /db_xref="taxon:955"
 /environmental_sample
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 Northfield, MN"
 /lat_lon="44.48 N 93.13 W"
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 gpV"
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 protein V"
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 gene complement(454..912)

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    /product="hypothetical protein"
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ORIGIN

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301 ctgctcttgc cgttaccac ggaagccaat ccgttaaaaa ttctcctatt tttaccgca
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ACCESSION  JAQZAU010000024 JAQZAU010000000
VERSION    JAQZAU010000024.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 8269)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 8269)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date                :: JUN-2019

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Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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CDS	<1..526 /locus_tag="wEsol_00176" /codon_start=1 /transl_table=11 /fullproduct="qcoverage 100 , hcoverage 94.0540540540541 , similarity 100 , identity 100 , evaluate 1.83e-112 , alnlength 174 , Bacteria , Proteobacteria , EEH12441.1 DnaJ domain protein, partial [Wolbachia endosymbiont of Muscidifurax uniraptor]" /translation="FLAPLLAGSILSLAVKSIYTRNGKEFNHQTNILLFFNFDQECEN FSKSDRTRLKWLKNSVILSNTICTSLMFFGVGLDLVANGFGITNSMMLSGLLLSLPFT LLIVTSPILNAASNYILKKTAINSIEEQFKGDDQFIEVDNEKPSSTMSNQSYFPIGQL ISSKLAILHSEVSS" /product="DnaJ domain protein, partial" /besthit="qcoverage 100 , hcoverage 94.0540540540541 , similarity 100 , identity 100 , evaluate 1.83e-112 , alnlength 174 , Bacteria , Proteobacteria , EEH12441.1 DnaJ domain protein, partial [Wolbachia endosymbiont of Muscidifurax uniraptor]"
gene	complement(494..1774) /locus_tag="wEsol_00177"
CDS	complement(494..1774) /locus_tag="wEsol_00177" /codon_start=1 /transl_table=11 /fullproduct="qcoverage 100 , hcoverage 99.3006993006993 , similarity 99.8 , identity 99.5 , evaluate 7.18e-314 , alnlength 426 , Bacteria , Proteobacteria , WP_197907432.1 MULTISPECIES: bifunctional folylpolyglutamate synthase/dihydrofolate synthase [unclassified Wolbachia]" /cog="FolC COG0285 427 Folylpolyglutamate synthase" /pfam="Mur_ligase_M" /tigr="TIGR01499 folC 400 bifunctional protein FolC" /product="bifunctional"

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AEQPITLFEAATIAAFLAFSRHKADITLIEVGMGGRLDTTNVIDSPILTIITSIALDH
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folylpolyglutamate synthase/dihydrofolate synthase
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CDS complement(1780..2370)
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ABC transporter substrate-binding protein [unclassified
Wolbachia]"
/cog="Ttg2D COG2854 202 ABC-type transport system
involved in resistance to organic solvents, auxiliary
component"
/pfam="Pfam-B_9033 Tol_Tol_Ttg2"
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associated membrane protein HpnM"
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Wolbachia]"
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[Wolbachia sp. wRi]"
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transport protein"
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        DKLYGKAIVK"
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gene      complement(3894..4163)
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CDS       complement(3894..4163)
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        WP_007551133.1 MULTISPECIES: DUF2671 domain-containing
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Wolbachia]"
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/pfam="GST_N Glutaredoxin GST_N_3 GST_N_2 GST_C GST_C_2"
/product="glutathione S-transferase family protein"
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Wolbachia]"
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subunits gamma and tau [Wolbachia pipientis wMelPop]"
/cog="DnaX COG2812 515 DNA polymerase III, gamma/tau
subunits"
/pfam="RuvB_N AAA_16 Pfam-B_18840 DNA_pol3_delta2 AAA_22
AAA AAA_17 AAA_18 TIP49 Pfam-B_5933 DNA_pol3_gamma3
DUF3646"
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LNKIPQSILLSGSSGVGKTTTARIIALCLNCSLGPIFEPCGSCENCLAIKNSSHPDVI
EIDAASHTSIDDIKVILGDICYSPISSKFKVYIIDEVHMLSSSAFNALLKTLEPPSS
VKFILATTEIKKIPITIIARCQRFDLHNIPVAKIVERLNDVAQKESYSIEKGALELIA
RHSGNSMRNALFLMNQAVLYSKDGAISTKNVTDILGLVDKDIIFDLLGAILEGDLQKA
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AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

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TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 6079)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
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/cog="Dcd COG0717 183 Deoxycytidine deaminase"
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, identity 100 , evalue 6.36e-134 , alnlength 185 ,
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gene complement(4906..5928)
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CDS complement(4906..5928)
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/codon_start=1
/transl_table=11
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100 , identity 100 , evalue 2.73e-235 , alnlength 340 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_141456986.1 MULTISPECIES: hypothetical protein
[unclassified Wolbachia]"
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KNNPGTHSGSGLTLKQVLNLVWKACNDQTRANNIAINTRISQRKYQLVKHLVESQTEY
GVRGGRGSSACFTGTFNSIVSSLYTFEEFSFLQKADKNTIKQEFENELQKKGEELFNQ
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WP_141456986.1 MULTISPECIES: hypothetical protein
[unclassified Wolbachia]"

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ORIGIN

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1981	gagccacgag	gggactctga	ctagtgacaa	aggtagcatt	taa	aatgatgt
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LOCUS      JAQZAU010000026          741 bp    dna        linear    ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_22294, whole genome
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ACCESSION  JAQZAU010000026  JAQZAU010000000
VERSION    JAQZAU010000026.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 741)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 741)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission

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JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##

FEATURES Location/Qualifiers
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/submitter_seqid="contig_22294"
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/isolation_source="galls on Solidago altissima"
/host="Eurosta solidaginis MN-2018-EFC"
/db_xref="taxon:955"
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Northfield, MN"
/lat_lon="44.48 N 93.13 W"
/altitude="280 m"
/collection_date="2018-11"
/metagenome_source="insect metagenome"
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gene complement(<1..215)
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CDS complement(<1..215)
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similarity 100 , identity 98.6 , evaluate 4.26e-35 ,
alnlength 71 , Bacteria , Proteobacteria , RLT59986.1
hypothetical protein WANA31_0645, partial [Wolbachia
endosymbiont of Drosophila ananassae]"
gene 665..>741
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CDS 665..>741
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/besthit="qcoverage 100 , hcoverage 13.3689839572193 ,
similarity 100 , identity 100 , evaluate 1.14e-06 ,
alnlength 25 , Bacteria , Proteobacteria , WP_179949445.1
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[Wolbachia endosymbiont of Drosophila santomea]"

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LOCUS      JAQZAU010000027          529 bp    dna        linear    ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_23028, whole genome
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ACCESSION  JAQZAU010000027  JAQZAU010000000
VERSION    JAQZAU010000027.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
  ORGANISM Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 529)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL   International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 529)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Direct Submission
  JOURNAL   Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage    :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
            ##Genome-Assembly-Data-END##
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            /isolation_source="galls on Solidago altissima"
            /host="Eurosta solidaginis MN-2018-EFC"
            /db_xref="taxon:955"
            /environmental_sample
            /country="USA: Cowling Arboretum, Carleton College,
            Northfield, MN"
            /lat_lon="44.48 N 93.13 W"
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QAVILRIAVEFPEILN"
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similarity 98.9 , identity 97.7 , evaluate 1.47e-116 ,
alnlength 176 , Bacteria , Proteobacteria ,
WP_006279250.1 toprim domain-containing protein, partial
[Wolbachia endosymbiont of Muscidifurax uniraptor]"
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ORIGIN

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LOCUS JAQZAU010000028 698 bp dna linear ENV 17-MAR-2023

DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_23078, whole genome
shotgun sequence.

ACCESSION JAQZAU010000028 JAQZAU010000000

VERSION JAQZAU010000028.1

DBLINK BioProject: PRJNA929258

BioSample: SAMN33142973

KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.

SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis

Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 698)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 698)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##

Assembly Date :: JUN-2019

Assembly Method :: FLYE v. 06-2019

Genome Representation :: Full

Expected Final Version :: Yes

Genome Coverage :: 100.0x

Sequencing Technology :: Illumina HiSeq; PacBio Sequel

##Genome-Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..698

/organism="Wolbachia pipientis"

/mol_type="genomic DNA"

/submitter_seqid="contig_23078"

/isolate="wEsol"

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Northfield, MN"
/lat_lon="44.48 N 93.13 W"
/altitude="280 m"
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simulans]"

ORIGIN

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1 cccctaacga cctatgtaca gacaatgcaa ttatggttgg atggacagga attgaaaggt
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121 gttattaaaa gctctcaatt ctgaattata gctaaagtga cttaggttct ctaattgcac
181 ataagtcaac aataattttc acacaaatca aaacagcata tcttctccat aatccttggt
241 aattttacat aagttaaaag tagcatatgg ttctctccgc ggtctgagat gacaataaat
301 ttgtcaagcc gcattatact tgtaggcgg aagtggacgg caacatattt accacgaagt
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LOCUS JAQZAU010000029 646 bp dna linear ENV 17-MAR-2023

DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_23080, whole genome
shotgun sequence.

ACCESSION JAQZAU010000029 JAQZAU010000000

VERSION JAQZAU010000029.1

DBLINK BioProject: PRJNA929258
BioSample: SAMN33142973

KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.

SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 646)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 646)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##

Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##

FEATURES Location/Qualifiers

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CDS       complement(527..>646)
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ORIGIN

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181  gatttgatat tgaaaatttt gaataggaaa cttgaggcat agctagtagt tggctagcaa
241  agcaacaaac caatatcaac tgttggtgtc atgaaagtag ctgacactgg aatccaggaa
301  ttttattaag ttggtaagca taaaagtata acttctacgt cataccgccg cggtatccgc
361  taacaagcag cgggggtgacg attgtcaggg tagctgtcat cccagtgcc agactacttg
421  gatccaggaa aaagaatggg gtcaccccag tgcgtgatac cctagtagaa atcgtttttg
481  taattgcaac attcgtgcaa tcttttagcca taaatattta aaaaatttac caaatgaaaa
541  aaaaggcaaa agaaaccctg gggttattat ccgctttaaa atattggcgt tttttatggt
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LOCUS      JAQZAU010000030          7725 bp    dna        linear    ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_25003, whole genome
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ACCESSION  JAQZAU010000030  JAQZAU010000000
VERSION    JAQZAU010000030.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)

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ORGANISM *Wolbachia pipientis*
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 7725)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of *Eurosta solidaginis* to gall-induction
 JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 7725)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
 ##Genome-Assembly-Data-END##

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 of *Tribolium confusum*]"
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 IAKWIGYSEKNNLTGQPTASWNYDESQVIATVYRYNTDSGKRYLPFDVVRSSFTPP
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 FIENNSKKIIVKQLLNIQEWSVERFIGPVPEQKFLVEGLFPLGVTSILAAMGDTGKGM
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 DRLFIVPLPNVSGSLTIKSVSGKVIETSPEFESITKQLNKKIDKLIVFDPLASFVH
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confusum]"
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ATPase [Wolbachia endosymbiont of Ceratitis capitata]"
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100 , identity 100 , evalue 1.32e-109 , alnlength 164 ,
Bacteria , Proteobacteria , WP_019236463.1 MULTISPECIES:
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/cog="RpoE COG1595 182 DNA-directed RNA polymerase
specialized sigma subunit, sigma24 homolog"
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factor, sigma-70 family"
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 , KAG8301083.1 hypothetical protein J6590_060860
 [Homalodisca vitripennis]"

ORIGIN

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121 tcagtttagc tgtatcttcc acagaccaa aagcgtatga acacctaaca ccattaacaa
181 gagcagatgt acctctaata gcatcacgtg cttgctcaac agtcgatata ggtttttcac
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301 cagataataa agacatcaaa taatcgccca cggctgggtc agtatttaaa tcagcatgca
361 caaatgatgc aagtggatca aatacgatta attttaagtc ttttatttta ttaagttggt
421 ttgttatcga ttcaaattca ggagaagtct ctataacttt acctgaaaca ctctttatga
481 ttgtaagtga tccactaaca tttggtaatg gtacaataaa gagcctatcc ttatatatta
541 atctttcgca ttgcgaatca agacgctcta aacgacgatg tatttcactc atatcatctt
601 ctgctgagaa aattaccaca gatccatgtt cagtaactaa aggacaaaaa ccacatggct
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961 gtgataaaac accaagaaaa gtaagctttt tcacaacttt ctcagcatat tgtttacctg
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1201 gaatattata taaaggcctg gtctctggtg gagtaaaact agaccttttt acatcaaaag
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1381 aaccaatcca cttagcaata tcttctatcg tgtcagtaaa ttgatttttt ccagtaacag
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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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REFERENCE  1  (bases 1 to 11993)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 11993)

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AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
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 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
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 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
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VERSION    JAQZAU010000032.1
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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 3012)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 3012)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date          :: JUN-2019

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Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
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SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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REFERENCE  1 (bases 1 to 2559)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 2559)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission

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JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##

FEATURES Location/Qualifiers

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ORIGIN

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[Wolbachia pipientis]"

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of Dactylopius coccus]"
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similarity 97.8 , identity 93.5 , evaluate 2.46e-22 ,
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 34.5707656612529 , similarity 97.3 , identity 88.6 ,
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CDS 15485..16027
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 39.1566265060241 , similarity 72.3 , identity 60.0 ,
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gene 16102..16884
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CDS 17244..17627
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evaluate 1.57e-53 , alnlength 115 , Bacteria ,
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gene 17747..18100
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94.1860465116279 , similarity 84.0 , identity 76.5 ,
evaluate 6.41e-29 , alnlength 81 , Bacteria ,
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98.7096774193548 , similarity 95.8 , identity 90.5 ,
evaluate 2.72e-186 , alnlength 306 , Eukaryota , Arthropoda
, GFS56378.1 putative transcriptional regulator [Nephila
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26.9911504424779 , similarity 73.8 , identity 45.9 ,
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[Wolbachia endosymbiont of Ctenocephalides felis wCfeT]"

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[Trichonephila clavata]"
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GFQ64080.1 ANK_REP_REGION domain-containing protein
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similarity 93.1 , identity 84.5 , evalue 2.34e-19 ,
alnlength 58 , Eukaryota , Arthropoda , GFT52245.1
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gene      complement(24453..24767)
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[Trichonephila clavata]"
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[Wolbachia endosymbiont of Pissodes strobi]"
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/tigr="TIGR00337 PyrG 526 CTP synthase"
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, identity 97.6 , evaluate 0.0 , alnlength 534 , Bacteria ,
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gene endosymbiont of *Pissodes strobi*]"
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 Pissodes strobi]"

ORIGIN

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26701	acggtttgtc	aaatgtctct	cagttttctca	aaaaaatcct	ttaacaaaaa	gagcattctg
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ACCESSION  JAQZAU010000035  JAQZAU010000000
VERSION    JAQZAU010000035.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 872)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 872)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA

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COMMENT      ##Genome-Assembly-Data-START##
              Assembly Date      :: JUN-2019
              Assembly Method    :: FLYE v. 06-2019
              Genome Representation :: Full
              Expected Final Version :: Yes
              Genome Coverage    :: 100.0x
              Sequencing Technology :: Illumina HiSeq; PacBio Sequel
              ##Genome-Assembly-Data-END##

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                                   /isolation_source="galls on Solidago altissima"
                                   /host="Eurosta solidaginis MN-2018-EFC"
                                   /db_xref="taxon:955"
                                   /environmental_sample
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                                   Northfield, MN"
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                                   melanogaster]"
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                                   melanogaster]"

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    241 ctctgccgcc aacgtttgtt cacctatatt ccaagctgca agacgagcac tacaaatcag
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    721 tcacctaaaa aggacacatt ttagacttct ttgttgaaat aaaacagaaa caaaagtgc
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ACCESSION  JAQZAU010000036  JAQZAU010000000
VERSION    JAQZAU010000036.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
  ORGANISM Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 849)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL   International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 849)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Direct Submission
  JOURNAL   Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method     :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage     :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
            ##Genome-Assembly-Data-END##
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                  Northfield, MN"
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VERSION    JAQZAU010000037.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 3037)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 3037)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage    :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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ORIGIN

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VERSION    JAQZAU010000038.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
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            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 14144)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL  International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 14144)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Direct Submission
  JOURNAL  Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date           :: JUN-2019
            Assembly Method          :: FLYE v. 06-2019
            Genome Representation     :: Full
            Expected Final Version    :: Yes
            Genome Coverage           :: 100.0x
            Sequencing Technology     :: Illumina HiSeq; PacBio Sequel
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gene

CDS

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gene

CDS

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ATP-binding protein [unclassified Wolbachia]"
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            BioSample: SAMN33142973
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SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 18036)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 18036)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##

FEATURES

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/besthit="qcoverage 98.2490272373541 , hcoverage 70.6293706293706 , similarity 78.4 , identity 68.5 , eval 1.22e-223 , alnlength 505 , Bacteria , Proteobacteria , WP_065106813.1 hypothetical protein [Wolbachia endosymbiont of Nomada ferruginata]"

gene complement(8127..8321)

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CDS complement(8127..8321)
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 evalue 1.10e-21 , alnlength 62 , Bacteria , Proteobacteria , WP_191111146.1 hypothetical protein
 [Candidatus Wolbachia massiliensis]"
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 [Wolbachia pipientis]"
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 DFWNFFESLFLNLFVDVDDPKIYQMLKEKKEKNWLLSIKFLRDKLKELIKIFARDL
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 GFVRPVVLSKPELDLLPKPIMPISIFKEVINNENREEIKPKVEEEKKAKPEEPKKEVCP
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gene 10386..11675
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CDS 10386..11675
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 LFEISPGFVRPVLSKPELDLLPKPIMPISIFKEVINNENREEIKPKVEEEKKAKPEEP
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 alnlength 430 , Bacteria , Proteobacteria ,
 WP_182309949.1 hypothetical protein [Wolbachia
 pipientis]"

gene 12096..12290
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CDS 12096..12290
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 /codon_start=1
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 [Candidatus Wolbachia massiliensis]"
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 hypothetical protein [Candidatus Wolbachia massiliensis]"

gene 12328..14520
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CDS 12328..14520
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 WP_065106813.1 hypothetical protein [Wolbachia
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similarity 78.1 , identity 68.8 , evaluate 0.0 , alnlength
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hypothetical protein [Wolbachia endosymbiont of Nomada
ferruginata]"
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CDS complement(14500..14769)
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19.4513715710723 , similarity 89.7 , identity 80.8 ,
evaluate 1.85e-37 , alnlength 78 , Eukaryota , Arthropoda ,
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gene complement(14726..15493)
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CDS complement(14726..15493)
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evaluate 1.35e-172 , alnlength 247 , Bacteria ,
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conserved in bacteria"
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62.0512820512821 , similarity 100 , identity 99.2 ,
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Proteobacteria , RLT59430.1 hypothetical protein
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ananassae]"

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CDS complement(15803..16048)
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protein,Transposase and inactivated derivatives
[Wolbachia endosymbiont of Drosophila simulans wAu]"
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conserved in bacteria"
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, identity 98.8 , evalue 9.11e-55 , alnlength 81 ,
Bacteria , Proteobacteria , CDR79199.1 phage
protein,Transposase and inactivated derivatives
[Wolbachia endosymbiont of Drosophila simulans wAu]"

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CDS 16120..16500
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derivatives"
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gene 16611..16952
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CDS 16611..16952
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/transl_table=11
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100 , identity 100 , evalue 1.53e-79 , alnlength 113 ,
Bacteria , Proteobacteria , AAS13810.1 transposase, IS5
family, OrfB [Wolbachia endosymbiont of Drosophila
melanogaster]"
/cog="COG3293 COG3293 124 Transposase and inactivated
derivatives"
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/product="transposase, IS5 family, OrfB"
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family, OrfB [Wolbachia endosymbiont of Drosophila
melanogaster]"
gene 17031..17378
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100 , identity 100 , evalue 2.74e-74 , alnlength 115 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
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protein [Wolbachia]"
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derivatives"
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protein [Wolbachia]"
gene 17578..17889
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CDS 17578..17889
/locus_tag="wEsol_00324"
/codon_start=1
/transl_table=11
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Bacteria , Proteobacteria , WP_155968470.1 transposase
[Wolbachia pipientis]"
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derivatives"
/pfam="DDE_3 DDE_1"
/product="transposase"
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[Wolbachia pipientis]"

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ORIGIN

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3541	ttctgttttt	gctacgagtg	gcactgaagc	tgaaattgca	aagagtatga	tgattgattc
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16081 aaaaggctat aatatctgaa atttttagtac ggggtaaaga tgagaaaaaa gtatccaaca
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16201 ggaggaaggc cgccaaagta tagcaaaaga gaaatattag aagcaatttt ctatgtattg
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16621 aatatactaa agttaaaaaa atgtgggctg acatgggata ccaaggaaga aatttaaaga
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LOCUS JAQZAU010000040 2750 bp dna linear ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_3091, whole genome

shotgun sequence.

ACCESSION JAQZAU010000040 JAQZAU010000000

VERSION JAQZAU010000040.1

DBLINK BioProject: PRJNA929258
BioSample: SAMN33142973

KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.

SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 2750)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 2750)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##

FEATURES Location/Qualifiers

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/environmental_sample
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Northfield, MN"
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/altitude="280 m"
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          /tigr="TIGR01933 hflK 261 HflK protein"
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VKEVNREEIGVSSSYGRDTRGEGVMLTGDENIVNVNFEVQWRVRDAKDYLKVRDYK
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ORIGIN

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1  gaatttagtg aattgctttt tgacaagctg ttagattggt cagagccttt tcttcccagt
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181 ttaataacct tcttaatttc atcgtaatgt tcagagaaaa cactgtcgat gaaataacta
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541 ttatggaact ttatttgcca ctccttcgcc taaaaaacta gcgccttttt tcagtgaatc
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661 ttttccggca gcgtatgttg atgcgtcctt aactttccca gcagtatatt ttgccccatc
721 aactgttttt tctgctgacc acttgagccc tttatatcca gattgaactg tttttacagc
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1801 tacggaaaca cctggtttgc gttatcactt cccctaccct attggcaagg tttttaaagt
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family, OrfB [Wolbachia endosymbiont of Drosophila
melanogaster]"

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ORIGIN

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601 ctgacatggg ataccaagga agaaatttaa agaatacat aaaggaagaa tatgacatag
661 atattgaaat tggttaaaagg cctccatgta gattttgggt gcacaaagat acgccacctg
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LOCUS      JAQZAU010000042      2288 bp      dna      linear      ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_31115, whole genome

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shotgun sequence.

ACCESSION JAQZAU010000042 JAQZAU010000000

VERSION JAQZAU010000042.1

DBLINK BioProject: PRJNA929258
BioSample: SAMN33142973

KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.

SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 2288)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 2288)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##

FEATURES Location/Qualifiers

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Proteobacteria , WP_213863621.1 transposase, partial
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ORIGIN

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781 ccatactctc ggtataacct attatcaact cctgcttcat ctatatataa gatgctggaa
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961 tattccaaat ccaagatttt gtttcatctc tgccagcgta tgatctggat tctttttaac
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1981 gtaagaagaa gatggtggct ataacagccc taatgcgtaa aattatagta attgctaata
2041 caagacttaa agaagcaatt aatttgcata cttaaaaatc ttcacaacgg taactgaaat
2101 tggctaataa atatgtgcgt ccacacagac ttaaaagcaca tattcattag cttaaagcaga
2161 aattgctgtg gtagctgttt gatataaaat tctattttcta tgacaaacgg gtttttattg
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DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_31598, whole genome
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ACCESSION  JAQZAU010000043 JAQZAU010000000
VERSION    JAQZAU010000043.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 1692)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 1692)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

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TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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 /isolation_source="galls on Solidago altissima"
 /host="Eurosta solidaginis MN-2018-EFC"
 /db_xref="taxon:955"
 /environmental_sample
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 Northfield, MN"
 /lat_lon="44.48 N 93.13 W"
 /altitude="280 m"
 /collection_date="2018-11"
 /metagenome_source="insect metagenome"
 /note="metagenomic"
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 29.7520661157025 , similarity 97.2 , identity 94.4 ,
 evaluate 1.07e-15 , alnlength 36 , Bacteria ,
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 CDS 109..435
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          [unclassified Wolbachia]"

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ORIGIN

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1  ataagacaga taaatcagat gcagctatga tagctagatt ttgtatcgcc aacaaacctg
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121 aaagatgata aggtgcaaca gacaaatcgc ttggaaaaca aaaatatgca ttccagttgc
181 aaagaagcta tatctaaagt aatttttgga atagaggagc aaattattgt tctcgaaaaa
241 gaaattaatg agcatataaa taactatcca catctaaaaa atatggtgga aaaccttaag
301 actataaaag gtataggata tcttactgct gttgctgttg tcgcagaaat gccatcagtt
361 gataactttg acaatgctaa acaatttaca gcttttgctg ccaggacatt atcaatcggg
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481 tctttatatg ccagctatag tagtcaaaaa ccataataat cattttcaaa agttttgtca
541 gcgtctagca agtaaaggca aatgtccaaa agtcatagtt cttgcgttaa tgcgaaaatt
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661 ataatttggt tgacagcaga gacagtatct gggatccaga ttgggcaact agttggtaaa
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1021 tgtaacaact cttttcttgc acaataactt tgagaaaagc aagactgcat gcaaggtaaa
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 family, OrfB [Wolbachia endosymbiont of Drosophila
 melanogaster]"
 /cog="COG3293 COG3293 124 Transposase and inactivated
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 /pfam="DDE_Tnp_1_2 DDE_Tnp_1"
 /product="transposase, IS5 family, OrfB"
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 , identity 100 , evalue 1.53e-79 , alnlength 113 ,
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 family, OrfB [Wolbachia endosymbiont of Drosophila
 melanogaster]"

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1 aaagtaaatt gtcatatagt ctcttgtggt gtattgataa ctttctccat ctagtctgct
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181 ccttcgatag ccttctattc ctattaaccc aagcaaaagt ctttctaca acccatcttc
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VERSION    JAQZAU010000045.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 37288)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 37288)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage     :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
            ##Genome-Assembly-Data-END##
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                                 Northfield, MN"
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NFNENTELPNNELSRRLRIATIGRPNVGKSTFLNGLLAENRLITSSEPGTTRDSVDITY
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CDS 2600..3142
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100 , identity 99.4 , evalue 3.15e-118 , alnlength 180 ,
Bacteria;Viruses , Proteobacteria;Uroviricota ,
WP_006279362.1 MULTISPECIES: demethoxyubiquinone
hydroxylase family protein [Wolbachia]"
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COQ7"
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WP_006279362.1 MULTISPECIES: demethoxyubiquinone
hydroxylase family protein [Wolbachia]"
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transposase [unclassified Wolbachia]"
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CDS complement(4260..4589)
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Bacteria , Proteobacteria , WP_141456678.1 MULTISPECIES:
transposase [unclassified Wolbachia]"
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Bacteria , Proteobacteria , WP_141456678.1 MULTISPECIES:
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gene 4813..5703
/locus_tag="wEsol_00350"
CDS 4813..5703
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7.13e-191 , alnlength 287 , Bacteria , Proteobacteria ,
WP_007548592.1 MULTISPECIES:
phospho-N-acetylmuramoyl-pentapeptide-transferase
[Wolbachia]"
/cog="Rfe COG0472 319 UDP-N-acetylmuramyl pentapeptide
phosphotransferase/UDP-N- acetylglucosamine-1-phosphate
transferase"
/pfam="Glycos_transf_4 Pfam-B_8659"
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[Wolbachia]"
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CDS complement(6401..7183)
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Bacteria , Proteobacteria , WP_015589382.1 MULTISPECIES:
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Wolbachia]"
/cog="VirB9 COG3504 265 Type IV secretory pathway, VirB9
components"
/pfam="CagX"
/tigr="TIGR02781 VirB9 248 P-type conjugative transfer
protein VirB9"
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transfer protein VirB9"
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WP_007548591.1 MULTISPECIES: outer membrane lipid
asymmetry maintenance protein MlaD [Wolbachia]"
/cog="Ttg2C COG1463 359 ABC-type transport system
involved in resistance to organic solvents, periplasmic
component"
/pfam="MCE"
/tigr="TIGR00996 Mtu_fam_mce 291 virulence factor Mce
family protein"
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lipid asymmetry maintenance protein MlaD"
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gene complement(7827..8141)
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CDS complement(7827..8141)
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NADH-ubiquinone oxidoreductase subunit NDUFA12 family
protein [Wolbachia]"
/cog="COG3761 COG3761 118 NADH:ubiquinone oxidoreductase
17.2 kD subunit"
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protein [Wolbachia]"
gene 8206..9672
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CDS 8206..9672
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100 , identity 100 , evalue 0.0 , alnlength 488 ,
Bacteria , Proteobacteria , WP_015589384.1 MULTISPECIES:
NADH-ubiquinone oxidoreductase [unclassified Wolbachia]"
/cog="HyfB COG0651 504 Formate hydrogenlyase subunit
3/Multisubunit Na+/H+ antiporter, MnhD subunit"
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K+:H+antiporter"
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oxidoreductase"
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FECLISGTIGATFYLFYGIGLLYSMTGTLNMSDMAERIVPLYDNNIIKLGTLFIFVGLS
IKMALFPLSRWLVNAYSEAPSFISIFFSGTVTKVMIYVFIRIFYTVFHFQNFLLFKPLL
DNVIIILALCAIVFGSIFAITAKDIKRLLAHSSISQIGYIILALSFNSTGVFAAILH
IVNHSIIKTSLFMAAGCISYKFDTTKIENLSGLKKSMPTALAFTLFSLALIGMPLTN
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CDS 9726..10616
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evalue 7.44e-189 , alnlength 295 , Bacteria ,
Proteobacteria , MBH5362260.1 rod shape-determining
protein RodA [Wolbachia endosymbiont of Kradibia
gibbosae]"
/cog="FtsW COG0772 381 Bacterial cell division membrane
protein"
/pfam="FTSW_RODA_SPOVE"
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protein RodA"
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RodA"
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QPSEFAKVGLILALARYFDKQSVYKMMFEKILLKALIIIFLPVFLVLKQPNLGTAVIM
LFIGISIIIFTAIIKRSHSVICGTLGIFAVPAIWPFLRPYHKQRILSFLDSSVDPLGIG
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evalue 7.44e-189 , alnlength 295 , Bacteria ,
Proteobacteria , MBH5362260.1 rod shape-determining
protein RodA [Wolbachia endosymbiont of Kradibia
gibbosae]"
gene 10681..10830
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CDS 10681..10830
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protein RodA"
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LPMLK"

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26.2295081967213 , similarity 100 , identity 100 , evaluate
1.21e-23 , alnlength 48 , Bacteria , Proteobacteria ,
AOV88385.1 rod shape-determining protein RodA, partial
[Wolbachia endosymbiont of Drosophila incompta]"
gene 10856..12241
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CDS 10856..12241
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100 , identity 100 , evaluate 0.0 , alnlength 461 ,
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/cog="PurF COG0034 470 Glutamine
phosphoribosylpyrophosphate amidotransferase"
/pfam="GATase_2 GATase_4 GATase_2 GATase_6 GATase_7
GATase_2 Pribosyltran"
/tigr="TIGR01134 purF 432 amidophosphoribosyltransferase"
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amidophosphoribosyltransferase"
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QIQGAYSFVAINQEVVIGVRDPGIRPLVLGKLNGSYVLASETCALDIVNAEFVREIE
PGELVTIDRNGNLASAFPFPQKSSFCIFEYVYFSRPDSIMENRSIYDIRKEIGKILA
EESPPKNNVDMVPIPDGIPAAIGYAKHSGLPMEGLIIRNHYIGRTFIQPTAEVRKV
RIKLKFNANKHTLKGKNIILIDDSIVRGSTLTNIIVMLKDAGVKEIHLKISSPPIKHS
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gene complement(12263..12769)
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CDS complement(12263..12769)
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100 , identity 100 , evaluate 1.13e-121 , alnlength 168 ,
Bacteria , Proteobacteria , WP_141456676.1 MULTISPECIES:
DNA-3-methyladenine glycosylase [unclassified Wolbachia]"
/cog="Mpg COG2094 200 3-methyladenine DNA glycosylase"
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DNA-3-methyladenine glycosylase"
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Bacteria , Proteobacteria , WP_141456676.1 MULTISPECIES:
DNA-3-methyladenine glycosylase [unclassified Wolbachia]"

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Bacteria , Proteobacteria , WP_015589388.1 hypothetical
protein [Wolbachia endosymbiont of Drosophila simulans]"
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DQKTRGVRCQIDKDGARIYEVANGSYQMALKWYVDGQECKIKILISDDGTIKPIEGNG
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Bacteria , Proteobacteria , WP_015589388.1 hypothetical
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CDS       complement(13776..14756)
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Holliday junction branch migration DNA helicase RuvB
[unclassified Wolbachia]"
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helicase subunit"
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Bac_DnaA DUF815 NB-ARC Mg_chelatase AAA_5 AAA_22 NTPase_1
AAA_3 AAA AAA_14 AAA_24 AAA_17 AAA_18 Pfam-B_17810
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RuvB"
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branch migration DNA helicase RuvB"
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GLLSAPLRDRFGIPLHLEFYSFEEELVDIIKRGARVLSAEIEEGAAREIACRARGTPRI
ALRLLRIRDFVEVKDDKKITYEVADSVLLKLGVDKMGMLNKLDMNYLRFLFNTSGPVG
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Bacteria , Proteobacteria , WP_141456674.1 MULTISPECIES:
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 DNA-binding subunit"
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 branch migration protein RuvA"
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 [unclassified Wolbachia]"
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 CDS complement(15983..16108)
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 family protein"
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 gene complement(17489..18739)
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 Bacteria , Proteobacteria , WP_007548582.1 MULTISPECIES:
 tyrosine--tRNA ligase [Wolbachia]"
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ligase"
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Bacteria , Proteobacteria , WP_041573543.1 MULTISPECIES:
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CDS complement(18971..19288)
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/cog="COG0799 COG0799 115 Uncharacterized homolog of
plant Iojap protein"
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/tigr="TIGR00090 iojap_ybeB 99 iojap-like
ribosome-associated protein"
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factor"
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99.6 , identity 99.1 , evaluate 1.05e-151 , alnlength 228 ,
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protein wHa_09360 [Wolbachia endosymbiont of Drosophila
simulans wHa]"
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simulans wHa]"
gene 20072..20560
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CDS 20072..20560
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Bacteria , Proteobacteria , WP_006279569.1 MULTISPECIES:
RNA pyrophosphohydrolase [Wolbachia]"
/cog="MutT COG0494 161 NTP pyrophosphohydrolases
including oxidative damage repair enzymes"
/pfam="NUDIX"
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pyrophosphohydrolase"
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gene 20557..21324
/locus_tag="wEsol_00370"
CDS 20557..21324
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100 , identity 100 , evaluate 1.34e-181 , alnlength 255 ,
Bacteria , Proteobacteria , WP_006280340.1 MULTISPECIES:
TatD family hydrolase [Wolbachia]"
/cog="TatD COG0084 256 Mg-dependent DNase"
/pfam="TatD_DNase"
/tigr="TIGR00010 TIGR00010 253 hydrolase, TatD family"
/product="TatD family
hydrolase"
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CDS complement(21352..22302)
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100 , identity 100 , evalule 3.51e-219 , alnlength 316 ,
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malate dehydrogenase [Wolbachia]"
/cog="Mdh COG0039 313 Malate/lactate dehydrogenases"
/pfam="UDPG_MGDP_dh_N Ldh_1_N Glyco_hydro_4 Ldh_1_C"
/tigr="TIGR01763 MalateDH_bact 305 malate dehydrogenase,
NAD-dependent"
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dehydrogenase"
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SELNISVEDISAFVLGGHGDTMVPLINCASVAGVPLTQIIDMGLITQKKVDEIVERTR
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gene complement(22306..22878)
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CDS complement(22306..22878)
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/cog="NuoC COG0852 176 NADH:ubiquinone oxidoreductase 27
kD subunit"
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oxidoreductase subunit C"
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Bacteria , Proteobacteria , WP_007548576.1 MULTISPECIES:
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gene complement(22871..23377)
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oxidoreductase subunit B [Wolbachia endosymbiont of
Cardiocondyla obscurior]"
/cog="NuoB COG0377 194 NADH:ubiquinone oxidoreductase 20
kD subunit and related Fe-S oxidoreductases"
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/tigr="TIGR01957 nuoB_fam 145 NADH-quinone
oxidoreductase, B subunit"
/product="NADH-quinone oxidoreductase
subunit B"
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FGLACCAVEMMHTASSRYDLDRYGIMFRASPRQSDVMIVAGTLTNKMAAALRKVYDQM
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Bacteria , Proteobacteria , WP_174516933.1 NADH-quinone
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gene complement(23381..23734)
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CDS complement(23381..23734)
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100 , identity 100 , evalue 3.18e-74 , alnlength 117 ,
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NADH-quinone oxidoreductase subunit A [Wolbachia]"
/cog="NuoA COG0838 123 NADH:ubiquinone oxidoreductase
subunit 3 (chain A)"
/pfam="Oxidored_q4"
/product="NADH-quinone
oxidoreductase subunit A"
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, identity 100 , evalue 3.18e-74 , alnlength 117 ,
Bacteria , Proteobacteria , WP_006279576.1 MULTISPECIES:
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gene complement(23753..24121)
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CDS complement(23753..24121)
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100 , identity 100 , evalue 2.37e-85 , alnlength 122 ,
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HIT domain-containing protein [Wolbachia]"
/cog="Hit COG0537 138 Diadenosine tetrphosphate (Ap4A)
hydrolase and other HIT family hydrolases"
/pfam="DcpS_C HIT"
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domain-containing protein"
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gene complement(24125..24382)
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CDS complement(24125..24382)
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hypothetical protein [Wolbachia]"
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DMVKVRELVSLSNLEDASGEAIKPLSTPNVEKNEERGKGRS"
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, identity 100 , evalue 1.37e-51 , alnlength 85 ,
Bacteria , Proteobacteria , WP_006279579.1 MULTISPECIES:
hypothetical protein [Wolbachia]"
gene complement(24399..25178)
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CDS complement(24399..25178)
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100 , identity 100 , evalue 8.70e-180 , alnlength 259 ,
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hypothetical protein [unclassified Wolbachia]"
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KSPEEIKKLALQGIADSINGDLKKLAGITGGEFKIHTDLKLLNGIAEKLYKEYDNQKQ
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, identity 100 , evalue 8.70e-180 , alnlength 259 ,
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gene 25362..25775
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CDS 25362..25775
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94.2622950819672 , similarity 100 , identity 97.4 ,
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Proteobacteria , EAL59246.1
UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-
D-alanyl-D-alanyl ligase, partial [Wolbachia endosymbiont
of Drosophila ananassae]"
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synthase"
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UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanyl ligase, partial"
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 UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanyl ligase, partial [Wolbachia endosymbiont of Drosophila ananassae]"
 gene 25723..26892
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 CDS 25723..26892
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 RDNKYYDYLSHANRNVISFGKDKNAEVCLNLIRNDESSVISALSSVIPVLDYLDPG
 SSIANEHIRRLYNKDWIPASRAGMTSNRVANRLSLKIRLSDNQIINCNLRVQGEHFAY
 SLLAVAAVVQSLGLDLSKLPLALKNFSVAKGRGNIHKIKYNRKYIHLIDDSYNASPAS
 MKTAIKTLSTYSNQRKVALLGDMLELGDESIEFHDTLVKIIITENNIDKVYTVGKFMLE
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 similarity 100 , identity 100 , evalule 1.90e-273 ,
 alnlength 389 , Bacteria , Proteobacteria , WP_015589396.1
 UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine
 ligase [Wolbachia endosymbiont of Drosophila simulans]"
 gene 26943..27893
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 CDS 26943..27893
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 /cog="COG0702 COG0702 275 Predicted
 nucleoside-diphosphate-sugar epimerases"
 /pfam="RmlD_sub_bind adh_short NAD_binding_10 Epimerase
 NmrA Saccharop_dh 3Beta_HSD F420_oxidored NAD_binding_4
 NAD_binding_4 RmlD_sub_bind"
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 subunit family protein"
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 AAKMKNVPMMIHFSAAGIENSKLSKYAKSKLEGEKAVTSAFQEAIIIRPSLVFGKEDN
 FFNKFARLATILPFLPLIGNGTTFKFQPICVTDLAEVVYRIISFNKQDKKIYNMGGPKV
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Wolbachia]"
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CDS       27910..28320
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91.304347826087 , similarity 100 , identity 98.4 , eval
6.28e-33 , alnlength 63 , Bacteria , Proteobacteria ,
KAB2977954.1 hypothetical protein DEF52_04360 [Wolbachia
endosymbiont of Nasonia oneida]"
gene      29076..30527
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CDS       29076..30527
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99.6 , identity 99.0 , eval 0.0 , alnlength 483 ,
Bacteria , Proteobacteria , WP_141456669.1 MULTISPECIES:
phage terminase large subunit [unclassified Wolbachia]"
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LRKRAINWFDQTLVTRLNDRKKGIVIVLVMHRLHQEDLTGHLLSKPKNIWHHICLPMIS
ENKQVIYISIKKPMPPVPVIRVAQHCATRRLYNKPASPVRILYSREESQLLYPLDGGKE
EIEMIKVELGSYAFAAQYQQNPLPLSSGIKPEWLKRYKKFPDNLSHITQSWDTAVST
SDMSNFSVCTTWAKIDNKFYLLDVYRAKLEYPKLKEQVLSLAARWTPHAILIEAKTSG
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large subunit"
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, identity 99.0 , eval 0.0 , alnlength 483 , Bacteria ,
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terminase large subunit [unclassified Wolbachia]"
gene      30919..33369
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CDS       30919..33369
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100 , identity 99.9 , eval 0.0 , alnlength 816 ,
Bacteria , Proteobacteria , WP_141456668.1 MULTISPECIES:
type I DNA topoisomerase [unclassified Wolbachia]"
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Toprim_C_rpt Toprim_C_rpt Toprim_C_rpt"
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gene 33427..34053
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protein [Wolbachia endosymbiont of Cardiocondyla
obscurior]"
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Wolbachia]"
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sulfurtransferase"
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VERSION    JAQZAU010000046.1
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SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 8587)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 8587)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,

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1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT ##Genome-Assembly-Data-START##
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Assembly Method    :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
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Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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ORIGIN

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SOURCE     Wolbachia pipientis (insect metagenome)
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REFERENCE  1  (bases 1 to 28030)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL  International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 28030)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Direct Submission
  JOURNAL  Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
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            Assembly Method          :: FLYE v. 06-2019
            Genome Representation     :: Full
            Expected Final Version    :: Yes
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            Sequencing Technology     :: Illumina HiSeq; PacBio Sequel
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100 , identity 100 , evalule 9.97e-66 , alnlength 106 ,
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family protein [Wolbachia endosymbiont of Cardiocondyla
obscurior]"
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VADK"
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family protein [Wolbachia endosymbiont of Cardiocondyla
obscurior]"
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CDS complement(9291..10370)
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100 , identity 100 , evalule 3.45e-259 , alnlength 359 ,
Bacteria , Proteobacteria , WP_015589490.1 MULTISPECIES:
DNA replication/repair protein RecF [unclassified
Wolbachia]"
/cog="RecF COG1195 363 Recombinational DNA repair ATPase
(RecF pathway)"
/pfam="SMC_N AAA_15 AAA_23 AAA_29 Pfam-B_17122 AAA_21
AAA_15"
/tigr="TIGR00611 recf 365 DNA replication and repair
protein RecF"
/product="DNA replication/repair protein RecF"
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EAISLLAKSNGMKKAKASEIQNRFSNEDWVVHYDFFNGTDFNSIGIAKSFDDKLIQID
GKTQSSYSSLYKISNVIWLIPQMDYVLLNSPSDRLKFLDRIVSLFEENYTCCYMKYRK
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Wolbachia]"
gene complement(10387..10854)
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CDS complement(10387..10854)
/locus_tag="wEsol_00407"
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100 , identity 100 , evalue 1.30e-107 , alnlength 155 ,
Bacteria , Proteobacteria , WP_015589489.1 MULTISPECIES:
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Wolbachia]"
/cog="Bcp COG1225 157 Peroxiredoxin"
/pfam="AhpC-TSA Redoxin DUF899"
/tigr="TIGR03137 AhpC 187 peroxiredoxin"
/product="
thioredoxin-dependent thiol peroxidase"
/translation="MELVVGNAPDFSLPTDSGENLSLSEFFDKKNVALYFYPKDDTP
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, identity 100 , evalue 1.30e-107 , alnlength 155 ,
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Wolbachia]"
gene complement(11039..12382)
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CDS complement(11039..12382)
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alnlength 447 , Bacteria , Proteobacteria ,
WP_015589488.1 MULTISPECIES: HAMP domain-containing
histidine kinase [unclassified Wolbachia]"
/cog="BaeS COG0642 336 Signal transduction histidine
kinase"
/pfam="NrfD Pfam-B_6312 HisKA Pfam-B_15665 HATPase_c"
/product="HAMP
domain-containing histidine kinase"
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QLLTNDEIDKLLSNQEILYTTGNTLTSIFPIFHENS AKPSFFLKILRSYNN SYVIAYG
LFLIFLGLLLIILILIMFYLFHFSNTKMLAKQHKTNIELQQIKEALEQENANKLKFFAS
VTHELRTPLNAIIGFAELIKNETLGSMDSQYKEYADDIYNAGTHLLALINDVLD FSK
AESSSLTVEKVKFNLNKIIDSCVNMLLPKLKEAGINLKKEMTNKQLLVIADSKRMKQV
IINLLSNSIKFTPKDGLIRMVIKENIEKNLLTIEFHDNGIGIMQQDIYKVMSVFGQAD
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similarity 99.8 , identity 99.8 , evalue 1.24e-308 ,
alnlength 447 , Bacteria , Proteobacteria ,
WP_015589488.1 MULTISPECIES: HAMP domain-containing

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          Wolbachia]"
          /cog="ArgD COG4992 404 Ornithine/acetylornithine
          aminotransferase"
          /pfam="Aminotran_3 Pfam-B_11691"
          /tigr="TIGR00707 argD 381 transaminase,
          acetylornithine/succinylornithine family"
          /product="aspartate
          aminotransferase family protein"
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          EPNIESVKKAISDIGVILIEPIQGQGGIKVMNEVFMKELRKLCDENDILLFFDCVQC
          GAGRTGKLFAYEHIGVEPDICALAKGIGGGFPLGACLATENAAKYMAVGMHGSTFGGN
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          Wolbachia]"
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          /locus_tag="wEsol_00410"
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          , similarity 100 , identity 100 , eval 7.96e-112 ,
          alnlength 168 , Bacteria , Proteobacteria ,
          WP_015589486.1 MULTISPECIES: ribosome maturation factor
          RimM [unclassified Wolbachia]"
          /cog="RimM COG0806 174 RimM protein, required for 16S
          rRNA processing"
          /pfam="RimM PRC"
          /tigr="TIGR02273 16S_RimM 166 16S rRNA processing protein
          RimM"
          /product="ribosome
          maturation factor RimM"
          /translation="MLDINMNDNLVCLGIITSPHGIKGAVKLKTFTEKPKNISLYGEL
          ISGDENYKIDSVSIIGDNLVIATISGVNSRNEAELLRNKKLYIERSKLPELNDEDEFY
          QSDLVDMEVRLESNELYGNVKSVMYVFGSGDILEILVISTKKRIMLSFTKEIFPHINIK
          GRYIVLNIPEFID"
          /besthit="qcoverage 97.1098265895954 , hcoverage 100 ,
          similarity 100 , identity 100 , eval 7.96e-112 ,
          alnlength 168 , Bacteria , Proteobacteria ,
          WP_015589486.1 MULTISPECIES: ribosome maturation factor
          RimM [unclassified Wolbachia]"
gene      14292..14858
          /locus_tag="wEsol_00411"

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CDS 14292..14858
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 /tigr="TIGR00038 efp 184 translation elongation factor P"
 /product="elongation factor P"
 /translation="MAERANDIRPGQVLEHNGGLFLVVGIMHTQPGKGGAYIQAEMKN IKTGAKHYERFRSDATIRRAILDEEEYVYLFTEGNIVNLMHPSNYEQITINLDLLGEK KIYLDQNMKIKVVAYQDKIISAHVDPDYVTLAVKETESVIKQTATASYKPAILENGMR VNVPQFIKEEDKIVVYTPDDSYERVKE"
 /besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 7.39e-130 , alnlength 188 , Bacteria , Proteobacteria , WP_012673415.1 MULTISPECIES: elongation factor P [Wolbachia]"

gene 14867..15565
 /locus_tag="wEsol_00412"

CDS 14867..15565
 /locus_tag="wEsol_00412"
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 /transl_table=11
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 /cog="SuhB COG0483 260 Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family"
 /pfam="Inositol_P"
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 /besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 3.55e-161 , alnlength 232 , Bacteria , Proteobacteria , WP_015589485.1 MULTISPECIES: inositol monophosphatase family protein [unclassified Wolbachia]"

gene complement(15557..16759)
 /locus_tag="wEsol_00413"

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 /cog="BioF COG0156 388 7-keto-8-aminopelargonate"

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synthetase and related enzymes"
/pfam="Aminotran_1_2 DegT_DnrJ_EryC1_Beta_elim_lyase
Cys_Met_Meta_PP_Aminotran_5 Pfam-B_8788"
/tigr="TIGR01821 5aminolev_synth 402 5-aminolevulinic
acid synthase"
/product="5-aminolevulinate synthase"
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EVIVWCSNNYLGMSQNESVIAAIQNSSVGAGGTRNISGTTKEVVELEKSLACLHKKEA
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LEQLLKSIDKKTPIIIVLESVYSMDGDVAPLKEICDLADQHNAITYLDEVHAVGMYGS
HGGGIAEREGLMDRITVIQGTLSKAFGVMGGYIASSKSLVDVIRSSAPGFIFTTAMSP
VLAAAKASVEHLKSSNIEREKQKQVVEKVKNSLRNAGINFILTETHIPIIIGDPPEL
SKKASKLLFDEYGIYVQHINYPTVPRGTERFRITPTPYHTDEMIEHLTESLVKVLEKL
SISVACLS"
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, identity 100 , evalue 1.47e-283 , alnlength 400 ,
Bacteria , Proteobacteria , WP_174516755.1
5-aminolevulinate synthase [Wolbachia endosymbiont of
Cardiocondyla obscurior]"
gene complement(16824..20426)
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CDS complement(16824..20426)
/locus_tag="wEsol_00414"
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Pfam-B_3281 Pfam-B_1200"
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103.267411865864 , similarity 96.3 , identity 96.3 ,
evalue 0.0 , alnlength 1201 , Bacteria , Proteobacteria ,
WP_197907087.1 hypothetical protein [Wolbachia
endosymbiont of Kradibia gibbosae]"
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VQPVESESKGDQGGSPPLSPQSSASGDVEGTEASANAAVTTPEEARSLSVSDGEHDKIV
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/besthit="qcoverage 100.083333333333 , hcoverage
103.267411865864 , similarity 96.3 , identity 96.3 ,
evalue 0.0 , alnlength 1201 , Bacteria , Proteobacteria ,
WP_197907087.1 hypothetical protein [Wolbachia
endosymbiont of Kradibia gibbosae]"
gene complement(20465..22360)

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Bacteria , Proteobacteria , WP_141456863.1 MULTISPECIES:
molecular chaperone HtpG [unclassified Wolbachia]"
         /cog="HtpG COG0326 623 Molecular chaperone, HSP90 family"
         /pfam="HATPase_c_3 HATPase_c HSP90"
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chaperone HtpG"
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[unclassified Wolbachia]"
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         /pfam="LYTB"
         /tigr="TIGR00216 ispH_lytB 282
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         /product="
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         /besthit="qcoverage 100 , hcoverage 100 , similarity 99.7
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Bacteria , Proteobacteria , WP_015589482.1 MULTISPECIES:
4-hydroxy-3-methylbut-2-enyl diphosphate reductase
[unclassified Wolbachia]"
gene     24832..26667
         /locus_tag="wEsol_00417"

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CDS 24832..26667
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 /transl_table=11
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 /cog="FtsI COG0768 599 Cell division protein FtsI/penicillin-binding protein 2"
 /pfam="PBP_dimer Transpeptidase"
 /product="penicillin-binding protein 2"
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 /product="hypothetical protein"
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gene complement(27154..27861)
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CDS complement(27154..27861)
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 /cog="ElbB COG3155 217 Uncharacterized protein involved in an early stage of isoprenoid biosynthesis"

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/pfam="DJ-1_PfpI"
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biosynthesis glyoxalase ElbB"
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/besthit="qcoverage 100 , hcoverage 100 , similarity 100
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Bacteria , Proteobacteria , WP_022626165.1 MULTISPECIES:
isoprenoid biosynthesis glyoxalase ElbB [Wolbachia]"

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ORIGIN

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ACCESSION  JAQZAU010000048  JAQZAU010000000
VERSION    JAQZAU010000048.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 22476)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 22476)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
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            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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[Wolbachia]"
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wHa]"

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ORIGIN

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  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL  International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 38835)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Direct Submission
  JOURNAL  Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
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            Assembly Method    :: FLYE v. 06-2019
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methyltransferase [Wolbachia]"
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methyltransferase, release factor-specific"
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methyltransferase [Wolbachia]"
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CDS complement(8050..8649)
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71.6417910447761 , similarity 100 , identity 100 , evalue
1.59e-134 , alnlength 192 , Bacteria , Proteobacteria ,
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[Wolbachia endosymbiont of Ceratosolen solmsi]"
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evaluate 2.16e-34 , alnlength 69 , Bacteria ,
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membrane protein [Wolbachia endosymbiont of Nasonia
oneida]"
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93.5532233883059 , similarity 100 , identity 100 , evaluate
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Wolbachia]"
/cog="VirB11 COG0630 312 Type IV secretory pathway,
VirB11 components, and related ATPases involved in
archaeal flagella biosynthesis"
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/tigr="TIGR02788 VirB11 308 P-type DNA transfer ATPase
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transfer ATPase VirB11"
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IIISGGTSTGKTTFTNATLRAIPDEERIITVEDAREIVLNDHPNKHVLIASKGGQGRA
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Wolbachia]"
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family protein [unclassified Wolbachia]"
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CDS complement(13557..14357)
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Bacteria , Proteobacteria , AGJ99506.1 Type IV secretion

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system protein VirB9 [Wolbachia endosymbiont of
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/cog="VirB9 COG3504 265 Type IV secretory pathway, VirB9
components"
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protein VirB9"
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VirB9"
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system protein VirB9 [Wolbachia endosymbiont of
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Wolbachia]"
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component VirB8"
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system protein"
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Wolbachia]"
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CDS complement(15097..16179)
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replication initiator protein DnaA [Wolbachia
endosymbiont of Drosophila ananassae]"
/cog="DnaA COG0593 408 ATPase involved in DNA replication
initiation"
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AFG1_ATPase AAA_25 AAA Bac_DnaA_C"
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initiator protein DnaA"
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protein DnaA"
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gene 21151..22053
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27.9296875 , similarity 100 , identity 100 , eval
3.49e-183 , alnlength 286 , Bacteria , Proteobacteria ,
WP_174516802.1 efflux RND transporter permease subunit
[Wolbachia endosymbiont of Cardiocondyla obscurior]"
gene 22046..24226
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RND transporter permease subunit [Wolbachia endosymbiont
of Cardiocondyla obscurior]"
gene 24315..25877
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CDS 24315..25877
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Wolbachia]"
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Wolbachia]"
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Wolbachia]"
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gene

CDS

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decarboxylase and related decarboxylases"
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gene

CDS

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ORIGIN

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SOURCE     Wolbachia pipientis (insect metagenome)
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AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 3095)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
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COMMENT    ##Genome-Assembly-Data-START##
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            Expected Final Version  :: Yes
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ORIGIN

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VERSION    JAQZAU010000051.1
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KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
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 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
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 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 34015)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
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gene

CDS

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KIYFGINVSINVERDDITDKNGKYENNKYTVTLFVVRKINDFISSNVNGVFKLKEEV
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FAFSDRSWELFGTTLSRLFIDGSTYLVDSFSGYVGEGERKFAFLDLTAGVLFTAETWL
KFLSLMLSGPFGVIAFLAILCATYAFLKCIISATLKYVISTVLVAFLLSLTPLFIVFI
LFQKTKPLFDNWIKTLAHVSLEPVILFSFLSLLNQLMYSVLYNLTNFSACYQCLISVN
FLSYDLCLMKSIPLGYSPGTSVDVALSTGERAGGHFAALPIDLIQAFIYLI IAGAME
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KNKEENGEE"
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system protein"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
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Proteobacteria , WP_174516844.1 MULTISPECIES: type IV

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CDS       complement(10856..13243)
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          /codon_start=1
          /transl_table=11
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100 , identity 100 , evaluate 0.0 , alnlength 795 ,
Bacteria , Proteobacteria , WP_174516845.1 MULTISPECIES:
type IV secretion system protein [unclassified
Wolbachia]"
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WLSGREYWFSKLDQDERKKEIENIINSIKQGENIDCSKLSSESSASKIDTHILNSLCRR
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LLIVSLIFSGPLGIVSFCLVIWGLITVSLSIFNALFSFITSIAIVALLLSLAPIFIIC
LLFAYTRQMFQNWVKNLARFAIHPVLLIFISLISQVMDYIVYSVFDFEVCSTCILNI
NLKIFNPCIFYGYASKYTPNITAMMAFVILGHAMKALVEASSAISDSLFGAYVASEPG
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system protein"
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CDS       complement(13253..15817)
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100 , identity 99.9 , evaluate 0.0 , alnlength 854 ,
Bacteria , Proteobacteria , WP_015589248.1 MULTISPECIES:
type IV secretion system protein [unclassified
Wolbachia]"
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QNKAREDVNKKDYDGKRAEKEALNSNVQESTESYYWPKNGVQYSEYIEVCHRNPLTF
NLFNKVDFNSRGKPGYIDFDVREKDTGYVDGSWSSKVDGGLECRVLKAGQSEPIHGAT
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GTGEEKVTIGNDDYKTIIRSKEKGLNGQGGKIFVGYDNAGCFSSYVSEACYNQAGSK
SLAPIPVTSMIVQCIKESLDNLVAGKGAPNGESFISVAQKRLKNTVTAVLVLALILFS
IKAMSGGVQRPQEMYMLIIKFALVIYFTTGSTISHYYGELTRLSNGLSEIVLKASSES
KGICNYKAGTDYEYTRAGKRVSYSYLAPWDRDLDCRILFYLGAPLDGIGGKIGTGGVAT
LAVLLGAAPVLLVAGSVIGIIFAGGQILVALVCIFMAVLMVVILWLCYVFILSLVAL
SVIIISPLFIPMVLVQHTKGYFEGWVKELITYSLYPVILFAFLSFMFIACDKIYFKN
LNFELDESYKNEQPDKSYEKKQAEISYSKKKQWFKLKDGECDKNETTLACMMQNYFSK
KSSILGLFDFTYMEFGSSSIGELLKLCVLFLFYHFLNILPGMAAELAGNHRAALGSG
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system protein"
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secretion system protein [unclassified Wolbachia]"
gene complement(15810..18215)
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CDS complement(15810..18215)
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/transl_table=11
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100 , identity 100 , evalue 0.0 , alnlength 801 ,
Bacteria , Proteobacteria , WP_010962886.1 MULTISPECIES:
VirB4 family type IV secretion/conjugal transfer ATPase
[Wolbachia]"
/cog="VirB4 COG3451 796 Type IV secretory pathway, VirB4
components"
/pfam="CagE_TrbE_VirB AAA_23 TrwB_AAD_bind AAA_10 AAA_22"
/tigr="TIGR00929 VirB4_CagE 792 type IV
secretion/conjugal transfer ATPase, VirB4 family"
/product="VirB4 family type
IV secretion/conjugal transfer ATPase"
/translation="MLRFRAIQSKNKSTLNREHVHAAEFIPYSCYWNSTTLMTKENWL
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N
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LVPFLGLAGPDTLAGAISMWHDNGSHAAIFDNKEDLLDFSRARVFGFEMASLLKDPVA
LGPVLIYLFHRISISLDGTPSIIIVLDEAWALIDNPVFAPKIKDWLKVLRKLNAFVIFA
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KNV"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 0.0 , alnlength 801 , Bacteria ,
Proteobacteria , WP_010962886.1 MULTISPECIES: VirB4
family type IV secretion/conjugal transfer ATPase
[Wolbachia]"
gene complement(18225..18521)
/locus_tag="wEsol_00497"
CDS complement(18225..18521)
/locus_tag="wEsol_00497"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 1.26e-62 , alnlength 98 ,
Bacteria , Proteobacteria , WP_007548615.1 MULTISPECIES:
type IV secretion system protein VirB3 [Wolbachia]"
/cog="VirB3 COG3702 105 Type IV secretory pathway, VirB3
components"
/pfam="VirB3"
/product="type IV secretion
system protein VirB3"
/translation="MSTGSIQTDQLFKGLTRPAMLFVSYMFALINVLICMLIFINSN

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Bacteria , Proteobacteria , WP_007548615.1 MULTISPECIES:
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gene 18630..20165
/locus_tag="wEsol_00498"
CDS 18630..20165
/locus_tag="wEsol_00498"
/codon_start=1
/transl_table=11
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99.8 , identity 99.8 , evaluate 0.0 , alnlength 511 ,
Bacteria , Proteobacteria , WP_015589250.1 MULTISPECIES:
lysine--tRNA ligase [unclassified Wolbachia]"
/cog="LysS COG1384 521 Lysyl-tRNA synthetase (class I)"
/pfam="tRNA-synt_1f Pfam-B_854"
/tigr="TIGR00467 lysS_arch 515 lysine--tRNA ligase"
/product="lysine--tRNA
ligase"
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THQSYGHHMNSLLCKFLDMFEFEYEFRSATECYKSGVYDEKLLLLLKNYDKVMDVMLP
SFREERQQTYSPFLPICPKTSQVLQVPVIETNTEKGTITYEDPNGEKIEVPVTKGKCK
LQWKPDWGMRWAAFGVNYEAHGKDLTPSAVLSSQICEILGEKPLLFCYELFLDKERK
KISKSKNGGISIEEWLTYAPTESLALYIFQSPKKAKRLYFDVIPKSTDEYLEFVKRYH
ENKEKDINNPAWHIHQGNVPSIETSGINFSLLLNLAAACNAENKEILWGFISSYAPNV
TPENNKMLDRLSDFAVKYYHDFIKPTKSYKTPNEKEKAALLDLKDTLHSLSTTATAEE
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CIL"
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, identity 99.8 , evaluate 0.0 , alnlength 511 , Bacteria ,
Proteobacteria , WP_015589250.1 MULTISPECIES:
lysine--tRNA ligase [unclassified Wolbachia]"
gene complement(21099..23732)
/locus_tag="wEsol_00499"
CDS complement(21099..23732)
/locus_tag="wEsol_00499"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
99.9 , identity 99.9 , evaluate 0.0 , alnlength 877 ,
Bacteria , Proteobacteria , WP_141457239.1 MULTISPECIES:
alanine--tRNA ligase [unclassified Wolbachia]"
/cog="AlaS COG0013 879 Alanyl-tRNA synthetase"
/pfam="tRNA-synt_2c tRNA_SAD"
/tigr="TIGR00344 alaS 847 alanine--tRNA ligase"
/product="alanine--tRNA
ligase"
/translation="MKLNEIRERFIKFFVNNDHEQVSSSPLIPEHDS TLMFTNAGMVQ
FKNIFTGAQKTEMKRAVSSQKCLRAGGKHNDLENVGYTTRHHTFFEMLGNFSFGDYFK
ETAIEFAWEFITKELSLDKNRLSITVYHTDDEAYEIWRKISGFSSDKIIRITDDNFW
SMGSTGPCGPCSEIFYDHGSPNLQEGDRIVEIWNLVFMEFNKDEEGNLHKLPPKKCIDT
GMGLERIAAVMQNVHDNYDIDLFSALINKSQEYCGRTENKIAHKIVADHLRAAFLIA
EGVLPGNEGRNYVLRRLIRRATRYIHLLGYNDSLLHRIFPVLIDSTSSAYMGAELVRA
KSLIETTLKSEENFKDTLMKGISLLEKFTADLKP GDTLP GELAFKLYD TYGFPLDIT
LDILKEKKINF DQKGFD DAMGEQKERARAKWAGSGEKSVEQVWFDLIDKFGKTKFVG Y
EFNEVND AKILAIVSSKNEVIDSAKEGEKITIILDKTPFYGESGGQV GDTGSLIKSDR
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MNQAIDEGAMALFGEKYGNQVRVVKIGDSRELCCGTHVEHTGEIGLFKIVTESSVAFG
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Proteobacteria , WP_141457239.1 MULTISPECIES:
alanine--tRNA ligase [unclassified Wolbachia]"
gene 23898..24341
/locus_tag="wEsol_00500"
CDS 23898..24341
/locus_tag="wEsol_00500"
/codon_start=1
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100 , identity 100 , evalue 5.38e-103 , alnlength 147 ,
Bacteria , Proteobacteria , WP_015589252.1 MULTISPECIES:
PAS domain-containing protein [unclassified Wolbachia]"
/cog="COG5388 COG5388 209 Uncharacterized protein
conserved in bacteria"
/pfam="Pfam-B_17152 PAS_5"
/product="PAS
domain-containing protein"
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/besthit="qcoverage 100 , hcoverage 100 , similarity 100
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Bacteria , Proteobacteria , WP_015589252.1 MULTISPECIES:
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gene 24440..24646
/locus_tag="wEsol_00501"
CDS 24440..24646
/locus_tag="wEsol_00501"
/codon_start=1
/transl_table=11
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100 , identity 100 , evalue 2.16e-36 , alnlength 68 ,
Bacteria , Proteobacteria , WP_015589253.1 MULTISPECIES:
50S ribosomal protein L35 [unclassified Wolbachia]"
/cog="RpmI COG0291 65 Ribosomal protein L35"
/pfam="Ribosomal_L35p"
/tigr="TIGR00001 rpmI_bact 63 ribosomal protein L35"
/product="50S ribosomal
protein L35"
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/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 2.16e-36 , alnlength 68 ,
Bacteria , Proteobacteria , WP_015589253.1 MULTISPECIES:
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gene 24667..25032
/locus_tag="wEsol_00502"
CDS 24667..25032
/locus_tag="wEsol_00502"
/codon_start=1
/transl_table=11
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Bacteria , Proteobacteria , WP_015589254.1 MULTISPECIES:
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 /pfam="Ribosomal_L20"
 /tigr="TIGR01032 rplT_bact 114 ribosomal protein L20"
 /product="50S ribosomal
 protein L20"
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 KDDFAKLVEAVSGKLAENS"
 /besthit="qcoverage 100 , hcoverage 100 , similarity 100
 , identity 100 , evalule 6.56e-78 , alnlength 121 ,
 Bacteria , Proteobacteria , WP_015589254.1 MULTISPECIES:
 50S ribosomal protein L20 [unclassified Wolbachia]"
 25060..25944
 /locus_tag="wEsol_00503"
 CDS 25060..25944
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 , similarity 100 , identity 100 , evalule 4.19e-208 ,
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 WP_015589255.1 MULTISPECIES: methionyl-tRNA
 formyltransferase [unclassified Wolbachia]"
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 /pfam="Formyl_trans_N Formyl_trans_C"
 /tigr="TIGR00460 fmt 315 methionyl-tRNA
 formyltransferase"
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 formyltransferase"
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 CDS 26025..27536
 /locus_tag="wEsol_00504"
 /codon_start=1
 /transl_table=11
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 99.8 , identity 99.8 , evalule 0.0 , alnlength 503 ,
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 bifunctional phosphoribosylaminoimidazolecarboxamide
 formyltransferase/IMP cyclohydrolase [unclassified
 Wolbachia]"
 /cog="PurH COG0138 515 AICAR transformylase/IMP
 cyclohydrolase PurH (only IMP cyclohydrolase domain in
 Aful)"
 /pfam="MGS AICARFT_IMPCHas"
 /tigr="TIGR00355 purH 511
 phosphoribosylaminoimidazolecarboxamide

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formyltransferase/IMP cyclohydrolase"
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phosphoribosylaminoimidazolecarboxamide
formyltransferase/IMP cyclohydrolase"
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AIGNNALEAYEKALSCDEVSSFSGGIVALNREIDLKLAEKLNEIFLEVVIAPSVNNEAL
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bifunctional phosphoribosylaminoimidazolecarboxamide
formyltransferase/IMP cyclohydrolase [unclassified
Wolbachia]"
gene 28377..29897
/locus_tag="wEsol_00505"
CDS 28377..29897
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/codon_start=1
/transl_table=11
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100 , identity 100 , evalue 0.0 , alnlength 506 ,
Bacteria , Proteobacteria , WP_015589257.1 MULTISPECIES:
2,3-bisphosphoglycerate-independent phosphoglycerate
mutase [unclassified Wolbachia]"
/cog="GpmI COG0696 509 Phosphoglyceromutase"
/pfam="Metalloenzyme iPGM_N Phosphodiester Alk_phosphatase
Sulfatase"
/tigr="TIGR01307 pgm_bpd_ind 504
2,3-bisphosphoglycerate-independent phosphoglycerate
mutase"
/product="
2,3-bisphosphoglycerate-independent phosphoglycerate
mutase"
/translation="MNIKSVVLCILDGWNGIENNKYNAISNANPPCWQYISSNYPKC
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, identity 100 , evalue 0.0 , alnlength 506 , Bacteria ,
Proteobacteria , WP_015589257.1 MULTISPECIES:
2,3-bisphosphoglycerate-independent phosphoglycerate
mutase [unclassified Wolbachia]"
gene complement(29937..30917)
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CDS complement(29937..30917)
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/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity

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100 , identity 100 , evalue 2.13e-225 , alnlength 326 ,
Bacteria , Proteobacteria , WP_015589258.1 MULTISPECIES:
ACP S-malonyltransferase [unclassified Wolbachia]"
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S-malonyltransferase"
/pfam="Acyl_transf_1 Pfam-B_728"
/tigr="TIGR00128 fabD 290 malonyl CoA-acyl carrier
protein transacylase"
/product="ACP
S-malonyltransferase"
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IANDNGGGQVVISGTREALEMLPDLFKNSSVRKLIKQVSGPFHSSLMKPADEKVLEF
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, identity 100 , evalue 2.13e-225 , alnlength 326 ,
Bacteria , Proteobacteria , WP_015589258.1 MULTISPECIES:
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DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_33766, whole genome
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ACCESSION  JAQZAU010000052  JAQZAU010000000
VERSION    JAQZAU010000052.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 6041)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 6041)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT     ##Genome-Assembly-Data-START##
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            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage     :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
            ##Genome-Assembly-Data-END##
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ORGANISM   Wolbachia pipientis

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Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 6975)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 6975)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University, 1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##

Assembly Date :: JUN-2019

Assembly Method :: FLYE v. 06-2019

Genome Representation :: Full

Expected Final Version :: Yes

Genome Coverage :: 100.0x

Sequencing Technology :: Illumina HiSeq; PacBio Sequel

##Genome-Assembly-Data-END##

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SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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REFERENCE  1 (bases 1 to 61158)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 61158)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
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            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
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CDS complement(1559..4042)
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regulator [Wolbachia endosymbiont of Cardiocondyla
obscurior]"
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EKGGELTIRTFNQKIDSLNSTPQDMFSPDKEAIEHGNVYVIEVIDTGCGMTSDTTEKI
FDPFFSTKDITSGTGLGLSTVYGIKQTEGYIYVASKVNHGTFKSIFLPMVYISDEND
REEDSEETKPVVSEIKNGIILLIEDEDSVREFISKALKRKGFDVIEASIGSEALEI
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gene 4203..5027
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CDS 4203..5027
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Wolbachia]"
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CDS 5076..6320
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TSEYEPITMYAEVNNNVIPPQKPSRTFEYKPKSTNYDALPSKEPIYAEVYDAKVSNSL
GENGYLSVSEESIYAEIYDSHKKSTENLSLED SGYLSISEEPIYCTIDDLSEQKPPAS
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gene 6489..6890
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CDS 6489..6890
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RsmE family"
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conserved in bacteria"
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(uracil(1498)-N(3))-methyltransferase [unclassified
Wolbachia]"
gene 6900..7175
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CDS 6900..7175
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conserved in bacteria"
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alnlength 91 , Bacteria , Proteobacteria , WP_146038223.1
RsmE family RNA methyltransferase, partial [Wolbachia sp.
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gene 7658..7858
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CDS 7658..7858

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/tigr="TIGR00030 S21p 58 ribosomal protein S21"
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gene 7896..9047
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100 , identity 100 , evaluate 8.51e-263 , alnlength 383 ,
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ADP-forming succinate--CoA ligase subunit beta
[unclassified Wolbachia]"
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subunit"
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[unclassified Wolbachia]"
gene 9051..9926
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CDS 9051..9926
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100 , identity 100 , evaluate 2.96e-203 , alnlength 291 ,
Bacteria , Proteobacteria , WP_015589444.1 MULTISPECIES:
succinate--CoA ligase subunit alpha [unclassified
Wolbachia]"
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alpha subunit"
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Wolbachia]"
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CDS complement(9935..10726)
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incompta]"
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epimerase [Wolbachia endosymbiont of Drosophila
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CDS complement(10704..11291)
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/tigr="TIGR02476 BluB 205 5,6-dimethylbenzimidazole
synthase"
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family protein"
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100 , identity 100 , evalue 6.38e-111 , alnlength 175 ,
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biotin transporter BioY [Wolbachia]"
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BioY"
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gene 11928..12290
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protein"
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protein"
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domain-containing protein [Wolbachia endosymbiont of
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gene 12459..13334
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CDS 12459..13334
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 Wolbachia]"
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 DSFESGDNEAAISLLNQIIAKFPYHKNALIGLNIYYANKEYKKAIVEIYTRLLKEHPS
 NPYILKNFLTIIISQYDPDLALSEMLKLYDIHKNYAPLLANLGLIYMKKEDYVKGKEYM
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 repeat protein"
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 Wolbachia]"
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 DNA gyrase subunit A [unclassified Wolbachia]"
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 gyrase/topo II, topoisomerase IV), A subunit"
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 A"
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 subunit A [unclassified Wolbachia]"
 gene 17095..17694
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CDS 17095..17694
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 /tigr="TIGR01416 Rieske_proteo 176 ubiquinol-cytochrome c reductase, iron-sulfur subunit"
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gene complement(17704..20046)
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CDS complement(17704..20046)
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 /pfam="Pfam-B_4868 ResIII DEAD AAA_19 Pfam-B_14354 Pfam-B_4868 Pfam-B_19902 Pfam-B_4868 Helicase_C"
 /fullproduct="qcoverage 100 , hcoverage 100 , similarity 99.9 , identity 99.9 , evalue 0.0 , alnlength 780 , Bacteria , Proteobacteria , WP_015589438.1 MULTISPECIES: primosomal protein N' [unclassified Wolbachia]"

gene 20191..21975
 /locus_tag="wEsol_00542"

CDS 20191..21975
 /locus_tag="wEsol_00542"

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/codon_start=1
/transl_table=11
/pfam="Pfam-B_150"
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 0.0 , alnlength 594 ,
Bacteria , Proteobacteria , WP_141456689.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
/translation="MVNDKITLNFIEIEKGEPIDRYYFSAHIKLTDESKNLLREKLGST
IQFDNLDDHFNLNHENFYIYYNKYSEHNGRSELHVRDDNGKYLTSLNPLNYYGFSMEL
SPDGASIADYGfYPLYAIYNPNHYNKAKEKVFDDHGELSPIASNVLDNFLSNTNSLT
QDILQNVFSQLQKKADEEAERLAREREAERQREEELNEKNEELKELVEKDEIKIFKV
KGNLDLGNHSAVVLQLDGEEDKIPLDSSKYIIAEYRHHPEWEGDEYLN FVSPDS
VNYENLFFVLNQSSYSDFESGFYSENRTDPHNYAKYSKEPYLSGDQLSEKLSNELEED
SNQIGTEFTIDDEQVDEEVVVESEAKSGEKGTVGEDNAKNTIQEEESNYIDQMADD
SSYPALQSNRDDYADTKKALQEKHLGDEIHKQSNEKAQKDIEVKKVTVETDSSSNKT
EKQTKPTEDEQETVMASVIENMDKNSDIEAETSNSVANSQHPLKIKTGSPLEVGKYK
ELQVTYDDVKNFYDTVRGKYHAGDGYNYEQVMVLYNEIVRPAHNHHYELFTLDEAHV
NDHLFIKGQDFGTLNDFNEMFYKSDELM"
/product="hypothetical protein"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 0.0 , alnlength 594 , Bacteria ,
Proteobacteria , WP_141456689.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
gene complement(22048..22902)
/locus_tag="wEsol_00543"
CDS complement(22048..22902)
/locus_tag="wEsol_00543"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 7.29e-205 , alnlength 284 ,
Bacteria , Proteobacteria , WP_015589436.1 MULTISPECIES:
FAD-dependent thymidylate synthase [Wolbachia]"
/cog="THY1 COG1351 273 Predicted alternative thymidylate
synthase"
/pfam="Thy1"
/tigr="TIGR02170 thyX 211 thymidylate synthase,
flavin-dependent"
/product="FAD-dependent
thymidylate synthase"
/translation="MNEATKRTIVKEIDAILYEEHKVLDHGFIRVVDYMGSDSAIVQA
ARVSYGKGTKQISQDEALIKYLMRHHHTTPFEMCEIKFHVKLPIFVARQWIRHRTANV
NEYSARYSILDNEFYTPKPEQVAKQSDNNKQSGEAFDPDTSKEIIDSLTNSNLVYS
HYEKFIEQGLAREIARTNLMLNYYTQFYWKIDLHNLHFLKLADKHAQYEIRVYAEV
MLDIIKKWVPLAYNAFVEYCLESAISRTGLEIIRKLIKGENVTREESNIGKREWEL
MSILDKQS"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 7.29e-205 , alnlength 284 ,
Bacteria , Proteobacteria , WP_015589436.1 MULTISPECIES:
FAD-dependent thymidylate synthase [Wolbachia]"
gene complement(22912..24189)
/locus_tag="wEsol_00544"
CDS complement(22912..24189)
/locus_tag="wEsol_00544"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 1.86e-301 , alnlength 425 ,
Bacteria , Proteobacteria , WP_006279833.1 MULTISPECIES:
UDP-N-acetylglucosamine 1-carboxyvinyltransferase

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[Wolbachia]"
/cog="MurA COG0766 421 UDP-N-acetylglucosamine
enolpyruvyl transferase"
/pfam="EPSP_synthase"
/tigr="TIGR01072 murA 416 UDP-N-acetylglucosamine
1-carboxyvinyltransferase"
/product="
UDP-N-acetylglucosamine 1-carboxyvinyltransferase"
/translation="MHKILIRNNYKPLVGKIKINGSKNAVLPIMAASLLSSSPVILHN
VPDLIDVHLSKLLLESLGAEVNFMHNKNYKANHTLKIDCSNINNHVMPYKASKLRTS
FLILGPMLSRFGKARTAFPGGCNIGKRPVDMHIKALEEMGAKIEIDGYNIIATVKGKL
QGKEITFEKISVGATENVIMAATFAEGVTTINNAATEPEVLDLIDFLKKMGADIEIDN
TKVIITGVEALNGCVHKIIPDRIEAGTYALAAIITGGKLELEGINLSDIRCITNELET
IGAMVELYDGGIVISRKNGSIKSANVATDPYPNFPSPDMQPOLMSAMCIADGISVIEEN
IFENRFTHADELRLKLGANISIEKSKATISGIKSLSGANLYATDLRSTAALVLASLVAG
GETIINNSHHLWRGYEAMHEKLNSCGADISISS"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 1.86e-301 , alnlength 425 ,
Bacteria , Proteobacteria , WP_006279833.1 MULTISPECIES:
UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Wolbachia]"
gene complement(24345..25181)
/locus_tag="wEsol_00545"
CDS complement(24345..25181)
/locus_tag="wEsol_00545"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 5.28e-195 , alnlength 278 ,
Bacteria , Proteobacteria , WP_010963091.1 MULTISPECIES:
CPBP family intramembrane metalloprotease [Wolbachia]"
/cog="COG1266 COG1266 226 Predicted metal-dependent
membrane protease"
/pfam="Abi"
/product="CPBP family
intramembrane metalloprotease"
/translation="MGVCMNLTINCTLFVVITYFLTCTIIAWCLPFKDITLLTTFVPA
SVAILLTIYNKQKVRDLFKLSSPKNCLLGFILILVSMLISNGLLSIYCGFSFFRESFT
LDRVKDLASVLSPLVMLFVLLSTFVMWIIMSLGEEIGWRGYLLKNLKSISNFYIRAI
IVGIIWSVWHIPTYVVGASALWKDGFTFTICAYTLYICAMSIMFTWLFEKDNSIWPV
TIAHATNNLVYSVLSILMPSPPLSTFDVIRLTLGAAGYFIVAIGVIWFDKARERHLS
NS"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 5.28e-195 , alnlength 278 ,
Bacteria , Proteobacteria , WP_010963091.1 MULTISPECIES:
CPBP family intramembrane metalloprotease [Wolbachia]"
gene complement(25421..26692)
/locus_tag="wEsol_00546"
CDS complement(25421..26692)
/locus_tag="wEsol_00546"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 8.96e-308 , alnlength 423 ,
Bacteria , Proteobacteria , WP_015589434.1 MULTISPECIES:
beta-ketoacyl-ACP synthase II [unclassified Wolbachia]"
/cog="FabB COG0304 412 3-oxoacyl-(acyl-carrier-protein)
synthase"
/pfam="ketoacyl-synt Thiolase_N Ketoacyl-synt_C"
/tigr="TIGR03150 fabF 407

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beta-ketoacyl-acyl-carrier-protein synthase II"
/product="beta-ketoacyl-ACP
synthase II"
/translation="MSRRVVVTGVGLITPLAADVDNTWLRRLIKGESGIKAINTRFDS
SDLACKIAGQVPLQSDNIEHHFNPLDYISEKDSKRTDRFIHYGIAAAIQAVDDSLILE
SQNINRERVGVTTIGSGIGGLPSIQENVITMQEKGPRRVSPFFVPASLINLISGHISIK
YEFTGPNDSAVTACATGAHAIINSARTIKLGEADVMIAGGAESALCRVGIAGFASMKA
LSTKFNDKPKEASRPWDAERDGFVMGEGAGILVLEEYEHAKKRGAKIYAEELNGYGLTG
DAHHTAPHPEGRGAFKAMQLALHSAQINPNQVGYINAHGTSTPLGDKIEVIAMKKLF
GDYAYKIPVSSTKSSTGHLLGAAGSVEAIFSILALNNGIIPPTLNHLHKPSEGCDLNFV
PFKAQEHKIQYALSNSFGFGGTNASLIFGQV"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 8.96e-308 , alnlength 423 ,
Bacteria , Proteobacteria , WP_015589434.1 MULTISPECIES:
beta-ketoacyl-ACP synthase II [unclassified Wolbachia]"
gene complement(26706..26978)
/locus_tag="wEsol_00547"
CDS complement(26706..26978)
/locus_tag="wEsol_00547"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 8.01e-51 , alnlength 90 ,
Bacteria , Proteobacteria , WP_007549723.1 MULTISPECIES:
acyl carrier protein [Wolbachia]"
/cog="AcpP COG0236 80 Acyl carrier protein"
/pfam="Pfam-B_5835 Pfam-B_10478 PP-binding Pfam-B_17829
Ribosomal_L50"
/tigr="TIGR00517 acyl_carrier 77 acyl carrier protein"
/product="acyl carrier
protein"
/translation="MVRNVNSELAKSTREDIEEKVKKIILEHISKDVEKFNSSSKLSE
HGTDSDLAVEIIMAAEEFGEIIPDEDAQKMETMEQIVEYINNKKG"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 8.01e-51 , alnlength 90 ,
Bacteria , Proteobacteria , WP_007549723.1 MULTISPECIES:
acyl carrier protein [Wolbachia]"
gene 27112..27903
/locus_tag="wEsol_00548"
CDS 27112..27903
/locus_tag="wEsol_00548"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 2.91e-180 , alnlength 263 ,
Bacteria , Proteobacteria , WP_141456688.1 MULTISPECIES:
polyprenyl synthetase family protein [unclassified
Wolbachia]"
/cog="IspA COG0142 322 Geranylgeranyl pyrophosphate
synthase"
/pfam="polyprenyl_synt"
/tigr="TIGR02748 GerC3_HepT 319 heptaprenyl diphosphate
synthase component II"
/product="polyprenyl
synthetase family protein"
/translation="MLDETTKNLLIVEVNKLLPENSENKLISAMRYILLAPAKHIRSF
LVIASSQVFNAEAKKVISVAAAEFVHAYSLIHDDLPCMDNSDTRRSQLSCHKKFDEA
TAVLAGDALLTLAFEVLSSLNEKRCEIIKVLSSQAIGIRGMVGGQALDIDTDFNKIKEI
HLMKTAKLFAASCEIGAIIGGATDEQRRALNYGINLGLIFQAKDDIEDYEQDKTNL
MSVLGKSEVEDYIDGLFKQGLDNLALSGLDNTNYLYDLLNQVKKDG"

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/blasthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 2.91e-180 , alnlength 263 ,
Bacteria , Proteobacteria , WP_141456688.1 MULTISPECIES:
polyprenyl synthetase family protein [unclassified
Wolbachia]"
gene 27896..28837
/locus_tag="wEsol_00549"
CDS 27896..28837
/locus_tag="wEsol_00549"
/codon_start=1
/transl_table=11
/pfam="FKBP_C FKBP_C"
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 1.48e-214 , alnlength 313 ,
Bacteria , Proteobacteria , WP_015589432.1 MULTISPECIES:
FKBP-type peptidyl-prolyl cis-trans isomerase
[unclassified Wolbachia]"
/translation="MVRKIILQMLISVVMILTTLTSAFVFTIVYINKGKPEKKDKLYEI
NATHGGLIQTIAYYLVKPILESALDRYIEKHGLTEYLEEMTQQKEEDSINFYEITEGS
GSKAFCGLEVLQIYKISNNNSATLPSKVSDVTLKIGQDDLKEVSLGAIGMKEGGERV
VTIANENKMNFNFSYYVKLIEVKDKYPDSVNNLMVFNDLINKTGKQVRCGDEISVKYSV
KEHNGEYIVKDQTVQFRVGDKKIPLAIELGVGMRAGNKRTILSPDLLTITDDMLIK
DIDYDEKNISIIDLSLDVKQEVAAHHSTVEKQPKEYS"
/product="FKBP-type
peptidyl-prolyl cis-trans isomerase"
/blasthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 1.48e-214 , alnlength 313 ,
Bacteria , Proteobacteria , WP_015589432.1 MULTISPECIES:
FKBP-type peptidyl-prolyl cis-trans isomerase
[unclassified Wolbachia]"
gene complement(28906..30396)
/locus_tag="wEsol_00550"
CDS complement(28906..30396)
/locus_tag="wEsol_00550"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 0.0 , alnlength 496 ,
Bacteria , Proteobacteria , WP_006280200.1 MULTISPECIES:
ATP-dependent protease ATPase subunit HslU [Wolbachia]"
/cog="HslU COG1220 444 ATP-dependent protease HslVU
(ClpYQ), ATPase subunit"
/pfam="MCM AAA_16 Zeta_toxin Sigma54_activat AAA_2 AAA_5
Mg_chelatase AAA AAA_17 AAA_33 AAA_18 AAA_22 AAA_2 AAA
ClpB_D2-small"
/tigr="TIGR00390 hslU 441 ATP-dependent protease HslVU,
ATPase subunit"
/product="ATP-dependent
protease ATPase subunit HslU"
/translation="MSSKQKTLCTNFSNPITLSEGRSCSSDITYDEKDNLYKDTKSGF
DSNDSQVQVNDSTQVLLDDLPPQKIVKELDRFIIGQDDAKRAVAIALRNRWRNQVPF
PLRDEIIPKNILMIGHTGVGKTEIARRLAKLAGAPFIKIEATKFTEIGYVGRDVSII
RDLVDAAIVLVKEKARKALAKKALILAEKTIVNSMVGENATEESKKIFRERLRNKEFE
DGEVSINVRESKSMPLPTFDIPGMPGGQVGVMMNVTEIMGKMFNGSKKTKTITVVKKEAR
EILINEESERLMDEDKIIKEAIDLVSNDGIVFLDEIDKIAARTEVKGEVNREGVQRDL
LPLLEGTTVTTKYGHVKTDYILFIASGAFHQSKPSDLLPELQGRLPFIRVELKALTQED
LIRILKEPESSLLKQYIALMKTENVTLFTDDGIKTIAEIAFTVNRQVENIGARRLHT
VMEKLLDEISFIASEKNSEKFIIDSKYVKDKLESISKQLDLSKFIL"
/blasthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 0.0 , alnlength 496 , Bacteria ,

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Proteobacteria , WP_006280200.1 MULTISPECIES:
 ATP-dependent protease ATPase subunit HslU [Wolbachia]"

gene complement(30398..30952)
 /locus_tag="wEsol_00551"

CDS complement(30398..30952)
 /locus_tag="wEsol_00551"
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 /transl_table=11
 /fullproduct="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 8.00e-123 , alnlength 184 , Bacteria , Proteobacteria , WP_006280198.1 MULTISPECIES:
 ATP-dependent protease subunit HslV [Wolbachia]"
 /cog="HslV COG5405 178 ATP-dependent protease HslVU (ClpYQ), peptidase subunit"
 /pfam="Proteasome Pfam-B_18807"
 /tigr="TIGR03692 ATP_dep_HslV 171 ATP-dependent protease HslVU, peptidase subunit"
 /product="ATP-dependent protease subunit HslV"
 /translation="MIQHDNNKMYGTTILSIRKDKSVVVIGDGQVSLGHTVIKSGAKK VRRLSGDSVIAGFAGATADAFTLFRLESKLDKHPGQLMRACVELAKDWRMDKYLRKL EAMMIVADKSISLVITGTGDVLEPEDGVAAIGSGGNFALSAARALIDIKGISIEEIAK KAMKIAGDICVYTNHNVVIEKIEE"
 /besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 8.00e-123 , alnlength 184 , Bacteria , Proteobacteria , WP_006280198.1 MULTISPECIES:
 ATP-dependent protease subunit HslV [Wolbachia]"

gene 31068..32228
 /locus_tag="wEsol_00552"

CDS 31068..32228
 /locus_tag="wEsol_00552"
 /codon_start=1
 /transl_table=11
 /fullproduct="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 9.13e-280 , alnlength 386 , Bacteria , Proteobacteria , WP_015589431.1 MULTISPECIES:
 glutamate--cysteine ligase [unclassified Wolbachia]"
 /pfam="GshA"
 /tigr="TIGR02049 gshA_ferroox 403 glutamate--cysteine ligase"
 /product="glutamate--cysteine ligase"
 /translation="MQNIIHPDLEKSINNWF EAKFNGLTSPFYSSIDL RNSGYKIVPV DANLFPAGFNNLSEESRTMAARLIKS YFKRHQYKKVLIIPENYTRNKMYIENVFVIEK ILQLAGFETRIGLLYNEVYNLIEQYETVVKENSLLKTTSGFVPDVII LNRDMTSHIPD TLKDVKQDIVPSPLYGWHSRQKFKYFEIYQELASEFCGEFKIDPWLISVLTESCDGVD FDDDL S LGAVATKVDQILSLVQKKYEEYEIKTQPYVFIKASNGTYGMGIITATSGEEI LNLNKKKRHKMKKIKEGIAINSVIIQEGVPTIDMFKSSSAEPLIYYIGDTPTCYLYRC NSRKDVYSSLNATDCEFH DVSQVVEGKILSLWSIVSKLAVLALAVEIKSFHP"
 /besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 9.13e-280 , alnlength 386 , Bacteria , Proteobacteria , WP_015589431.1 MULTISPECIES:
 glutamate--cysteine ligase [unclassified Wolbachia]"

gene complement(32232..33029)
 /locus_tag="wEsol_00553"

CDS complement(32232..33029)
 /locus_tag="wEsol_00553"
 /codon_start=1
 /transl_table=11
 /pfam="DUF3278"

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/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evaluate 2.60e-184 , alnlength 265 ,
Bacteria , Proteobacteria , WP_006280195.1 MULTISPECIES:
hypothetical protein [Wolbachia]"
/translation="MPNKLKKKSNILAQRVHDIYDHDFRKVICITTGLTALLCKISLQ
FCCEFIDNNRSNIFLIRNVARLVKFPTSILYIAHSAFTLQDLIKDYRNPESKKELAKI
VGKSANLASSTIEALMMLKIIHFCTGSNTDIISYINLTSTILFLFISEPISYYTCKE
YLDNKDPEKSAECKKDLIISTLTLSLGLLNFILRRIETPTIPINLGNIGIYNFNLSVT
VSIIYSAVFLAVQLDKLFQQPVNDPSTELDDVHNINGHSNDSTVEV"
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/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evaluate 2.60e-184 , alnlength 265 ,
Bacteria , Proteobacteria , WP_006280195.1 MULTISPECIES:
hypothetical protein [Wolbachia]"
gene complement(33100..34047)
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CDS complement(33100..34047)
/locus_tag="wEsol_00554"
/codon_start=1
/transl_table=11
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100 , identity 100 , evaluate 3.43e-230 , alnlength 315 ,
Bacteria , Proteobacteria , WP_010082099.1 MULTISPECIES:
ferrochelatase [Wolbachia]"
/cog="HemH COG0276 320 Protoheme ferro-lyase
(ferrochelatase)"
/pfam="Ferrochelatase"
/tigr="TIGR00109 hemH 322 ferrochelatase"
/product="ferrochelatase"
/translation="MKKAVILFNLGGPDSLNAVVRPFLFNLFYDRRIINLPNPFRLLA
KFISAKRENTARKIYEEIGGKSPILENTKMQANASELKLNNRNHVHKVFICMRYWRP
FADEVIESVKQFDPDEVILLPLYPQYSTTTTLSSIENWQKNAKRYGLKCNTKMIHRY
DNQDFIEAHTNLIKYYKLARKIGKPRVLFSASLSPLSIIKKGDPYASQVERSVELIV
EKLAINNLDWSICYQSKIGPVKWLEPSTESELLRAKADGVPVVLSPISFVSEHSETLV
ELDIEYKAIKDGYYFRVPTLSTDPLFIKCLADLCINLP"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evaluate 3.43e-230 , alnlength 315 ,
Bacteria , Proteobacteria , WP_010082099.1 MULTISPECIES:
ferrochelatase [Wolbachia]"
gene complement(34048..34869)
/locus_tag="wEsol_00555"
CDS complement(34048..34869)
/locus_tag="wEsol_00555"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evaluate 6.56e-182 , alnlength 273 ,
Bacteria , Proteobacteria , WP_015589429.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
/translation="MGECKNNTTKQAEPTTKKQAKSTTKKLVSNFKSSLFCGTKGFL
TFNLAFLSFLEYSLLHNTLKKGAAFAMKRNTIPFLEMAIIVPFVCFALPAMLGSM
MQCALLCASLMIATCFIVRTFHLREKLMEKITNHSRKEIDAEFKKDTIKFPIFDQNRK
HTEYNPSNSGRLLDETSSTSLFVKVLLFPLKVLLNVLQSCIMLSLAAVELLETVP
SLFVDTFFDWNFTSTKSNLKRSGHLLYASVRNLVPITKFDECVANFIGTPEVTCCSSA"
/product="hypothetical protein"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evaluate 6.56e-182 , alnlength 273 ,
Bacteria , Proteobacteria , WP_015589429.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
gene 34983..35402

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CDS
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 34983..35402
 /locus_tag="wEsol_00556"
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 /transl_table=11
 /fullproduct="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 5.71e-92 , alnlength 139 , Bacteria , Proteobacteria , WP_015589428.1 MULTISPECIES: nucleoside-diphosphate kinase [Wolbachia]"
 /cog="Ndk COG0105 135 Nucleoside diphosphate kinase"
 /pfam="NDK"
 /product="nucleoside-diphosphate kinase"
 /translation="MAIEKTLKILKPDVKNNTGNINSYIEQSGLKITAQKMMLLTKKQAEIFYEIHKDRPFFGELVEFMTSGSVVQVLVGENAVSKYRQIMGATDPKQADKGTIRGDFADDISENRVHGSDSLENARKEIAFFFAECELV"
 /besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 5.71e-92 , alnlength 139 , Bacteria , Proteobacteria , WP_015589428.1 MULTISPECIES: nucleoside-diphosphate kinase [Wolbachia]"

gene
 complement(35714..35890)

CDS
 /locus_tag="wEsol_00557"
 complement(35714..35890)
 /locus_tag="wEsol_00557"
 /codon_start=1
 /transl_table=11
 /fullproduct="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 4.12e-32 , alnlength 58 , Bacteria , Proteobacteria , WP_182309489.1 hypothetical protein [Wolbachia pipientis]"
 /translation="MKKKAKETLGLLSALKYWRFLCFKRLTSEIQPLLIATNLRCKCLRNLRSRKKDKESPS"
 /product="hypothetical protein"
 /besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 4.12e-32 , alnlength 58 , Bacteria , Proteobacteria , WP_182309489.1 hypothetical protein [Wolbachia pipientis]"

gene
 36383..36988

CDS
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 36383..36988
 /locus_tag="wEsol_00558"
 /codon_start=1
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 /cog="RecR COG0353 198 Recombinational DNA repair protein (RecF pathway)"
 /pfam="RecR Toprim_4 Toprim"
 /tigr="TIGR00615 recR 196 recombination protein RecR"
 /product="recombination mediator RecR"
 /translation="MNVNIKNLVHAFSKLPSLGPSSSRRLVIHLLQNKEKVMLPLASLIKELADLIIECEVCGNLDTKSPCSICTNPKRDTKLLCVVEELGDLWAFEKGNIYSGLYHVLGGRLSAINGIGPKELNLDITLKRVTESKIEEIIIIAINPTLEGQVTAQYIIELLKNLDVKISRLACGIPMGGEIDYLDDEGTLRIALTSRQEYELNIK"
 /besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 3.33e-137 , alnlength 201 , Bacteria , Proteobacteria , WP_010963080.1 MULTISPECIES:

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gene      recombination mediator RecR [Wolbachia]"
          36992..38212
          /locus_tag="wEsol_00559"
CDS       36992..38212
          /locus_tag="wEsol_00559"
          /codon_start=1
          /transl_table=11
          /pfam="KAP_NTPase AAA_22"
          /fullproduct="qcoverage 100 , hcoverage 100 , similarity
          100 , identity 100 , evalue 4.75e-283 , alnlength 406 ,
          Bacteria , Proteobacteria , WP_015589427.1 MULTISPECIES:
          hypothetical protein [Wolbachia]"
          /translation="MCLKKLISLITFKKKEIAPPLKVVAWENDRLNYKQFSGKFNNII
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          FLFEDLFVSYKVKRSVIQQFKNINQELFSLNTLGKLISKSPAMLVSFLDAAKEADKK
          DIGFVLSELSSLQRRKESTRDFKTQLADVVNKIRKDKNIYIMVDNLDVCRPKFVVDLF
          ESIKYMLDVEGLVFIIPVSKDKSNVQRAISTILGPNFDLKSFTDLSLHLPKQPIEKFT
          KELFENIKLPKKSKNLIVDSFIFYAESLSLSLKTIEYCVKKIKLCLLNHTREELPDPN
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gene      complement(38258..39082)
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CDS       complement(38258..39082)
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          SPKQQNNQKVETSKKTYNPLDWNPIYQGKKLFSGLNMSSNSSSCSEKSNISDVSDKSN
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gene      complement(39152..40480)
          /locus_tag="wEsol_00561"
CDS       complement(39152..40480)
          /locus_tag="wEsol_00561"
          /codon_start=1
          /transl_table=11
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          100 , identity 100 , evalue 3.26e-306 , alnlength 442 ,
          Bacteria , Proteobacteria , WP_141456686.1 MULTISPECIES:
          pyruvate dehydrogenase complex dihydrolipoamide
          acetyltransferase [unclassified Wolbachia]"
          /cog="AceF COG0508 404 Pyruvate/2-oxoglutarate
          dehydrogenase complex, dihydrolipoamide acyltransferase
          (E2) component, and related enzymes"
          /pfam="Biotin_lipoyl Biotin_lipoyl_2 E3_binding

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2-oxoacid_dh"
/tigr="TIGR01349 PDHac_trf_mito 437 pyruvate
dehydrogenase complex dihydrolipoamide acetyltransferase"
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dehydrogenase complex dihydrolipoamide acetyltransferase"
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acetyltransferase [unclassified Wolbachia]"
gene 40551..41042
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CDS 40551..41042
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/transl_table=11
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100 , identity 100 , evalue 8.31e-117 , alnlength 163 ,
Bacteria , Proteobacteria , WP_015589424.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
/cog="COG3807 COG3807 171 Uncharacterized protein
conserved in bacteria"
/pfam="Pfam-B_9058 SH3_4 SH3_4 SH3_3"
/product="hypothetical protein"
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gene complement(41097..41534)
/locus_tag="wEsol_00563"
CDS complement(41097..41534)
/locus_tag="wEsol_00563"
/codon_start=1
/transl_table=11
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99.3 , identity 99.3 , evalue 1.27e-91 , alnlength 145 ,
Bacteria , Proteobacteria , WP_015589423.1 hypothetical
protein [Wolbachia endosymbiont of Drosophila simulans]"
/translation="MSLKNKISELIEQQFSIKYHDNYLAYAIHKWAASEISNSIAFCI
IGCGNCKIGYQDAANSFNITKEEIEQGNIASIESKIKSEAEKSGSEFSELSIRVDQSL
REQSEKSIVQILDSSAEEMLRSFCDSPVQSPEHEEVSAIILCFT"
/product="hypothetical protein"
/besthit="qcoverage 100 , hcoverage 100 , similarity 99.3
, identity 99.3 , evalue 1.27e-91 , alnlength 145 ,
Bacteria , Proteobacteria , WP_015589423.1 hypothetical
protein [Wolbachia endosymbiont of Drosophila simulans]"
gene complement(41656..44463)
/locus_tag="wEsol_00564"

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CDS      complement(41656..44463)
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          /transl_table=11
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          /fullproduct="qcoverage 99.2513368983957 , hcoverage 100
, similarity 99.8 , identity 99.8 , evaluate 0.0 ,
alnlength 928 , Bacteria , Proteobacteria ,
WP_174516895.1 hypothetical protein [Wolbachia
endosymbiont of Cardiocondyla obscurior]"
          /translation="MSGYRYFMRSVRLNLFLLIFFLILGLSYQGYADCPTFVESNTWLE
AIVGGDWVKEIKVQAIKDQGVDFYFNPKIRVCAYDGGQSYCYDLQSGESCRQIYGTQGT
GAGVSAAAFIDWEGDKTKAGGEIARGLKWEWADGVTDEEKRRFANSPKICACSQKGAC
MSGISSWGSRVFSGENIFRPGEMEKVCDTCYQTAVKCAPVPLAPSPPPFCEQLAMSP
QVRIVPITNEDNDYFDPRVGVIISGLEERKELGFPHVVSNNENIPNHSYTVTDKDTHTY
YFKTYRKKGQLCAEYLGTSINEQNPFVRCFPAPPAPPEPEIVEIVNKNLTKVEMKMS
ESTCAKAHGTYSNGSCTFNVNTDLNHPINIGPLSLKVVKPAIVAKTTDSNIDNIIIEGI
LESNPQQFKVLKEYGYVPDVQIKCSKGGSFYSFNDFEKKLKDKSIOCFNNSGQPEIE
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VFGSGDYDVGDSQITSSRVEIEVWGCGEAGHIKDTPTYTTPNSTESRVGMPGDYIKAE
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IYEEKDYTEPIIDDSVKLKEKTTTTGLRVTEDNKIIYIENGEIKHETVKCSKGFSSK
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928 , Bacteria , Proteobacteria , WP_174516895.1
hypothetical protein [Wolbachia endosymbiont of
Cardiocondyla obscurior]"
gene      complement(44423..46777)
          /locus_tag="wEsol_00565"
CDS      complement(44423..46777)
          /locus_tag="wEsol_00565"
          /codon_start=1
          /transl_table=11
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100 , identity 100 , evaluate 0.0 , alnlength 784 ,
Bacteria , Proteobacteria , WP_141456684.1 MULTISPECIES:
type VI secretion protein [unclassified Wolbachia]"
          /cog="VirB4 COG3451 796 Type IV secretory pathway, VirB4
components"
          /pfam="CagE_TrpE_VirB_TrwB_AAD_bind AAA_10"
          /tigr="TIGR00929_VirB4_CagE_792_type_IV
secretion/conjugal transfer ATPase, VirB4 family"
          /product="type VI secretion
protein"
          /translation="MQLKVPTVNSKLKKKNNLALLESIDLDFVPYACHYDEETILTKQ
GELLKIIKLEDYSSVDNYSDLRTEIRKSISKNNINSLCFTVWIHTVRKRNLKSLKWNKT
EDFSDNLHSTWFNKLTDSKLQYINELYIVILFSDFGKHTNNSFFFNRIKNKHLKSLQE
SHQELQKITDVIQNDLGPFGAKKLSLRFSEGKIYSEMIEFLHYIVTLTHKDYPIHERD
LSQYIRNFKIAFGFNTFQTIFENQQKFGSIFSISKEYREISLGNIDRCLQLESEFIITE
IMIFTSNNKAIKEFKKQINMLQISEDNTLLKSSGIEEIIIELEKTSSIDFCQKIIIFTI
FADDRNKLAESISDLSSIMSLVGFMFRTDLHMESHFWAQLPGNFASFITQPKNILT KY
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TSLINFLLSERKFNPRIVILDNTGKSIIFTKAVSGKYIIDPKYKDKSLKFNPLNIE
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Proteobacteria , WP_141456684.1 MULTISPECIES: type VI
secretion protein [unclassified Wolbachia]"
gene complement(46822..47196)
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CDS complement(46822..47196)
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/pfam="MMPL"
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100 , identity 100 , evalue 1.03e-71 , alnlength 124 ,
Bacteria , Proteobacteria , WP_022626145.1 MULTISPECIES:
hypothetical protein [Wolbachia]"
/translation="MRIQLNKVLVFIALLSFIFASYSSEASSASDELKGIQETVKNFI
SSFSVKDTVENMSPSTIIIGLCIAAVILAVVFRGLIFFMIMFGVLVLMFGSTEKATDYL
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/product="hypothetical protein"
/blasthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 1.03e-71 , alnlength 124 ,
Bacteria , Proteobacteria , WP_022626145.1 MULTISPECIES:
hypothetical protein [Wolbachia]"
gene complement(47291..48514)
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CDS complement(47291..48514)
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100 , identity 100 , evalue 2.62e-230 , alnlength 407 ,
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hypothetical protein [unclassified Wolbachia]"
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KEGASPEVLTELEKSLREQLKSPEKQEEYQKHYKYYIENFLPALKDEVIKSEELAVP
TVFNNEREQSQRPQTIRGKIVKTILDITNRSSSVSSIPNAVEENIEDQMQLKHIEEQN
NTQETPLNVAEKKSGDNKILSNSDVAEEVFEEKYSKVVKIEEKKTSKLSSGNDSDSGI
DSPRTSKESLKSPPVSSRRSSLTLVTSTSSSEESLNSTLSSVEGDNGLQPEGGEKTELLE
SNLESPKENETQVQPEQTVKKEPKMQENENSQGANPDQVKKDILLKNQPNRNLHVA
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LVDDKSLQHVHSGKN"
/product="hypothetical protein"
/blasthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 2.62e-230 , alnlength 407 ,
Bacteria , Proteobacteria , WP_015589419.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
gene complement(48637..49665)
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CDS complement(48637..49665)
/locus_tag="wEsol_00568"
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/transl_table=11
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100 , identity 100 , evalue 6.00e-240 , alnlength 342 ,
Bacteria , Proteobacteria , WP_015589418.1 MULTISPECIES:

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nitronate monooxygenase [unclassified Wolbachia]"
/cog="COG2070 COG2070 336 Dioxygenases related to
2-nitropropane dioxygenase"
/pfam="NMO ThiG His_biosynth FMN_dh DHO_dh IMPDH"
/tigr="TIGR03151 enACPred_II 307 putative
enoyl-[acyl-carrier-protein] reductase II"
/product="nitronate
monooxygenase"
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IKSAARNAIPSVQISADFPVIPVRAIANKASDDFMKRQKEVIDEYQKGQISKEDGQLE
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gene complement(49671..50192)
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CDS complement(49671..50192)
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100 , identity 100 , evalue 5.30e-118 , alnlength 173 ,
Bacteria , Proteobacteria , WP_015589417.1 MULTISPECIES:
cytochrome b [unclassified Wolbachia]"
/cog="CybB COG3038 181 Cytochrome B561"
/pfam="Cytochrom_B_N Ni_hydr_CYTB Cytochrom_B561 DUF4405"
/product="cytochrome b"
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TFIDKQNIKFKMI"
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, identity 100 , evalue 5.30e-118 , alnlength 173 ,
Bacteria , Proteobacteria , WP_015589417.1 MULTISPECIES:
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gene complement(50607..50783)
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CDS complement(50607..50783)
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100 , identity 100 , evalue 3.40e-31 , alnlength 58 ,
Bacteria , Proteobacteria , WP_215401836.1 hypothetical
protein [Wolbachia endosymbiont of Drosophila simulans]"
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Bacteria , Proteobacteria , WP_215401836.1 hypothetical
protein [Wolbachia endosymbiont of Drosophila simulans]"
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CDS 51492..52688

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Bacteria , Proteobacteria , WP_015589416.1 MULTISPECIES:
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/cog="Pgk COG0126 395 3-phosphoglycerate kinase"
/pfam="PGK"
/product="phosphoglycerate
kinase"
/translation="MSIPSIENCDLHNKAVLLRVDFNVPIKDGEIRDVTRILRALPTI
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SVMDAGDIILLENLRFYKEEQSDSNFAKQLASLADIYVNDASFCSHRAHASISRITE
FLPSYAGFCLQDELKYLEKAVSFKA KPITAIVGGAKISTKIKVLMKLTEKVDYLVGG
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, identity 100 , evalue 5.73e-280 , alnlength 398 ,
Bacteria , Proteobacteria , WP_015589416.1 MULTISPECIES:
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gene 52738..53025
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CDS 52738..53025
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100 , identity 100 , evalue 6.10e-64 , alnlength 95 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_012673373.1 MULTISPECIES: hypothetical protein
[Wolbachia]"
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SSQPATVSELTD FDRGVLKVC GDWGAHPDKEDFKILLSCPQH QE VVKGIYK"
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, identity 100 , evalue 6.10e-64 , alnlength 95 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_012673373.1 MULTISPECIES: hypothetical protein
[Wolbachia]"
gene 53022..53366
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CDS 53022..53366
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/codon_start=1
/transl_table=11
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100 , identity 100 , evalue 5.31e-85 , alnlength 114 ,
Bacteria , Proteobacteria , WP_227738569.1 EndoU
domain-containing protein [Wolbachia endosymbiont of
Drosophila simulans]"
/translation="MITPDADLELLKDELANIWFTNSESEKETIGFGHIFCGEPNDKL
GGMHFVGRYVEAQEDKWAGAIWNDSKSLCNKSDIKPPVYTFGMKYL GKDGEVKVKCPNG
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/product="EndoU domain-containing protein"
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Bacteria , Proteobacteria , WP_227738569.1 EndoU
domain-containing protein [Wolbachia endosymbiont of
Drosophila simulans]"
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CDS       53323..53532
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          /transl_table=11
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, similarity 100 , identity 100 , evalue 1.85e-45 ,
alnlength 69 , Bacteria , Proteobacteria , KDB19218.1
hypothetical protein wGmm_0106 [Wolbachia endosymbiont of
Glossina morsitans morsitans]"
          /translation="MDTHITFMPIISATKVFKELGKDGMClyEMEDDDYQSVFVRKND
AILTFYPDLTPKCDDKSTYCSCGKS"
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Glossina morsitans morsitans]"
gene      53630..53980
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CDS       53630..53980
          /locus_tag="wEsol_00575"
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Bacteria , Proteobacteria , WP_007549043.1 MULTISPECIES:
diacylglycerol kinase [Wolbachia]"
          /cog="DgkA COG0818 123 Diacylglycerol kinase"
          /pfam="DAGK_prokar"
          /product="diacylglycerol
kinase"
          /translation="MKKGIIRLIKAIQYSCEGIKSAFISEIAFRQELLLFIVCVSILF
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gene      complement(53992..54804)
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CDS       complement(53992..54804)
          /locus_tag="wEsol_00576"
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100 , identity 100 , evalue 1.84e-191 , alnlength 270 ,
Bacteria , Proteobacteria , AGK00383.1 Pseudouridine
synthase [Wolbachia endosymbiont of Drosophila simulans
wHa]"
          /cog="RluA COG0564 289 Pseudouridylate synthases, 23S
RNA-specific"
          /pfam="PseudoU_synth_2 Pfam-B_415"
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RluA family"
          /product="Pseudouridine synthase"

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KNEAAHSFLSELLSNRKIKREYLAVVWGTLSQQGTIKTNIAPKRGNKEMMCVTKITG
KLAITHYLVQKVIGQVSLVKCTLETGRTHQIRVHMSHIGHISIVGDQVYGKNSSKSTKY
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, identity 100 , evalue 1.84e-191 , alnlength 270 ,
Bacteria , Proteobacteria , AGK00383.1 Pseudouridine
synthase [Wolbachia endosymbiont of Drosophila simulans
wHa]"
gene complement(54927..56630)
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SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 6859)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 6859)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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FEATURES Location/Qualifiers

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SOURCE     Wolbachia pipientis (insect metagenome)
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REFERENCE  1  (bases 1 to 8361)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 8361)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
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ORIGIN

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REFERENCE  1  (bases 1 to 23382)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 23382)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date          :: JUN-2019
            Assembly Method        :: FLYE v. 06-2019
            Genome Representation   :: Full
            Expected Final Version :: Yes
            Genome Coverage        :: 100.0x
            Sequencing Technology   :: Illumina HiSeq; PacBio Sequel
            ##Genome-Assembly-Data-END##
FEATURES   Location/Qualifiers
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                                     Northfield, MN"
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KIKNAQSKAKVIGMLQNEGQRSATQELVKNGTIQNFSEDDMKKLREKGTSTYESDKEA
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isomerase SurA [Trichonephila clavata]"
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 /cog="TrmU COG0482 356 Predicted
 tRNA(5-methylaminomethyl-2-thiouridylate)
 methyltransferase, contains the PP-loop ATPase domain"
 /pfam="Asn_synthase Pfam-B_78 NAD_synthase ThiI
 tRNA_Me_trans ExsB Pfam-B_18759"
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 (5-methylaminomethyl-2-thiouridylate)-methyltransferase"
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 2-thiouridine(34) synthase MnmA"
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Wolbachia]"
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GLPVTEPEGSMIVDIGGGTTEVAIISLGGIVYSRSARVGGDIMDEAIIKSYIRENHKLL
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CDS 11558..12853
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Wolbachia]"
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FRPLLNFSRSEIEKYAKLHRLKWIEDRSNYDLKYRRTLYRNLLKASDNQEILTERICL
TALHMKRAAKALMHYTRLAFNDCVNVHDLGYIEIKLSEFYQLPEEIALRLLYSIMAI
ASKHYKPRYN SLIVIFNKILQKDSNVNCTLSGCKIRKHGENILIIRESSKIQEITLNL
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synthetase Tils"
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tRNA lysidine(34) synthetase Tils [unclassified
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gene 12866..14704
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WP_012673393.1 MULTISPECIES: ATP-dependent zinc
metalloprotease FtsH [Wolbachia]"
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metallopeptidase HflB"
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Bacteria , Proteobacteria , ACN95910.1 thymidylate kinase
[Wolbachia sp. wRi]"

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gene 16797..18515
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Proteobacteria , WP_141456699.1 MULTISPECIES: monovalent cation:proton antiporter-2 (CPA2) family protein
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ORIGIN

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VERSION    JAQZAU010000058.1
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            BioSample: SAMN33142973
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SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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REFERENCE  1 (bases 1 to 19355)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 19355)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
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            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
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VERSION    JAQZAU010000059.1
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 9449)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

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TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 9449)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 5710)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
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COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
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Genome Coverage :: 100.0x
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VERSION    JAQZAU010000061.1
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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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REFERENCE  1 (bases 1 to 2713)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 2713)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
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COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date                :: JUN-2019

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Assembly Method      :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
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ORIGIN

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SOURCE     Wolbachia pipientis (insect metagenome)
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  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL  International Journal Molecular Sciences
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  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Direct Submission
  JOURNAL  Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
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            Assembly Method         :: FLYE v. 06-2019
            Genome Representation    :: Full
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ORIGIN

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VERSION    JAQZAU010000063.1
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 10423)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

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TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 10423)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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Wolbachia]"
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PAGSARVEIEFTVNVDGILTVTAREKTTGIEQTVEVNSSFGLSEADVQNMVNQSINSF
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catalytic chain"
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[Wolbachia]"

ORIGIN

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 Anaplasmataceae; Wolbachieae; Wolbachia.
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 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 8664)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
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CDS complement(2104..2304)
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protein WP0973 [Wolbachia endosymbiont of Culex quinquefasciatus Pel]"
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 pipientis]"
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 Ceratititis capitata]"
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 endosymbiont of Ceratitidis capitata]"
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VERSION    JAQZAU010000066.1
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REFERENCE  1  (bases 1 to 42782)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 42782)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
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Wolbachia]"
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subunit (mitochondrial delta subunit)"
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CDS complement(927..2378)
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beta,F0F1-type ATP synthase, beta subunit,ATP synthase
F1, beta subunit,ATP synthase alpha/beta family,
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CDS complement(2456..3556)
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transporter, permease protein, putative [Wolbachia
endosymbiont of Drosophila simulans wHa]"
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system, permease component"
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endosymbiont of Drosophila simulans wHa]"
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CDS 3992..4129
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CDS 4216..4479
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CDS 7839..8915
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Methyltransf_12 Methyltransf_11"
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Wolbachia]"
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LIAKQYRGHELVMIIITKIFNNSTSELNILDLCGTGICGHFLKINSIGNHIIIGIDIS
SRMLNIARGCFIKGKPVYNELIHHMEMKEFLKQEKNNQYDVIIFAEVLHYLHDFQEELE
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Wolbachia]"
gene 8974..10758
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CDS 8974..10758
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[Wolbachia]"
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VYLPVSHPEIEEFDLRKPTGGDPNRKALNIHHAVIVTDKFMQAVENDQEWNLISPHN
NKVISTVKARDIWIKILTARVETGEPYIIFLDATNNNKPE SYKKLNLDIKMSNLCSEI
TLTTGYDHLNKSRTAVCC LSSVNLEYEEWKDNKLFIEDIMRFLDNVLEDFINKAPNE
MQRAKYSAARERSIGLGVMGFHSFLQSKMVPFESVTAQQWNKKIFKYLREQADIVSKK
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SFVVRNKFLQKLLAEKNQDNDKIWSSISTNEG SVQHLDLSEHEKLTFTAYELDQRW
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Proteobacteria , WP_006280151.1 MULTISPECIES:
ribonucleoside-diphosphate reductase subunit alpha
[Wolbachia]"
gene 11726..13288
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CDS 11726..13288
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glutamine-hydrolyzing GMP synthase [unclassified
Wolbachia]"
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MIVNEQRKIYCTQFHPEVRPTTNGSKLLSNFLDIANCERDWTMKS FIEEQKEKIKNVV
GEKKVIAAVSGGVDSSVAAALTYKAIGKQLNCIFIDTGLLRKNQTIAMLKEIPINYVD
KSNLFLSRLKGITDPEEKRKIIIGNTFIEVFEEEA KKIGDVDFLMQGTIYSDVVESGHA
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GLAVRIISEVDKEKVQILQEVD EIIYINTMKNYDLYDKIWQAFVLLPIKTVGVMGDGR
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Wolbachia]"
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CDS complement(13321..14028)
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involved in tellurium resistance"
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protein, YkoY family"
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GLGLALLMR FVILFFTSSILSMQKPIFHTASARDLLMIAGGLFLIVKSSMELRDDIFV
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gene 14289..14402
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CDS 14289..14402
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melanogaster]"
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protein WD_0193 [Wolbachia endosymbiont of Drosophila
melanogaster]"
gene 14426..14608
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CDS 14426..14608
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ILEEPTKITENFDSTL"
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Bacteria , Proteobacteria , WP_006279522.1 MULTISPECIES:
hypothetical protein [Wolbachia]"
gene 14794..15612
/locus_tag="wEsol_00707"
CDS 14794..15612
/locus_tag="wEsol_00707"
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100 , identity 100 , evalue 1.47e-173 , alnlength 272 ,

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Bacteria , Proteobacteria , WP_141456816.1 MULTISPECIES:
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 Wolbachia]"

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 KSMKKQANTKKESAMVGS LVPGVIIIGGFLGVVLGAGVCVAVSLSGGMILGVMIASSLV
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/product="ankyrin repeat
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 , identity 100 , evalue 1.47e-173 , alnlength 272 ,
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 Wolbachia]"

gene 16037..18601

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CDS 16037..18601

/locus_tag="wEsol_00708"

/codon_start=1

/transl_table=11

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 repair protein MutS [Wolbachia endosymbiont of Drosophila
 simulans wHa]"

/cog="MutS COG0249 843 Mismatch repair ATPase (MutS
 family)"

/pfam="MutS_I MutS_II MutS_III MutS_IV MutS_V"

/product="DNA mismatch repair protein MutS"

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 NDEYAI SWLELSTGKFFHTLTSLKALDSDLLRISP REL LISEKFTED EKIRSILKNYK
 ISITQHAQSFFEYSKSHRTLCEFYKIRELG SIGNFSKVEIMACGALLEYVRVTQRGSI
 PRLEFPKTYKQQNFMLIDASARRNLELFSTQFGEKKGSLISVIDHTVTASGGRLLKQM
 LASPLACSKAINLRLSTAQFFVN NHEPRRKIREILSNIPDIERSLSRLILGRGSPKDM
 NLLKIGL GKTLELSEFLSTLHNYCLSEKSEINSQMSFQCLTGEKEPVSTTQVISSDES
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gene complement(18923..19099)

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CDS complement(18923..19099)

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 protein WANA31_0944 [Wolbachia endosymbiont of Drosophila
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Bacteria , Proteobacteria , RLT60659.1 hypothetical
protein WANA31_0944 [Wolbachia endosymbiont of Drosophila
ananassae]"
gene complement(19591..19989)
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CDS complement(19591..19989)
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Bacteria , Proteobacteria , WP_007548550.1 MULTISPECIES:
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CDS 20063..21301
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99.5110024449878 , similarity 98.8 , identity 97.5 ,
evalue 1.49e-286 , alnlength 407 , Bacteria ,
Proteobacteria , ERN55977.1 ribonuclease D [Wolbachia
pipientis wMelPop]"
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/tigr="TIGR01388 rnd 363 ribonuclease D"
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pipientis wMelPop]"
gene 21613..22200
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CDS 21613..22200
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WP_006280338.1 MULTISPECIES: dephospho-CoA kinase
[Wolbachia]"
/cog="CoaE COG0237 201 Dephospho-CoA kinase"
/pfam="CoaE AAA_17 AAA_18"
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WP_006280338.1 MULTISPECIES: dephospho-CoA kinase
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gene 22864..24288
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CDS 22864..24288
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99.2 , identity 98.1 , evalule 0.0 , alnlength 474 ,
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monooxygenase family protein [Wolbachia endosymbiont of
Drosophila ananassae]"
/translation="MKDC EEVLKNKIKKIVISGKEVWPIIEGGKGIAVSDGRSSGAFA
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KGHGRIHMNVLWEMGAAERVLHGILEGAKGLIHGITCGAGMPYRLGEIAAKYQVYYYP
IISSVRAFKALWKRAYQRISSYLLGGVVYEDPWLAGGHNGLSNSEDPELPQAPFERVA
ELRSFMNEIGLSETPIVMAGGVWHLKDWEHWFNNLQIGPIAFQFGTRPLLTKESPISA
EWKKKLLTLEEGDVFLNKFSPTGFYSSAVKNNFIRELQERNRQIKFSENASEEFNNE
FAMGSRGRKIYLTAKDKELANTWTKAGYTEAMKTPDSTVIFVTPDKFKQIREDQINCM
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protein"
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, identity 98.1 , evalule 0.0 , alnlength 474 , Bacteria ,
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family protein [Wolbachia endosymbiont of Drosophila
ananassae]"
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CDS complement(24380..24544)
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/codon_start=1
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100 , identity 100 , evalule 5.23e-31 , alnlength 54 ,
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/cog="Tra5 COG2801 232 Transposase and inactivated
derivatives"
/pfam="rve_3 rve rve_2"

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        transposase"
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        , identity 100 , evalue 5.23e-31 , alnlength 54 ,
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gene      complement(24534..24698)
        /locus_tag="wEsol_00715"
CDS       complement(24534..24698)
        /locus_tag="wEsol_00715"
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        100 , identity 98.1 , evalue 4.17e-28 , alnlength 54 ,
        Bacteria , Proteobacteria , WP_167482801.1 hypothetical
        protein [Wolbachia endosymbiont of Carposina sasakii]"
        /cog="Tra5 COG2801 232 Transposase and inactivated
        derivatives"
        /pfam="rve"
        /product="hypothetical protein"
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        , identity 98.1 , evalue 4.17e-28 , alnlength 54 ,
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        protein [Wolbachia endosymbiont of Carposina sasakii]"
gene      complement(24702..24899)
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CDS       complement(24702..24899)
        /locus_tag="wEsol_00716"
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        100 , identity 100 , evalue 1.88e-40 , alnlength 65 ,
        Bacteria , Proteobacteria , WP_010082070.1 hypothetical
        protein [Wolbachia endosymbiont of Drosophila incompta]"
        /translation="MQKNDIRAILRRKFKIKKQQTNDRAVAPNILDQNFIVDQPNKVW
        DYLHQNQGGMAIFGSNNSHVW"
        /product="hypothetical protein"
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        , identity 100 , evalue 1.88e-40 , alnlength 65 ,
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        protein [Wolbachia endosymbiont of Drosophila incompta]"
gene      complement(25121..25414)
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CDS       complement(25121..25414)
        /locus_tag="wEsol_00717"
        /codon_start=1
        /transl_table=11
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        99.0 , identity 99.0 , evalue 6.55e-60 , alnlength 97 ,
        Bacteria , Proteobacteria , WP_155968835.1 transposase
        [Wolbachia pipientis]"
        /cog="COG2963 COG2963 116 Transposase and inactivated
        derivatives"
        /pfam="HTH_Tnp_1 HTH_23 HTH_28"
        /product="transposase"
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Bacteria , Proteobacteria , WP_155968835.1 transposase
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/locus_tag="wEsol_00718"
CDS complement(25585..26757)
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porin [unclassified Wolbachia]"
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KDGDPGYDQDKVFWVKPNIYSDYNELELGLKQSSINYISPEIYNFQLGFSYVPGKNNL
QYSNLIAAGLSYKNSLSDDIGFTTALTGEFARENLTDCSDGTSKNYECRNQLLHWNFG
LKLKLFDLDCIFS YGNGGKS GEKRN PETNNTYYMNAGIAYRSDSYKSSLT YFSSGRDI
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/besthit="qcoverage 100 , hcoverage 100 , similarity 99.7
, identity 99.7 , evalue 4.74e-284 , alnlength 390 ,
Bacteria , Proteobacteria , WP_141456814.1 MULTISPECIES:
porin [unclassified Wolbachia]"
gene complement(26820..27182)
/locus_tag="wEsol_00719"
CDS complement(26820..27182)
/locus_tag="wEsol_00719"
/codon_start=1
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EHFYKNCRSDDFLGYIDENKVLFLVILINCDVKSTSKIINRIHSAINKQLLMQKLPSVSI
IYG NIAQKQAAKSTSGAF"
/besthit="qcoverage 95.83333333333333 , hcoverage
46.7479674796748 , similarity 100 , identity 99.1 ,
evalue 4.08e-71 , alnlength 115 , Bacteria ,
Proteobacteria , ONI56753.1 hypothetical protein
N500_0192 [Wolbachia pipientis wUni]"
gene complement(27221..27637)
/locus_tag="wEsol_00720"
CDS complement(27221..27637)
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/codon_start=1
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, similarity 97.1 , identity 96.4 , evalue 1.05e-86 ,
alnlength 138 , Bacteria , Proteobacteria , EAL59419.1
conserved hypothetical protein [Wolbachia endosymbiont of
Drosophila ananassae]"
/translation="MDDFITARRKDDAVVSVCQDNKKKNVLILGLNQAARNLLKYEFG
NLLNKPLINILSARAADDMKNYLEYTENGHDLLDILPKVIDFSLTDAKGEDIRTKVKV
FRTAQFASNKINYELLIRDISLSHKLGI FRDEISNG"
/product="conserved hypothetical protein"
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similarity 97.1 , identity 96.4 , evalue 1.05e-86 ,

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alnlength 138 , Bacteria , Proteobacteria , EAL59419.1
conserved hypothetical protein [Wolbachia endosymbiont of
Drosophila ananassae]"
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CDS       28218..28658
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          /codon_start=1
          /transl_table=11
          /product="hypothetical protein"
          /pfam="adh_short_C2"
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MGLCKAALEASVKYIACDLGPQNIRVNAISAGPIRTLASSGISDFHFISEWNRNNSPL
RRNVTIEDVGKAALYLLSDLSSGTTGEILHVDSGYNVVG MKVVD"
          /cog="FabI COG0623 259 Enoyl-"
          /besthit="qcoverage 93.8356164383562 , hcoverage
52.6923076923077 , similarity 100 , identity 100 , eval
1.13e-90 , alnlength 137 , Eukaryota , Arthropoda ,
GFY65360.1 enoyl-[acyl-carrier-protein] reductase 1
[Trichonephila inaurata madagascariensis]"
gene      complement(28655..30163)
          /locus_tag="wEsol_00722"
CDS       complement(28655..30163)
          /locus_tag="wEsol_00722"
          /codon_start=1
          /transl_table=11
          /fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 99.8 , eval 0.0 , alnlength 502 ,
Bacteria , Proteobacteria , WP_015588851.1 MULTISPECIES:
protein translocase subunit SecD [unclassified
Wolbachia]"
          /cog="SecD COG0342 506 Preprotein translocase subunit
SecD"
          /pfam="Sec_GG SecD_SecF MMPL"
          /tigr="TIGR01129 secD 397 protein-export membrane protein
SecD"
          /product="protein translocase subunit SecD"
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LKGGASLLLNIDLDYFKEKLSMLANEIKETLLTKNIESNVQNSIITLNNIDDYKKAS
VLINAINPNLELN RKDSSILISYKPHYKNSLISEVAAESINNVQRRDLKLTKEVSVQ
KQGQNKILVQVPGVEDTKQIKSLLGKTAKLAFHLANTNIAKVQDIDHETTVM LKDSL
NSYPIFRKTEIGGDSL VNASVRFGHLGKPTVHFKFDSIASKRF AKITKENVGKPF
IAIVLDNTVLTVP TIREPILNGEGEISGNFTEKQASELA ILLKSGALPAPLK IIEEKNIG
PSLGEESIKAGEMAATISIIAVALFIIITYGKLGVLASVALFSNVILILSILT LLEATLT
LPGIAGIALTVGMAVDANVLIFERIREEIKSGKRVERAIEEGFKNAIKTILDSNITTL
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, identity 99.8 , eval 0.0 , alnlength 502 , Bacteria ,
Proteobacteria , WP_015588851.1 MULTISPECIES: protein
translocase subunit SecD [unclassified Wolbachia]"
gene      complement(30668..30820)
          /locus_tag="wEsol_00723"
CDS       complement(30668..30820)
          /locus_tag="wEsol_00723"
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          /transl_table=11
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100 , identity 100 , eval 6.45e-28 , alnlength 50 ,
Bacteria , Proteobacteria , WP_007548649.1 transposase
[Wolbachia endosymbiont of Drosophila ananassae]"

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DYLHKN"
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/besthit="qcoverage 100 , hcoverage 100 , similarity 100
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Bacteria , Proteobacteria , WP_007548649.1 transposase
[Wolbachia endosymbiont of Drosophila ananassae]"
gene complement(31044..31175)
/locus_tag="wEsol_00724"
CDS complement(31044..31175)
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/codon_start=1
/transl_table=11
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100 , identity 100 , evalue 1.06e-21 , alnlength 43 ,
Bacteria , Proteobacteria , ONI56748.1 hypothetical
protein N500_0187 [Wolbachia pipientis wUni]"
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/product="hypothetical protein"
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, identity 100 , evalue 1.06e-21 , alnlength 43 ,
Bacteria , Proteobacteria , ONI56748.1 hypothetical
protein N500_0187 [Wolbachia pipientis wUni]"
gene complement(31175..31309)
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CDS complement(31175..31309)
/locus_tag="wEsol_00725"
/codon_start=1
/transl_table=11
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100 , identity 100 , evalue 5.41e-20 , alnlength 44 ,
Bacteria , Proteobacteria , WP_007548354.1 MULTISPECIES:
IS3 family transposase [Wolbachia]"
/cog="COG2963 COG2963 116 Transposase and inactivated
derivatives"
/pfam="HTH_Tnp_1"
/product="IS3 family
transposase"
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, identity 100 , evalue 5.41e-20 , alnlength 44 ,
Bacteria , Proteobacteria , WP_007548354.1 MULTISPECIES:
IS3 family transposase [Wolbachia]"
gene complement(31373..32857)
/locus_tag="wEsol_00726"
CDS complement(31373..32857)
/locus_tag="wEsol_00726"
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, similarity 100 , identity 100 , evalue 0.0 , alnlength
494 , Bacteria , Proteobacteria , WP_065095043.1
MULTISPECIES: IMP dehydrogenase [unclassified Wolbachia]"
/pfam="IMPDH CBS CBS NanE B12-binding His_biosynth PcrB
FMN_dh Glu_synthase DeoC NMO Ribul_P_3_epim His_biosynth
Dus PcrB"
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inosine-5'-monophosphate dehydrogenase"
/product="IMP dehydrogenase"

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QGVNSASAMKLLHENRIEKLVLVDENSCCIGLITVKDIEKYNRYPNCKDSKGRLRVA
AAIGTGKKDGIDRCEALIGEEVDVVVDVTAHGHSENVINTIREIKKMPNTQLIGGNI
ATKEAAEALIDAGVDAVKVGIGPGSICTTRIVTGVGVQPQSAIKNVAEACRARNVRLI
ADGGVKYSGDVAKAIAAGADSVMIGSIFAGTDESPGEIIMYKGRAYKGYRGMGSISAM
KRGASRYFQDKDSKLKLVPOGVEGRVPFKGPASGVIHQGLIGGLQAAMGYTGNRNIEE
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/besthit="qcoverage 100 , hcoverage 99.3963782696177 ,
similarity 100 , identity 100 , evaluate 0.0 , alnlength
494 , Bacteria , Proteobacteria , WP_065095043.1
MULTISPECIES: IMP dehydrogenase [unclassified Wolbachia]"
gene complement(32983..33636)
/locus_tag="wEsol_00727"
CDS complement(32983..33636)
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/codon_start=1
/transl_table=11
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, similarity 100 , identity 99.5 , evaluate 1.69e-148 ,
alnlength 217 , Bacteria , Proteobacteria ,
WP_015588849.1 MULTISPECIES: 16S rRNA
(adenine(1518)-N(6)/adenine(1519)-N(6))-
dimethyltransferase RsmA [unclassified Wolbachia]"
/cog="KsgA COG0030 259 Dimethyladenosine transferase
(rRNA methylation)"
/pfam="RrnaAD"
/tigr="TIGR00755 ksgA 256 dimethyladenosine transferase"
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(adenine(1518)-N(6)/adenine(1519)-N(6))-
dimethyltransferase RsmA"
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LSVLSQLLCDIKKEFDIEPKEFFPRPKIHSSVITVNPLPIPKFAVNLETLTRLTRAFF
SQRRKMLRNSLQNITNHAETVLENAKLSGNQRPENLTIEQFCLLANNVECLFCNKMY"
/besthit="qcoverage 100 , hcoverage 80.3703703703704 ,
similarity 100 , identity 99.5 , evaluate 1.69e-148 ,
alnlength 217 , Bacteria , Proteobacteria ,
WP_015588849.1 MULTISPECIES: 16S rRNA
(adenine(1518)-N(6)/adenine(1519)-N(6))-
dimethyltransferase RsmA [unclassified Wolbachia]"
gene 34000..34698
/locus_tag="wEsol_00728"
CDS 34000..34698
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, similarity 100 , identity 100 , evaluate 9.59e-166 ,
alnlength 232 , Bacteria , Proteobacteria ,
WP_015588848.1 MULTISPECIES: triosephosphate isomerase
[Wolbachia]"
/cog="TpiA COG0149 251 Triosephosphate isomerase"
/pfam="TIM"
/tigr="TIGR00419 tim 228 triose-phosphate isomerase"
/product="triosephosphate
isomerase"
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WP_015588848.1 MULTISPECIES: triosephosphate isomerase
[Wolbachia]"
gene complement(34922..36010)
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CDS complement(34922..36010)
/locus_tag="wEsol_00729"
/codon_start=1
/transl_table=11
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100 , identity 100 , evaluate 6.36e-252 , alnlength 362 ,
Bacteria , Proteobacteria , WP_015588847.1 MULTISPECIES:
DNA-processing protein DprA [unclassified Wolbachia]"
/cog="Smf COG0758 350 Predicted Rossmann fold
nucleotide-binding protein involved in DNA uptake"
/pfam="DNA_processg_A Pfam-B_17296"
/product="DNA-processing
protein DprA"
/translation="MKINKLNNKELEVWLSLARTIGPTKFFSILRTHGSLDEVLYKYN
RVANNKVYGIQDAREEINNAERIGAKIIPACDPDYPDLLRNISSCPPVITALGDISLL
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AVTASGIDVVYPKENFDLYKKITGNGGLVITELPFATKPKPQYFPQRNRIISGLSLGV
AVIEASKRSGSLITADFALNQGREVFAVSGFPLDSRCSGSNYLIKNGAKLIESADDII
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Bacteria , Proteobacteria , WP_015588847.1 MULTISPECIES:
DNA-processing protein DprA [unclassified Wolbachia]"
gene 36072..36446
/locus_tag="wEsol_00730"
CDS 36072..36446
/locus_tag="wEsol_00730"
/codon_start=1
/transl_table=11
/pfam="Fer4_11 Fer4_6 Fer4_10 Fer4_2 Fer4_4 Fer4_7 Fer4_9
Fer4_10 Fer4 Fer4_6 Fer4_2 Fer4_15 Fer4_8 Fer4_4 Fer4_17
Fer4_16 DUF3470"
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100 , identity 100 , evaluate 4.06e-87 , alnlength 124 ,
Bacteria , Proteobacteria , WP_141456813.1 MULTISPECIES:
ferredoxin family protein [unclassified Wolbachia]"
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VCIPECPVDAIVTDDSIKDILELDEELLNSEQKIFKSFYNINVEYSQKWPNITAKKQP
LYTAEYKEKKDKTTYFEENLE"
/product="ferredoxin family
protein"
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, identity 100 , evaluate 4.06e-87 , alnlength 124 ,
Bacteria , Proteobacteria , WP_141456813.1 MULTISPECIES:
ferredoxin family protein [unclassified Wolbachia]"
gene 36640..37092
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CDS 36640..37092
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EEMIKEYYSLFKKISWSCGITAGGAQDANASSFNEAYKLGSKELALAIMSDFKKSVDQ
ELFKKYKKEEMSYPEGEGVQFIRELRVLSRILTISLIRKLDEVYSRRN"
/besthit="qcoverage 97.33333333333333 , hcoverage
55.9386973180077 , similarity 100 , identity 100 , evaluate
3.56e-93 , alnlength 146 , Bacteria , Proteobacteria ,
WP_015588845.1 MULTISPECIES: hypothetical protein
[unclassified Wolbachia]"
gene 37067..37417
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CDS 37067..37417
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44.0613026819923 , similarity 100 , identity 100 , evaluate
2.25e-70 , alnlength 115 , Bacteria , Proteobacteria ,
WP_015588845.1 MULTISPECIES: hypothetical protein
[unclassified Wolbachia]"
gene 37513..38460
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/codon_start=1
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100 , identity 100 , evaluate 5.46e-227 , alnlength 315 ,
Bacteria , Proteobacteria , AGJ99620.1
D-alanine--D-alanine ligase [Wolbachia endosymbiont of
Drosophila simulans wHa]"
/cog="DdlA COG1181 317 D-alanine-D-alanine ligase and
related ATP-grasp enzymes"
/pfam="Dala_Dala_lig_N ATP-grasp_4 RimK CPSase_L_D2
Dala_Dala_lig_C"
/tigr="TIGR01205 D_ala_D_alaTIGR 318 D-alanine--D-alanine
ligase"
/product="D-alanine--D-alanine ligase"
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NSSTIMEKMIVEEYIPGIELHTAVLLDEAIGTIEVRPKNKFYDYEAKYTDGFAEHIFP
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, identity 100 , evaluate 5.46e-227 , alnlength 315 ,
Bacteria , Proteobacteria , AGJ99620.1
D-alanine--D-alanine ligase [Wolbachia endosymbiont of
Drosophila simulans wHa]"
gene 38441..39199
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9361	ggcaaaacat	caggaattgt	tccattttat	gtagtcaaaa	atgctctaac	gcttgcaatt
9421	agtcagggat	ccctaaggcg	agggaagttca	gcagctctacc	ttcctgtatc	tcatccggag
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9541	aatatacatc	atgctgtaat	agtaacagat	aaatttatgc	aggctgttga	gaatgatcaa
9601	gaatggaatt	taataagccc	tcacaacaat	aagggttattt	caactgtaaa	agcgcgggat
9661	atatggatca	aaatattaac	agcaagagtt	gaaactggag	aaccttacat	tattttcctt
9721	gatgcaacaa	ataacaataa	gccagaatct	tacaaaaaagc	tcaacttaga	catcaagatg
9781	tcaaactctat	gcagtgaat	aactttaacc	acagggttatg	atcacctgaa	taagtcacgc
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9901	aaactcttca	tagaagatat	aatgcgcttt	cttgataatg	tattggaaga	tttcataaat
9961	aaagcaccga	atgaaatgca	gcgagcaaaa	tattctgcag	ccagagaacg	cagtattggg
10021	cttgggtgtga	tgggcttttca	ctcatttttta	caaagcaaaa	tggttccttt	tgaatcagta

10081	acagcacaac	aatggaataa	aaaaatattt	aagtattttac	gcgagcaagc	agatatagtt
10141	tctaaaaaat	tagcagaaga	aaagggagca	tgttctgatg	ccaaagaagt	tgatctaagt
10201	gaaaggttta	cacacaaact	cgctattgct	cctactgctt	cgatctccat	tattgcaggt
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10321	ggctcatttg	tagtgcgaaa	taaattcttg	caaaaactat	tagcagaaaa	aatcaagac
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10501	atagaacatg	caagtgatag	aacttcgtat	atttgtcaat	ctcaatcagt	aaatctgttc
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10621	ggattgaaga	gcttatatta	ctgcagatca	caatcaatgc	agagagccga	taaggtctcg
10681	catgacatat	tcaaaaaaag	tgaaatattg	caacaaaaaa	cagatattga	ctacgatgaa
10741	tgtctgtcat	gccaatagcg	gccttactca	aaaaagtaga	gagaaagtta	agcaaatggg
10801	taaatagact	tcttgcataa	ccatataacg	cacttttatt	gggaatagaa	acgaaaaaac
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11281	at ttggtaaa	tttcttaaac	at ttatggct	aaacgacaat	cg tcatcccg	ctacttgtta
11341	gcgggatcta	ttgccgagat	accgcgaatg	aatcgcggtg	tgacgggttcg	cggtggcatg
11401	acgataaagt	ttatacctcg	tcatcccgct	gcttggttagc	gggatctctt	gttagcggct
11461	gagataccgc	gaatgaatcg	cggtatgacg	gttcgtggca	gcatgaagat	aatcccgcta
11521	cttggttagcg	gctgagatac	tgcgggcggtg	tgacgtagat	tgctgtcatt	ccgctactag
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11701	at tttaataa	atatggagga	gcaaattgtc	agcaattgcc	attattgatt	ttggttcaca
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12001	ttat ttttgg	gcaaaagtaa	aagagagttt	caaacaggag	tttggtagaa	ctaaaatcaa
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12121	attaatgaac	catgcggaca	gtgttgatac	tataccacag	ggatttactg	ttatcgcac
12181	aggtgtgata	aatcaaacaa	ttgcaatgat	tg ttaacgaa	cagcgaaaaga	tttactgtac
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12361	aaaaatcaaa	aatgtagtag	gagagaaaaa	agtaatcgct	gcagtaagtg	gtgggggttg
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12781	aaagatgaat	ctgaagttag	tggagccttt	acgttacctc	tttaaagatg	aggtaaggct
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13441	aaatccatga	agtatgaggt	acacaccgac	aagtaaaaata	aataaaaatgg	cgattatttt
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13561	catggaaaaat	gtaaatgctg	tagcaattat	taccatgtta	taagtttagtg	ctatagcagt
13621	taatatcgaa	tcaaccgaaa	aaactaaatc	tattaatatata	at ttgtagca	caactaaaaa

13681	aaat t t t t g a t	t t a a c g t t t g	c t t t c t t t t t	a t t t t t c t t a	c a t a c a a a g a	t g t c a t c c c g
13741	t a a c t c c a t a	g a g c t c t t a a	c a a t a a g g a a	t a a t c c c c c t	g c g a t c a t a a	g t a a a t c c c t
13801	t g c t g a t g c a	g t g t g a a a t a	t a g g t t t t t g	c a t t g a c a a t	a t a g a t g a t g	t a a a a a a t a g
13861	t a t t a c a a a a	c g c a t t a a t a	g t g c t a a t c c	a a g g c c c a t a	a g g c g c a c t c	t t t c t c t c a g
13921	c g c a t t t g g t	a c c t t a t c t a	t t g c t a g a g a	a a t a a a g a t t	a a a t t g t c t a	c a c t a a g t a t
13981	a g t t t c a a g t	a g t g t a a g t g	t c a g t a a a g t	c c a a g c a t c a	g t t a g c a t t t	t t g t t t c a a a
14041	t t c g g t t c t t	c t t a c t c t a c	a a t a g a t g t g	t a a a a a t t a a	g t g a c t t c a c	t c a g a a g t t t
14101	t a t a g c a g t t	c t c c a g a a a a	a c a g g a t a t a	t a a a g t t c a g	c a g c t t c t t c	t a t t t t c g t t
14161	t t t g a g c a a a	a t c a a t a a t a	a g a g a g t t t c	t t a t t t t c a t	g c a c g c a a a t	a a g a t a a a g c
14221	c t t a t t t t t c a	t t t t t g a c t t	t a t t t g a a a a	t a a t a t a t a c	t a t a a a a a t a	g t g t g c t a g g
14281	t t g a a t g a a t	g t a t a t t a a a	g g a t c a c c a t	c a g g c a a a g t	a t t c g c t g g t	t a t c a g g c a t
14341	t t a t a c c a a g	c c c c t t g c c a	c c a a a a t t t g	a a t g g g a c a a	t g a t t t a g t t	a a t a g t c t t t
14401	a a a c c c t t a c	t t t a c t a t a a	g g a a a g t g g t	t g a a a a c t t a	g g t g t c g t a t	t t a c a a c a g c
14461	c c a a a g a g c a	a t c g t a a a g c	t t g a a g a t t t	a g g c a t c g t t	t c a c a a a c t t	c t c a a g g a a a
14521	g a g a g a t c g g	g t t t a t t g t g	c a a c t g a t a t	t t t g a a t a t t	c t a g a a g a a c	c a a c t a a g a t
14581	t a c a g a g a a c	t t c g a t a g c a	c a t t g t a g c t	a t t g t g a t g a	a t a a a t t c a g	c a a a c a g c a a
14641	g c t t a a a g a g	t c t g a t c c a a	t g g a c a t g c t	g a a c a a a a a g	t a a g g a g c t c	c t t t t g g a g g
14701	a t t a t a t t a a	c t t a t t a a t t	a a t t g c t t g a	c t t t t a g c a g	g a t t t a t t a t	a t t a t t t a t t
14761	a a t g a g c a a t	g c a a t c a a a c	c a a g g a g g a t	a g c a t g a t a a	a t a a t t t g g a	t t c a a t a a t t
14821	c t t g g a a t a a	a a g a t g g t g a	a a a g g c g a t t	g a a g a t t t a a	g g g t t g t t c t	t a a a a a a a g a
14881	a a a g a a g a a g	t t a t t a c t a c	a c a g a c a t t t	a a t t a c g c t t	t a c g a t g c c c	a a a a a c t a c a
14941	a a g g a a g c g a	t a g t a c a c g a	a a t t c t g c t t	c a t t t t t a t a c	a a a a t c c t g g	c g a g c a a t c a
15001	c t a g a a c a a g	t g a t a c a a t g	c t t a g a t a g a	g c a a t a c a a t	c t g g g a t a t a	t g c a a a a a a c
15061	a a c c c a a t a a	g a a a t c t a g a	t g a a g a a t t t	c g t a c t c a t a	t a a a c t t t a a	a g a t g a a g a g
15121	g g a a a t a c a t	t a c t a c a t c a	t g c a g t t a t a	g g t a a t a a a a	c t g a a g a a a t	a a t c a c c c t t
15181	c t t g t t a c a t	a t a g t g c a a a	t c c t t t g a t a	c a a a a c g c g g	a t a a t a a a a t	t c c t t t a g a t
15241	t t a g c t c a a g	g a g a a c a a a a	a g a a g t g c t t	a t t a a a a g t a	t g a a a a a a c a	a g c t a a t a c g
15301	a a a a a a g a a a	g c g c t a t g g t	a g g c a g t t t g	g t g c c t g g c g	t a a t a a t t g g	t g g t t t t c t t
15361	g g t g t t g t a c	t t g g a g c t g g	t g t g t g t g t t	g c a g t a a g t c	t t t c t g g t g g	t a t g a t a c t a
15421	g g t g t a a t g a	t a g c a t c t t c	t c t t g t t g c t	a g t a t a g c t a	t t g g a c t g g c	c a t g t a t t t t
15481	t t g a g t c a a g	a c t a t g a a c a	g g c t a a a g c g	a t a g a a a a a a	c t a t t a g c a c	t g t t a g c t c t
15541	g a a a t a t c t g	t t g a t g a t a c	a a c t g c c g c t	a a t a a a a a t a	a t a a a g a a g g	g c c a c a a c t t
15601	a c a t a t a g c t	g a c c c a a g c a	a c a c g t c a t a	c c g c g a t t c a	t t c g c g g t a t	a g a t t c c g c t
15661	a a c t a g t a g c	g g a a t g a c g a	a t g t g t c g t t	t t t c a a a a t t g	t c g t a a g t c a	c t t t a g c t a t
15721	a a t a c a c a c a	a g g a g g g t g t	c a t c c c a g c g	c c c c t a t g a t	g t c a t c c c a g	t g c t t g a c a c
15781	t g g g a t c c a g	a a a a g t t t g c	t t g t a a a c t a	g c a t g g a a a g	t a g c t g a t c t	t a c a c t a a a t
15841	g a a t g t t t t t t	g a t g a g g t t g	c a t a g a a g c t	g g a t t c c a g c	g t c a c g c g c t	g g a a t g a c a a
15901	c t g c g t t t t t t	t g t t t t t t t t g	t c a t c a a a t a	c t c c t a c t c t	t t a t g t c a t c	c a a g t g t c c t
15961	g a c t a c t t g g	a t c c a a g a a a	t t t a a t t g t t	t t a a a t t t t t t	c c c t c t a t a c	a c c t a t t t t a a
16021	a a t t t a t g t t	a t c c a c a t g t	g c a a t a t a a t	c t a t a a t a a c	g t t t a t c a a t	a c a a t a t a t t
16081	a a a a a a t a t t	a t g a g c t t c g	t a a a a g a a a a	a a a c a c c c c t	g t g a t g g a g c	a g t a t t t g a a
16141	c c t g a a a g c t	c a a t a c a a a g	a t c a t c t g c t	a t t t t a t a g g	c t a g g a g a t t	t t t a t g a a t t
16201	g t t t t t c g a t	g a t g c t a t t a	a a g c t g c g a a	a t t g c t g a a t	a t a g t g c t c a	c t a a g a g a g g
16261	t a a t t c g t g t	g g g c a a g a a a	t a c c a a t g t g	t g g a g t g c c a	g c a c a c a g t a	g t g a a t c t t a
16321	c c t a c a c a a g	c t a a t a g a t t	t a g g a t t c a a	a g t a g c a a t c	t g t g a c c a a t	t a g a a a c t g c
16381	t g a t g a a g c a	a a a a a g a g g g	g c t a t a a a t c	c a t a g t a a a a	c g t g a t g t a g	t g c g a g t t g t
16441	a a c t c c a g g t	a c a a t t a t a g	a a g a t t c a c t	a c t g g a g g a t	a a a a g c a a t a	a t t a t c t c g c
16501	g t c c a t a g t t	g a a c a a a a t g	a c g a a t a t g c	t a t t a g t t g g	c t t g a a t t a t	c g a c g g g a a a
16561	a t t t t t t c a c	a c t t t a a c g a	g t t t g a a a g c	t c t a g a t a g t	g a t t t a t t g c	g t a t a t c a c c
16621	a a g a g a a t t a	t t a a t t t c t g	a a a a a t t c a c	t g a g g a t g a a	a a a a t t a g a t	c g a t t t t a a a
16681	a a a t t a t a a a	a t a t c a a t t a	c g c a a c a c g c	a c a g a g t t t t	t t t g a g t a t a	g t a a a t c t c a
16741	c a g a a c g t t a	t g c g a g t t t t	a t a a a a t c a g	g g a a c t t g g g	a g t a t a g g a a	a t t t c a g c a a
16801	a g t a g a a a t c	a t g g c g t g t g	g t g c a c t g c t	t g a a t a t g t c	a g a g t a a c g c	a a a g g g g c t c
16861	c a t t c c a a g g	c t t g a a t t c c	c a a a a c c t a	t a a g c a a c a a	a a t t t c a t g c	t t a t t g a t g c
16921	t t c a g c a a g g	a g a a a t c t t g	a g t t g t t t t c	a a c t c a a t t t	g g t g a a a a g a	a a g g t t c a c t
16981	a a t t t c a g t t	a t t g a t c a t a	c a g t t a c a g c	t t c t g g t g g a	c g c c t g c t c a	a a c a a a t g c t
17041	c g c t t c a c c c	c t t g c t t g c t	c c a a g g c a a t	c a a t t t g a g g	c t c a g c a c c g	c t c a a t t t t t
17101	t g t a a a t a a t	c a t g a g c c a c	g c a g a a a a t	a c g a g a g a t a	t t a t c t a a c a	t t c c a g a t a t
17161	t g a g a g g t c t	t t a t c g c g c t	t a a t a c t a g g	g c g t g g t t c a	c c a a a g g a t a	t g a a c c t a t t
17221	g a a a a t a g g c	c t a g g a a a g a	c t t t a g a g t t	g t c t g a g t t t	c t g t c t a c c t	t g c a t a a t t a

17281	ttgtttaagt	gaaaaatcag	aaattaactc	tcagatgtca	ttccagtgtc	tgaccggaga
17341	aaaggaacca	gtgtctacta	ctcaggtgat	aagtagtgac	gagagtgaac	tcagcacaat
17401	acataagagc	cttggtaatc	ataaagacct	atgtgaactg	ctaaatagt	ctatacttga
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17641	ttacgttgaa	gtatcagcaa	atcacaaaat	aacttcggat	atattttattc	ataggcaaag
17701	cttagcaaat	agcatgcgct	acactactaa	tgaattgaaa	gaactagaaa	ataaaattct
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DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_39139, whole genome
            shotgun sequence.
ACCESSION  JAQZAU010000067  JAQZAU010000000
VERSION    JAQZAU010000067.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 35791)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 35791)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date          :: JUN-2019
            Assembly Method        :: FLYE v. 06-2019
            Genome Representation   :: Full
            Expected Final Version :: Yes
            Genome Coverage        :: 100.0x
            Sequencing Technology  :: Illumina HiSeq; PacBio Sequel
            ##Genome-Assembly-Data-END##
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specificities (related to short-chain alcohol
dehydrogenases)"
/pfam="Shikimate_DH Pfam-B_3397 adh_short KR
NAD_binding_10 Epimerase Saccharop_dh adh_short_C2"
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3-oxoacyl-[acyl-carrier-protein] reductase"
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contains TPR repeats"
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Pfam-B_333 TPR_11 TPR_12 NARP1 Pfam-B_1822 TPR_16 TPR_11
TPR_2 TPR_12 TPR_1 Pfam-B_392 Pfam-B_324 TPR_11"
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[Wolbachia]"
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[Wolbachia]"
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protein, YhbC family"
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Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_012673176.1 MULTISPECIES: F0F1 ATP synthase subunit
alpha [Wolbachia]"
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subunit"
/pfam="ATP-synt_ab_N HAS-barrel ATP-synt_ab
ATP-synt_ab_C"
/tigr="TIGR00962 atpA 503 ATP synthase F1, alpha subunit"
/product="F0F1 ATP synthase
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alpha [Wolbachia]"

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subunit (mitochondrial oligomycin sensitivity protein)"
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subunit delta"
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distantly related to archaeal Holliday junction
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          /tigr="TIGR00059 L17 112 ribosomal protein L17"
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protein L17"
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DNA-directed RNA polymerase subunit alpha [Wolbachia]"
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subunit/40 kD subunit"
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Pfam-B_14457"

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gene complement(8814..9455)

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 50S ribosomal protein L18 [Wolbachia]"
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 /tigr="TIGR00060 L18_bact 114 ribosomal protein L18"
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 protein L18"
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 , identity 100 , evalue 1.26e-76 , alnlength 123 ,
 Bacteria , Proteobacteria , WP_006279867.1 MULTISPECIES:
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 complement(12160..12705)
 gene

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50S ribosomal protein L6 [Wolbachia]"
         /cog="RplF COG0097 178 Ribosomal protein L6P/L9E"
         /pfam="Ribosomal_L6 Ribosomal_L6"
         /tigr="TIGR03654 L6_bact 175 ribosomal protein L6"
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protein L6"
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gene     complement(12722..13117)
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100 , identity 100 , evalue 1.18e-87 , alnlength 131 ,
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30S ribosomal protein S8 [Wolbachia]"
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         /pfam="Ribosomal_S8"
         /product="30S ribosomal
protein S8"
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Bacteria , Proteobacteria , WP_007551150.1 MULTISPECIES:
30S ribosomal protein S8 [Wolbachia]"
gene     complement(13139..13447)
CDS      /locus_tag="wEsol_00758"
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         /transl_table=11
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Bacteria , Proteobacteria , WP_006279345.1 MULTISPECIES:
30S ribosomal protein S14 [Wolbachia]"
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protein S14"
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CDS complement(13464..13997)
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100 , identity 100 , evaluate 2.23e-121 , alnlength 177 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_010962750.1 MULTISPECIES: 50S ribosomal protein L5
[Wolbachia]"
/cog="RplE COG0094 180 Ribosomal protein L5"
/pfam="Ribosomal_L5 Ribosomal_L5_C"
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protein L5"
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Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
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[Wolbachia]"
gene complement(14004..14321)
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CDS complement(14004..14321)
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100 , identity 100 , evaluate 1.08e-64 , alnlength 105 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_006279347.1 MULTISPECIES: 50S ribosomal protein L24
[Wolbachia]"
/cog="RplX COG0198 104 Ribosomal protein L24"
/pfam="KOW Pfam-B_10078"
/tigr="TIGR01079 rplX_bact 104 ribosomal protein L24"
/product="50S ribosomal
protein L24"
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, identity 100 , evaluate 1.08e-64 , alnlength 105 ,
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WP_006279347.1 MULTISPECIES: 50S ribosomal protein L24
[Wolbachia]"
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CDS complement(14321..14680)
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100 , identity 100 , evaluate 1.06e-73 , alnlength 119 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,

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WP_006279348.1 MULTISPECIES: 50S ribosomal protein L14
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/tigr="TIGR01067_rplN_bact 122 ribosomal protein L14"
/product="50S ribosomal
protein L14"
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, identity 100 , eval 1.06e-73 , alnlength 119 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_006279348.1 MULTISPECIES: 50S ribosomal protein L14
[Wolbachia]"
gene complement(14694..14930)
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CDS complement(14694..14930)
/locus_tag="wEsol_00762"
/codon_start=1
/transl_table=11
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100 , identity 100 , eval 1.62e-49 , alnlength 78 ,
Bacteria , Proteobacteria , WP_007549925.1 MULTISPECIES:
30S ribosomal protein S17 [Wolbachia]"
/cog="RpsQ COG0186 87 Ribosomal protein S17"
/pfam="Pfam-B_14863 Ribosomal_S17"
/tigr="TIGR03635_S17_bact 72 30S ribosomal protein S17"
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protein S17"
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Bacteria , Proteobacteria , WP_007549925.1 MULTISPECIES:
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gene complement(14923..15126)
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CDS complement(14923..15126)
/locus_tag="wEsol_00763"
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Bacteria , Proteobacteria , WP_006279350.1 MULTISPECIES:
50S ribosomal protein L29 [Wolbachia]"
/cog="RpmC COG0255 69 Ribosomal protein L29"
/pfam="Ribosomal_L29"
/tigr="TIGR00012_L29_56 ribosomal protein L29"
/product="50S ribosomal
protein L29"
/translation="MDIADIESRSSQELHEILVNLNRKEFVNLFQKKLGQCNNISRFS
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Bacteria , Proteobacteria , WP_006279350.1 MULTISPECIES:
50S ribosomal protein L29 [Wolbachia]"
gene complement(15138..15551)
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CDS complement(15138..15551)

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Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_010962752.1 MULTISPECIES: 50S ribosomal protein L16
[Wolbachia]"
/cog="RplP COG0197 146 Ribosomal protein L16/L10E"
/pfam="Ribosomal_L16"
/tigr="TIGR01164 rplP_bact 126 ribosomal protein L16"
/product="50S ribosomal
protein L16"
/translation="MFIPKKSKYKKVFKGRIKNTKGGSTLSFGDYGLKAMEAGRIQS
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, identity 100 , evalue 1.71e-92 , alnlength 137 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_010962752.1 MULTISPECIES: 50S ribosomal protein L16
[Wolbachia]"
gene complement(15566..16180)
/locus_tag="wEsol_00765"
CDS complement(15566..16180)
/locus_tag="wEsol_00765"
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100 , identity 100 , evalue 5.31e-140 , alnlength 204 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_010962753.1 MULTISPECIES: 30S ribosomal protein S3
[Wolbachia]"
/cog="RpsC COG0092 233 Ribosomal protein S3"
/pfam="KH_2 Ribosomal_S3_C"
/tigr="TIGR01009 rpsC_bact 212 ribosomal protein S3"
/product="30S ribosomal
protein S3"
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WP_010962753.1 MULTISPECIES: 30S ribosomal protein S3
[Wolbachia]"
gene complement(16220..16567)
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CDS complement(16220..16567)
/locus_tag="wEsol_00766"
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100 , identity 100 , evalue 1.53e-71 , alnlength 115 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_007549821.1 MULTISPECIES: 50S ribosomal protein L22
[Wolbachia]"
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/pfam="Ribosomal_L22"
/tigr="TIGR01044 rplV_bact 103 ribosomal protein L22"

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protein L22"
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RYSNITVKLGEII"
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Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_007549821.1 MULTISPECIES: 50S ribosomal protein L22
[Wolbachia]"
gene complement(16573..16857)
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CDS complement(16573..16857)
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100 , identity 100 , evalue 3.99e-64 , alnlength 94 ,
Bacteria , Proteobacteria , WP_006279181.1 MULTISPECIES:
30S ribosomal protein S19 [Wolbachia]"
/cog="RpsS COG0185 93 Ribosomal protein S19"
/pfam="Ribosomal_S19"
/tigr="TIGR01050 rpsS_bact 92 ribosomal protein S19"
/product="30S ribosomal
protein S19"
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Bacteria , Proteobacteria , WP_006279181.1 MULTISPECIES:
30S ribosomal protein S19 [Wolbachia]"
gene complement(16861..17685)
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CDS complement(16861..17685)
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100 , identity 100 , evalue 9.52e-196 , alnlength 274 ,
Bacteria , Proteobacteria , WP_015589143.1 MULTISPECIES:
50S ribosomal protein L2 [Wolbachia]"
/cog="RplB COG0090 275 Ribosomal protein L2"
/pfam="Ribosomal_L2 Ribosomal_L2_C"
/tigr="TIGR01171 rplB_bact 275 ribosomal protein L2"
/product="50S ribosomal
protein L2"
/translation="MGMKFFNPVTPSSRGTVLVSKVGLSKDEPEKSLTSGKKSSGGRN
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YILAPQGMKPGDVVTAGNDADILPGNCLLLKHIPVGSFVHNVELKPGNGAAIARAAGC
YAQIVGRDGQYVLLRLRSGQIRLILSSCKATIGVVSNPDKNRKLGKAGRSRWLGIRP
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Bacteria , Proteobacteria , WP_015589143.1 MULTISPECIES:
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gene complement(17687..17974)
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CDS complement(17687..17974)
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Bacteria , Proteobacteria , WP_015589144.1 MULTISPECIES:
50S ribosomal protein L23 [Wolbachia]"
/cog="RplW COG0089 94 Ribosomal protein L23"
/pfam="Ribosomal_L23"
/product="50S ribosomal
protein L23"
/translation="MIKYNNIIKSPIITEKASFLREKFNKYSLYVFNVNKRQIKLAI
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Bacteria , Proteobacteria , WP_015589144.1 MULTISPECIES:
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gene complement(17971..18585)
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CDS complement(17971..18585)
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100 , identity 100 , evaluate 2.35e-143 , alnlength 204 ,
Bacteria , Proteobacteria , WP_015589145.1 MULTISPECIES:
50S ribosomal protein L4 [unclassified Wolbachia]"
/cog="RplD COG0088 214 Ribosomal protein L4"
/pfam="Ribosomal_L4"
/tigr="TIGR03953 rplD_bact 188 50S ribosomal protein L4"
/product="50S ribosomal
protein L4"
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AGTHKTKGISDVSGTTAKPYDQKRTGRARQGSRLSPQFRGGGIIIFGPVVRSHYSLNK
KVRKFGLKIALSLKYLNQVIILNLDNLNIDVKKTSEMCKCIKNFKFSSFLIVGDYGGDL
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, identity 100 , evaluate 2.35e-143 , alnlength 204 ,
Bacteria , Proteobacteria , WP_015589145.1 MULTISPECIES:
50S ribosomal protein L4 [unclassified Wolbachia]"
gene complement(18588..19310)
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CDS complement(18588..19310)
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100 , identity 100 , evaluate 4.68e-170 , alnlength 240 ,
Bacteria , Proteobacteria , WP_006279218.1 MULTISPECIES:
50S ribosomal protein L3 [Wolbachia]"
/cog="RplC COG0087 218 Ribosomal protein L3"
/pfam="Ribosomal_L3"
/tigr="TIGR03625 L3_bact 202 50S ribosomal protein L3"
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protein L3"
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Bacteria , Proteobacteria , WP_006279218.1 MULTISPECIES:
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CDS complement(19320..19640)
/locus_tag="wEsol_00772"
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100 , identity 100 , evalue 7.02e-66 , alnlength 106 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_012673184.1 MULTISPECIES: 30S ribosomal protein S10
[Wolbachia]"
/cog="RpsJ COG0051 104 Ribosomal protein S10"
/pfam="Ribosomal_S10"
/tigr="TIGR01049 rpsJ_bact 99 ribosomal protein S10"
/product="30S ribosomal
protein S10"
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EVKV"
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, identity 100 , evalue 7.02e-66 , alnlength 106 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_012673184.1 MULTISPECIES: 30S ribosomal protein S10
[Wolbachia]"
gene complement(19655..20827)
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CDS complement(19655..20827)
/locus_tag="wEsol_00773"
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100 , identity 99.7 , evalue 1.77e-279 , alnlength 390 ,
Bacteria , Proteobacteria , WP_141456826.1 elongation
factor Tu [Wolbachia endosymbiont of Carposina sasakii]"
/cog="TufB COG0050 394 GTPases - translation elongation
factors"
/pfam="GTP_EFTU MMR_HSR1 Miro GTP_EFTU_D2 GTP_EFTU_D3"
/tigr="TIGR00485 EF-Tu 394 translation elongation factor
Tu"
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EVPVVVGSALKALDDSSSEYGKKSIDKLMEKLDEYVAVPPRPVDLPFLLPIDVFSIS
GRGTVVVTGRIEKGEIKTGEEIEIIGLKATQKTICTGVEMFKLLDKGSAGLNVGILLR
GTKREEVERGQVLAKPGTITPHRKFKAEVYILKKEEGGRHTPFFANYQPQFYLRRTDV
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/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 99.7 , evalue 1.77e-279 , alnlength 390 ,
Bacteria , Proteobacteria , WP_141456826.1 elongation
factor Tu [Wolbachia endosymbiont of Carposina sasakii]"
gene complement(21178..22269)
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CDS complement(21178..22269)
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100 , identity 100 , evaluate 6.50e-266 , alnlength 363 ,
Bacteria , Proteobacteria , WP_015589146.1 MULTISPECIES:
glutamine-hydrolyzing carbamoyl-phosphate synthase small
subunit [unclassified Wolbachia]"
/cog="CarA COG0505 368 Carbamoylphosphate synthase small
subunit"
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/tigr="TIGR01368 CPSaseIIsma11 361 carbamoyl-phosphate
synthase, small subunit"
/product="
glutamine-hydrolyzing carbamoyl-phosphate synthase small
subunit"
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SNFKSDLNAKYRVVIVDFGVKISIVSRLIELGCTVELIRPSTGFAQKVLSMNPDGIVL
SNGPGDPQEIGESVSVSEIDIIKSKIPIFGICMGHQLLAITLGAKTIKMDIGHRGSNH
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Bacteria , Proteobacteria , WP_015589146.1 MULTISPECIES:
glutamine-hydrolyzing carbamoyl-phosphate synthase small
subunit [unclassified Wolbachia]"
gene 22475..22969
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CDS 22475..22969
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100 , identity 100 , evaluate 4.38e-99 , alnlength 164 ,
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ORIGIN

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SOURCE     Wolbachia pipientis (insect metagenome)
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REFERENCE  1 (bases 1 to 60654)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL  International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 60654)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Direct Submission
  JOURNAL  Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##

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Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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FEATURES

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gene complement(4066..4827)
/locus_tag="wEsol_00792"
CDS complement(4066..4827)
/locus_tag="wEsol_00792"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 1.81e-169 , alnlength 253 ,
Bacteria , Proteobacteria , WP_015588978.1 MULTISPECIES:
twin-arginine translocase subunit TatC [unclassified
Wolbachia]"
/cog="TatC COG0805 255 Sec-independent protein secretion
pathway component TatC"
/pfam="TatC"
/tigr="TIGR00945 tatC 215 twin arginine-targeting protein
translocase TatC"
/product="twin-arginine
translocase subunit TatC"
/translation="MWNSSKYASFYEHFAELRKRVIKFLFFCVAFGFCYYFKENIY
RFLAPLIEATKGSEGFSLIYTDLTEAFFVYLQVAIMSALLFSFPVFAWQFYMFLAPG
LYKSERAVLLPYLIATPVLFVTGATVVYYYIFPLAWKFFITFEHSGKSFGIPIEFMPS
VSEYLDLVLQFMFAFGTAFQIPVILTLMVRVGLLTAQSLSNKRRIAIVVIFIIAAILT
PPDVLSQVGLAIPMLILYELSILICRYIEKKKTKI"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100

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, identity 100 , evalue 1.81e-169 , alnlength 253 ,
Bacteria , Proteobacteria , WP_015588978.1 MULTISPECIES:
twin-arginine translocase subunit TatC [unclassified
Wolbachia]"

gene complement(4824..5921)
/locus_tag="wEsol_00793"

CDS complement(4824..5921)
/locus_tag="wEsol_00793"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 1.32e-266 , alnlength 365 ,
Bacteria , Proteobacteria , WP_174516762.1 MULTISPECIES:
glyceraldehyde-3-phosphate dehydrogenase [unclassified
Wolbachia]"
/cog="GapA COG0057 335 Glyceraldehyde-3-phosphate
dehydrogenase/erythrose-4-phosphate dehydrogenase"
/pfam="Gp_dh_N Gp_dh_C"
/tigr="TIGR01534 GAPDH-I 330 glyceraldehyde-3-phosphate
dehydrogenase, type I"
/product="glyceraldehyde-3-phosphate dehydrogenase"
/translation="MTVRVGINGLGRIGRGVLRRAIFEIEEYSKQIEVAVNGSLSAKQ
HAHLIKYDSVHGKFSGDIDFNESQNWISINGKKFSLYRERNPENIPWNVDVILECTGA
FNKREEAIRHNAEKVIVSAPVPDADVTIVYGVNDMDLEKEHKVISAGSCTTNCLAPIV
KVLHSSLGIKSGFMTTIHAYTNDQNVLDGNHKKDLRRARACGLSMVPTTTGAAKTIGSV
IPELKGKLDGTAVRVPVSNVSMVDFKFTTDKKATVEEINEIFKDAALSSTS FQRM TLE
SNFWIPVSATRMTSEGTRMTEGYPM SNVLSICEEPLVSIDFVHNPHYSAIVDLTGTYVT
GDICRVAAWYDNEWAFSLRMLDIALLSYSKV"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 1.32e-266 , alnlength 365 ,
Bacteria , Proteobacteria , WP_174516762.1 MULTISPECIES:
glyceraldehyde-3-phosphate dehydrogenase [unclassified
Wolbachia]"

gene 7210..7743
/locus_tag="wEsol_00794"

CDS 7210..7743
/locus_tag="wEsol_00794"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 1.57e-121 , alnlength 177 ,
Bacteria , Proteobacteria , WP_006280514.1 MULTISPECIES:
HK97 family phage prohead protease [Wolbachia]"
/cog="COG3740 COG3740 194 Phage head maturation protease"
/pfam="Peptidase_U35"
/tigr="TIGR01543 proheadase_HK97 142 phage prohead
protease, HK97 family"
/product="HK97 family phage
prohead protease"
/translation="MNKKFLYSPLSIK SIGENG VFSGYASVFNI VDKQNDLILPGA FK
ENLNRN KIKLLWQHNPDEPIGSIID IYENDVGLYITAHLLLGIQKAE EVYLM LKTGAI
NGLSIGYIPIEYD VDHKSGARVLKQVELWEVSLVTFPANLAAQVINVKNN EQEVL A
RAIEKANAVLADMYISA"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 1.57e-121 , alnlength 177 ,
Bacteria , Proteobacteria , WP_006280514.1 MULTISPECIES:
HK97 family phage prohead protease [Wolbachia]"

gene 7879..8937
/locus_tag="wEsol_00795"

CDS 7879..8937
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 /codon_start=1
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 RWAENILYYDKTTANNEVQTDAFKTIIDGSVQVLDKPEVAVRESQSGVISKDGEVQTNK
 VTFHDIAMQTEYVETTDKNSDQAQQVEDLQSKNGLLEVKIEELRSIIIRLKADLQSKN
 SSLKKENRELQSIIIRLKKNYRELVEVTDKQEKEFLVKLKAKSEMIGCQGRELTELRA
 EFTNKINELFERVEEVKREKSKKKKEELQEQVEHLNAKLERARNVAIFSIGERTKTLDE
 ENLTLKNQQIESSPAKDEQQNGKLTEKDTQGQTKTKAPDTVSTVSTAKSTTGSMKSKF
 QRVYLSFVGMRIAINFYL"
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 64.7177419354839 , similarity 99.4 , identity 99.4 ,
 evalue 1.73e-176 , alnlength 321 , Bacteria ,
 Proteobacteria , WP_007549292.1 hypothetical protein
 [Wolbachia endosymbiont of Drosophila ananassae]"

gene 8998..9180
 /locus_tag="wEsol_00796"

CDS 8998..9180
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 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
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 VVNEHCNTNSHCTTNR"
 /besthit="qcoverage 100 , hcoverage 14.8514851485149 ,
 similarity 100 , identity 98.3 , evalue 1.84e-27 ,
 alnlength 60 , Bacteria , Proteobacteria , WP_213863522.1
 hypothetical protein [Wolbachia endosymbiont of Ceratitis
 capitata]"

gene 9232..9753
 /locus_tag="wEsol_00797"

CDS 9232..9753
 /locus_tag="wEsol_00797"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /pfam="HTH_23 HTH_28 HTH_1 HTH_29 HTH_Tnp_IS630 HTH_32
 Pfam-B_19535 HTH_Tnp_Tc3_2 HTH_24 HTH_33"
 /translation="MALRSKLLDEKVVESAKAMLKVKVRNNAYVTKKLNAVIAAKKHSI
 TAVAKICCSIRTALTAWIKHLKFNREEKLFAPPQRRRKTRLNQSQRQVEAWIQENPN
 ITIKEMRIKIQERFGLDISKSTVHRNMQRMKFSYITPRPVHNGQDKSKQEEFKKSQR
 NYWQISRKRAIFL"
 /cog="COG3415 COG3415 138 Transposase and inactivated
 derivatives"
 /besthit="qcoverage 90.1734104046243 , hcoverage
 47.1299093655589 , similarity 100 , identity 100 , evalue
 8.70e-97 , alnlength 156 , Bacteria , Proteobacteria ,
 WP_155968376.1 MULTISPECIES: IS630 family transposase
 [Wolbachia]"

gene complement(9856..10188)
 /locus_tag="wEsol_00798"

CDS complement(9856..10188)
 /locus_tag="wEsol_00798"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /translation="MEWVREVTNLHKVRSSRVIVSYILLHKMFCCIYNQNLSTGLSSG
 EYGGRYIISIFLGTFFKFFDLCLQAQSITRKVSRIPRYCDICSRNIFMQSVLTFELELS

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PFLGLTAL"
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96.6101694915254 , similarity 86.0 , identity 82.5 ,
evaluate 5.00e-24 , alnlength 57 , Bacteria ,
Proteobacteria , ONI56732.1 hypothetical protein
N500_0170 [Wolbachia pipientis wUni]"
gene complement(10271..10612)
/locus_tag="wEsol_00799"
CDS complement(10271..10612)
/locus_tag="wEsol_00799"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evaluate 1.53e-79 , alnlength 113 ,
Bacteria , Proteobacteria , AAS13810.1 transposase, IS5
family, OrfB [Wolbachia endosymbiont of Drosophila
melanogaster]"
/cog="COG3293 COG3293 124 Transposase and inactivated
derivatives"
/pfam="DDE_Tnp_1_2 DDE_Tnp_1"
/product="transposase, IS5 family, OrfB"
/translation="MRTKYTKVKMWADMGYQGRNLKNHIKEEYDIDIEIVKRPPCRF
WVHKDTPPELLPTREQGFKVQPRRWVVERTFAWVNRNRRLSKEYDLLTTSTENFIYLA
MSRVMLKREYA"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evaluate 1.53e-79 , alnlength 113 ,
Bacteria , Proteobacteria , AAS13810.1 transposase, IS5
family, OrfB [Wolbachia endosymbiont of Drosophila
melanogaster]"
gene complement(10723..11103)
/locus_tag="wEsol_00800"
CDS complement(10723..11103)
/locus_tag="wEsol_00800"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evaluate 1.16e-87 , alnlength 126 ,
Bacteria , Proteobacteria , AOV87106.1 transposase
[Wolbachia endosymbiont of Drosophila incompta]"
/cog="COG3293 COG3293 124 Transposase and inactivated
derivatives"
/pfam="DUF4096"
/product="transposase"
/translation="MRKKYPTDLSEREWARIEKHFRVSYKKGGRPPKYSKREILEAIF
YVLRGTGCQWRYLPNDFPLWKTVYEQFRQWKKQGIFEKMNIEITKYSRRKIGRNEQPSA
CIVDSQSVKTTEKGGSKAMMEVKK"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evaluate 1.16e-87 , alnlength 126 ,
Bacteria , Proteobacteria , AOV87106.1 transposase
[Wolbachia endosymbiont of Drosophila incompta]"
gene 11179..11619
/locus_tag="wEsol_00801"
CDS 11179..11619
/locus_tag="wEsol_00801"
/codon_start=1
/transl_table=11
/pfam="Pfam-B_2272"
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evaluate 2.11e-95 , alnlength 146 ,
Bacteria , Proteobacteria , WP_213863558.1 hypothetical

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protein [Wolbachia endosymbiont of Ceratitis capitata]"
/translation="MGKELRDDTLKAKLSPSVRKCVKKLEFNKQEGVNKIVDSILHSF
NSKNNNNNDSGELLKEIVTGKLTEAKMKCFSNKIQELQLALSIRDKFLSPDQGMCNQT
QGGVNEYQLTEKAKKEHIPNSSMSSPNIASIHSLNSQKAVRIGS"
/product="hypothetical protein"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 2.11e-95 , alnlength 146 ,
Bacteria , Proteobacteria , WP_213863558.1 hypothetical
protein [Wolbachia endosymbiont of Ceratitis capitata]"
gene complement(11603..12778)
/locus_tag="wEsol_00802"
CDS complement(11603..12778)
/locus_tag="wEsol_00802"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
99.7 , identity 99.7 , evalue 1.21e-282 , alnlength 391 ,
Bacteria , Proteobacteria , WP_015588983.1 MULTISPECIES:
CCA tRNA nucleotidyltransferase [unclassified Wolbachia]"
/cog="PcnB COG0617 412 tRNA
nucleotidyltransferase/poly(A) polymerase"
/pfam="PolyA_pol PolyA_pol_RNAbd"
/product="CCA tRNA
nucleotidyltransferase"
/translation="MQVDQETSLIIDAIIEEFGGEARLVGGCVRDSILQRDVHDIDLAT
NLLPDQTMKALKLRNIKTIPTGLNHGTITAILNQRSFEITTLRHDKCDGRHAKVEFT
NNWQADASRRDFTFNALYADKHGHIYDYFGGIEDLKARRLNFIGNAEDRIKEDYLRIL
RAFRFHAKICAGDLSDEILSVCKKHSHMIQNLSGERIRDEILKLLCNDPFPPTLKSQM
ESDVLQKIIPKEVKCEILSSSLLFGTDVLVKLALLLRTTKKNDRLSLGEYIIMFLRLS
NKQKKKLLFLLSNDIKTELSEKEQKKYISLFGRELYCDLVRICGVESGENVDEYISFA
NTFNIPKFPLSGDDLIGIGHQPGKSLGRNLELLKQHWEDSSYTTLTKEELVLYAKSLF"
/besthit="qcoverage 100 , hcoverage 100 , similarity 99.7
, identity 99.7 , evalue 1.21e-282 , alnlength 391 ,
Bacteria , Proteobacteria , WP_015588983.1 MULTISPECIES:
CCA tRNA nucleotidyltransferase [unclassified Wolbachia]"
gene complement(12779..13774)
/locus_tag="wEsol_00803"
CDS complement(12779..13774)
/locus_tag="wEsol_00803"
/codon_start=1
/transl_table=11
/pfam="OTU"
/fullproduct="qcoverage 99.3957703927493 , hcoverage
99.6969696969697 , similarity 91.2 , identity 90.0 ,
evalue 7.12e-208 , alnlength 329 , Bacteria ,
Proteobacteria , WP_015588984.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
/translation="MAEPRKRKLSNDFYDTGSPKRFKSSGQEITLLNSNPYPDNFHV
GAIGNGSCFFDSFRQGLEQQKGIEVTVEQLREDCKEFAQKNPPKWFTNAIVNSHDNNG
QHRSETVDDYTANIMRNDRWGDPDVEGRILCQKYDVKLHVIENQTVDNQDLFLHELID
NSGSKSAGEYNKVNYDDSSVLHVINKGHAHFEPLLDNRKSLAKQEQEDFLLAKKLQLD
EILEYCNLSKDISERAEVKKRFDELLAENADGKIGDVVGQCVSDIKQRIERSEKQNP
SLPRCSMEESRTEKIFHQQQISQLKCKINLHSPVYFYIGVCASISYNMNLQYVLT"
/product="hypothetical protein"
/besthit="qcoverage 99.3957703927493 , hcoverage
99.6969696969697 , similarity 91.2 , identity 90.0 ,
evalue 7.12e-208 , alnlength 329 , Bacteria ,
Proteobacteria , WP_015588984.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
gene 13893..14987

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CDS      /locus_tag="wEsol_00804"
13893..14987
/locus_tag="wEsol_00804"
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/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 1.90e-254 , alnlength 364 ,
Bacteria , Proteobacteria , WP_015588985.1 MULTISPECIES:
redox-regulated ATPase YchF [unclassified Wolbachia]"
/cog="COG0012 COG0012 372 Predicted GTPase, probable
translation factor"
/pfam="FeoB_N MMR_HSR1 FH2 YchF-GTPase_C"
/tigr="TIGR00092 TIGR00092 368 GTP-binding protein YchF"
/product="redox-regulated
ATPase YchF"
/translation="MSFNCGIVGLPNIGKSTLFNALTESSAAEAANYPFCTIEPNIGK
ISIKDQRLKQIAAIAGSEKIIYNQLEVVDIAGLVKGASKGEGLGKFLSHIREVDAIV
HLLRCFTDDDISHVHISKIDPISDAEVVEMELILADIDSIEKRLPQLEKKAKQGDKELK
RQLELMQEVLATLKLGPARSLENINEDMKLLQLLTTPVMYVCNVEDTNVITGNEL
SKKVERMAEENKSKFYCISAKLEADIANLDSEEEKQSFLSEFGLQESGLDGVARIMYE
VLSMITFFTVGPKEARAWPVKIGSTADKAAGVIHTDFEKGFIKAETISFADYIKYGSE
SACKDAGKIRFEGRDYIVQDGDIMHFRFNV"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 1.90e-254 , alnlength 364 ,
Bacteria , Proteobacteria , WP_015588985.1 MULTISPECIES:
redox-regulated ATPase YchF [unclassified Wolbachia]"
gene     15601..16803
CDS      /locus_tag="wEsol_00805"
15601..16803
/locus_tag="wEsol_00805"
/codon_start=1
/transl_table=11
/pfam="Pfam-B_5409 Ank_2 Ank_4 Ank_5 Ank Ank_3 Ank_4"
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 7.50e-261 , alnlength 400 ,
Bacteria , Proteobacteria , WP_015588986.1 MULTISPECIES:
Ankyrin repeat domain protein [unclassified Wolbachia]"
/translation="MKNILYFILLVVVFGSLSLFAIEQREEKKIGSVHKNENVGARKQ
DLLSSTNQKDELKSNVDAKQTQEAESKRLDGTDDKEKLQHNNENKASVVEKTISEGEKI
DKDLPNQLEGSTDKFAQNLPNMANKEVNKDLKPEPLPLSADLNENTTDPQKNLQADQ
KIDIKDNELSKSDASQLLEGKKEKVENQSEEKKVKETNSNSKDRNRVKPITKKDESEK
KNLQKWTKLNREPIKEWGHKDIQSKSIYKRQYDSLNEHLPTTVFIDDYSKQFFYCIKK
NNLTCLRGVISKLEKIGLTIQEILRFRNKLGDTPLIYSVKQGEVDIVRFLLLQGADLR
VVNNNFQSPIDIAIEKKQINIINAIAEMMPHLLLEDRKIDNKESAMYDWA VKTKENNE
SQCDKQDD"
/product="Ankyrin repeat
domain protein"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 7.50e-261 , alnlength 400 ,
Bacteria , Proteobacteria , WP_015588986.1 MULTISPECIES:
Ankyrin repeat domain protein [unclassified Wolbachia]"
gene     16796..18601
CDS      /locus_tag="wEsol_00806"
16796..18601
/locus_tag="wEsol_00806"
/codon_start=1
/transl_table=11
/pfam="Pentapeptide_4 Pentapeptide Pfam-B_10960
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Pentapeptide_4 Pentapeptide_3 Pentapeptide Pfam-B_18433
Pentapeptide_4 Pentapeptide_3 CfAFP Pentapeptide
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Pentapeptide_4 Pentapeptide_3 Pentapeptide Pfam-B_18433
Pentapeptide Pentapeptide_3"
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 9.37e-88 , alnlength 601 ,
Bacteria , Proteobacteria , WP_015588987.1 MULTISPECIES:
pentapeptide repeat-containing protein [unclassified
Wolbachia]"
/translation="MIRFLILILVGHLGNETNDEKNQISDFLALHDVKYVSYSKK
DFAEFLVQCHKEGVPEDFKKGFGSNLNGANFNQLYLSKSVFDGVSIGADFSNTDLS
VSFIDVDLRGANFSNANLHGIIKIKGTNLSFTKFVSANLTDIVFDQSNVSYADFISSDL
KKVSMHNVIGLHTNFSNVKMNFNSLSNSNVSHVNFSDSEINDTVMQKNLNDNASFFGV
DAYKLKIQFSSLKNANIYGAEKESDFTGSNLSDACLNSSIIINSNFDETNLSNTQIS
YVNDNSSFVQSILNGSKIKHAYVSETNLQDADLSNIDFSFSELHQVNVSNADIRHGK
FHNTKVANSNMNGSFFDHSLFTSAKIEDSDLSTTSMYKIKIQDSQVYNSTLSRHNIDS
SEIENSTFFNLLADNSSWSNLKVTNSNFIESDFRSSLHANAFRKTSFFLSNLSNSTI
SDMSFLSSSIYKSSVANSHLTGCKFDNSILIDNQGQKLAGLENAITSIEDLQEKISQ
GEKFNVNYSYFEFKDMNLENADFSNSTLSRAKFVNVLNKANFEKTDLRYTVFDNSSL
IGTNLSNSNLEGSSFLNSDPKSTMLKNAKKNDRKK"
/product="pentapeptide
repeat-containing protein"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 9.37e-88 , alnlength 601 ,
Bacteria , Proteobacteria , WP_015588987.1 MULTISPECIES:
pentapeptide repeat-containing protein [unclassified
Wolbachia]"
gene 18585..19190
/locus_tag="wEsol_00807"
CDS 18585..19190
/locus_tag="wEsol_00807"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 7.23e-132 , alnlength 201 ,
Bacteria , Proteobacteria , WP_015588988.1 MULTISPECIES:
guanylate kinase [unclassified Wolbachia]"
/cog="Gmk COG0194 191 Guanylate kinase"
/pfam="Guanylate_kin AAA_33 AAA_17 AAA_18"
/tigr="TIGR03263 guanyl_kin 180 guanylate kinase"
/product="guanylate kinase"
/translation="MTVKSEGVLLVLSSPSGAGKTTISAKLLEQSTNLVRSVSMTTRK
PRPGEINGKDYFFVTEEFKHELCKAGQMLEYAKVFENFYGIPRNFIEQNLSNGISVLL
SIDWQGAFHFLFKLMRKKVVSFILPPSMEEELRLRLQKRNSDDASEIERRLAEAQKEIS
KRDKYDYVIINDIDKSVEEISSILNKERLKKLKEKPSLED"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 7.23e-132 , alnlength 201 ,
Bacteria , Proteobacteria , WP_015588988.1 MULTISPECIES:
guanylate kinase [unclassified Wolbachia]"
gene 19477..21789
/locus_tag="wEsol_00808"
CDS 19477..21789
/locus_tag="wEsol_00808"
/codon_start=1
/transl_table=11
/pfam="LacI Ank_2 Ank_5 Pfam-B_14646 Ank_2 Ank_4 Ank_2
Ank_4 Ank_5 MOZART1"
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
99.9 , identity 99.9 , evalue 0.0 , alnlength 770 ,

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Bacteria , Proteobacteria , WP_174516766.1 ankyrin repeat domain-containing protein [Wolbachia endosymbiont of Cardiocondyla obscurior]"
 /translation="MGIDITALTTNADKLGECIDKNKKQEQRKDEQLYGIIKRKVKK
 EEHKREKPRGQDGTLLKCKRLEFKDASPEVLTKLEESLREQEKEYRYVQCFLPVLDK
 AIERSKKISNETKERVQKAISEITYNSKYCNQNDRRDSGIESDYSSDAGDDYEKHSIS
 NPNTANEDQEVEKSNGTTHNNVQLLKAIKNGNNRKLKKYLDCTDISSIKAEEGKNIL
 HLIASLEKKQKCKFLGTLIKTVTKEDLAQLINSENQTPFQVALINKVTKEKHESNTIR
 SNDNTLKFLLTKLLEHGASSDNLELSTEELQNLKEEQKTYRNFLEKLAEQGGKSKLKP
 EIRINTEAKIKEIIPHTINTPDSNDNYLLHPVIKNSDKLFEKELLEKGADISLKDTDG
 NNALHLIVKPETKQKLKLLNILLETGQKEQFIKAVNDKKEGQTPHLHQILQRIQESKE
 PSLKNKIKNVVKNVVKKEFKDTGRYKTLLEFLQNGADITVQDKDGKNALHYIASFKGE
 QKVTCLLELILNSVEKEKFSKAANAANEKERTPLQVALITKTTKDKHNLVNPKSRDNTI
 KFCVKLLQNGVDPKQLILPERLWSKEYYKTIKIEKSMGRALIPDDMRTELKCNFGRK
 LKARDIVKYINNVACKAVTTLVFAALACAAIFSASQGIITIATASSIIAVIGVCYLIY
 LNLENIYEGFGKIKGKFTEEKQLTLQDNAPKNDTQCNNSVKDIENKSNDDLEEQEVQKS
 SNQSEHTESPDPDKMSAISINSLKNCVGIV"
 /product="ankyrin repeat domain-containing protein"
 /besthit="qcoverage 100 , hcoverage 100 , similarity 99.9 , identity 99.9 , evalue 0.0 , alnlength 770 , Bacteria , Proteobacteria , WP_174516766.1 ankyrin repeat domain-containing protein [Wolbachia endosymbiont of Cardiocondyla obscurior]"
 complement(21790..23589)
 /locus_tag="wEsol_00809"
 CDS complement(21790..23589)
 /locus_tag="wEsol_00809"
 /codon_start=1
 /transl_table=11
 /fullproduct="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 0.0 , alnlength 599 , Bacteria , Proteobacteria , WP_015588990.1 MULTISPECIES: succinate dehydrogenase flavoprotein subunit [unclassified Wolbachia]"
 /cog="SdhA COG1053 562 Succinate dehydrogenase/fumarate reductase, flavoprotein subunit"
 /pfam="Thi4 FAD_binding_2 Pyr_redox_2 DAO Succ_DH_flav_C Pfam-B_6713"
 /tigr="TIGR01816 sdhA_forward 584 succinate dehydrogenase, flavoprotein subunit"
 /product="succinate dehydrogenase flavoprotein subunit"
 /translation="MDKSAYEIIIEHEYDVVVVGAGGAGLRATLGMAATNFSVACISKI
 FPTRSHTVAAQGGISAAAGNIGEDDWRWHAYDTIKGSDWLGDQDAIEYMCKNAAKAVI
 ELENFGVPFSRTEDGKIYQRSFSGMTTHFGKGKSAQRTCAAADKTGHAILHTLYQQCL
 KFNAEFFVEYFVIDLIMDSETCCGVLAWSLCDGTLHRFRAHRVVLATGGYGRVYFSAT
 SAHTCTGDGNGMVVRAGLPLEDMFVQFHPTGIYGSGLMTEGCRGEGGYLVNSQGEK
 FMERYAPKAKDLASRDVVSRAITIEIREGRGVGPKKDYMYLTIAHLDPVVKLRPLGI
 SETARTFAGVDVTKDPIPIPTVHYNMGGIPTNYYGEVITLKQGKEEVVDGLFAIGEA
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 complement(24469..25890)
 gene

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 /pfam="tRNA-synt_1c Pfam-B_1171 Pfam-B_1171"
 /tigr="TIGR00464 gltX_bact 470 glutamate--tRNA ligase"
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 gene 26283..26795
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 gene 26868..28943
 CDS 26868..28943
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[unclassified Wolbachia]"
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carboxylase, alpha subunit"
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ATP-grasp_5 Dala_Dala_lig_C ATP-grasp RimK Biotin_carb_C
Biotin_lipoyl Biotin_lipoyl_2"
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carboxylase biotin carboxylase subunit"
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carboxylase biotin carboxylase subunit [unclassified
Wolbachia]"
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CDS complement(28892..29920)
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100 , identity 100 , evaluate 1.14e-228 , alnlength 342 ,
Bacteria , Proteobacteria , WP_174516784.1 MULTISPECIES:
COX15/CtaA family protein [unclassified Wolbachia]"
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for cytochrome oxidase assembly"
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ALIIFALLSYQFFDYQIRPQQTKLVSGNTIYYARMILVLIVIQIIFGAFVAGLNAGL
IYNTFPLMDGQVVPEDLFFLQPIWLNIFENRATVQFIHRALALLILTLVVILTVKNAS
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PICTFFPS"
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gene complement(29902..31491)

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involved in cell wall biogenesis"
         /pfam="Glyco_tranf_2_3 Glycos_transf_2 Glyco_transf_21
Glyco_trans_2_3 Pfam-B_2922"
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QKVDYSKLNPIYITILLPVFEESAVIGQLIESVKSLDYPKSKLDVKLLVESDDQETLA
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RARWIKGYMQTYIVHLKNIKSLYKHTGFKGILLNLFVGSAAFIFFTPFLLLSLILT
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gene     complement(31497..31973)
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100 , identity 100 , evalue 1.26e-86 , alnlength 158 ,
Bacteria , Proteobacteria , WP_141457161.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
         /cog="AtpF COG0711 161 F0F1-type ATP synthase, subunit b"
         /pfam="Mt_ATP-synt_B ATP-synt_B Pfam-B_1635 Peptidase_M41
HrpE"
         /tigr="TIGR01144 ATP_synt_b 147 ATP synthase F0, B
subunit"
         /product="hypothetical protein"
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EKFRKDMLEYKKSSEKYKKLDAEVNEMMNEALDKANSIIKHNRQQLDQTLDDNAHSN
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, identity 100 , evalue 1.26e-86 , alnlength 158 ,
Bacteria , Proteobacteria , WP_141457161.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
gene     complement(31982..32461)
CDS      /locus_tag="wEsol_00817"
         complement(31982..32461)
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Bacteria , Proteobacteria , WP_015589036.1 MULTISPECIES:
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 subunit"
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 subunit B"
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 EVLDSFNSSVHLLRLTEDQVAKYNAALTQARIQAKKIIDDALAQAEMRANVKNILEE
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 , identity 99.4 , evalue 2.89e-97 , alnlength 159 ,
 Bacteria , Proteobacteria , WP_015589036.1 MULTISPECIES:
 ATP synthase subunit B [unclassified Wolbachia]"
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 /pfam="ATP-synt_C"
 /tigr="TIGR01260 ATP_synt_c 58 ATP synthase F0, C
 subunit"
 /product="F0F1 ATP synthase
 subunit C"
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 /pfam="ATP-synt_A"
 /tigr="TIGR01131 ATP_synt_6_or_A 227 ATP synthase F0, A
 subunit"
 /product="F0F1 ATP synthase
 subunit A"
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 GVLPSFTVTSHVIVTFALSMVVFYITIVGFKERGVEFLRILLPKGTPSWLAPIIII
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Wolbachia]"
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gene 34114..36453
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CDS 34114..36453
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phenylalanine--tRNA ligase subunit beta [unclassified
Wolbachia]"
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subunit"
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/tigr="TIGR00472 pheT_bact 798 phenylalanine--tRNA
ligase, beta subunit"
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EKFGYSNKLFIIDNPFNNSFNIMRPSIMP NLLQVTADNIAHGISDLAIFEIGPIYDGE
AQSKYVLSGIRSGNNLPRNHYNTRKVDVFD AKADCIAALEFFNVNCDNL TIEKAEKE
HYHPGKSGTLSFKNKVAGYFGELHPNILD LFDIKQKVVGFEVILENIENLPVSRKKFI
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/blasthit="qcoverage 100 , hcoverage 100 , similarity 100
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Wolbachia]"

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TYDKLKELLDEFRLKVVSSIDFKLTTHLIYNAYQVAFIQAIKFQRRRGEDFSLEDEI
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Ceratosolen solmsi]"
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8.42e-77 , alnlength 133 , Bacteria , Proteobacteria ,
WP_015589040.1 hypothetical protein [Wolbachia
endosymbiont of Drosophila simulans]"
gene      complement(39156..41063)
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          /codon_start=1
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RKQADFHISDRIRV I I K T E E E K I K E A I N T W F E Y I K E Q T L A L S L D I N T E I G T N F Y S K E Y
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FVFYDGPFPFANGLP HYGHLLTGFIKDAFARYQTMLQKRVERRFGWDCHGLPAEMGAEK
ELGISGRTEVEKFGIDKFNDHCRTSVMKISSEWEKYVNRQARWVDFHNDYKTMDKLFM
ESVMWAFKQLYDKGLVYESMRVVPYSWACETPLSNFETRLDNAYREKVSKAVTVAFEL
LENPQQFKSVKRKCKLLAWTTTPWTLPSNLALAIGKDIEYCAVSVHSLMSFQVRTLES
ISGSQCRSTGMTEVNERSSVNSEIYIFAESYLEKFISHSEQNNIPYENCNIKLKANDL
AGLPYKPLFDYFKD TKK CIPRFSS LIM"
/cog="IleS COG0060 933 Isoleucyl-tRNA synthetase"
/besthit="qcoverage 98.6149584487535 , hcoverage
31.8141197497766 , similarity 98.0 , identity 98.0 ,
evaluate 1.43e-252 , alnlength 356 , Bacteria ,
Proteobacteria , WP_141457155.1 MULTISPECIES:
isoleucine--tRNA ligase [unclassified Wolbachia]"
gene 42696..44162
/locus_tag="wEsol_00827"
CDS 42696..44162
/locus_tag="wEsol_00827"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evaluate 0.0 , alnlength 488 ,
Bacteria , Proteobacteria , WP_007548626.1 MULTISPECIES:
oligopeptide:H+ symporter [Wolbachia]"

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/cog="PTR2 COG3104 498 Dipeptide/tripeptide permease"
/pfam="Pfam-B_3817 MFS_1 PTR2 MFS_1"
/tigr="TIGR00924 yjdL_sub1_fam 475 amino acid/peptide
transporter (Peptide:H+ symporter)"
/product="oligopeptide:H+
symporter"
/translation="MDQKTDKFPQFLKMLCFVEMWERFSYYGMRALLVLFLTSHLGFT
DERAFTIYSLFAATGYAIPILGGFLADKLMGFRNMVLLGGIVMIAGHACMSLVKFEPG
LLYLGLSLIAIGTGMFKGNVTNLLSSCYGKDDPERSRGFTLFYVGVNIGAILASISCG
YVAHLFGWHYGFGLAGIGMSIGLIFFLKFNLLGDSGLSPYPELMNKRILGIKIFGIV
LIGSFLSSSIIAKMLIHSEFFTNMLIFIGITALGIFIYIISKLSAEQRRKLVALSILV
VFFLCFFALEMQLGSLVNLFTERNVINNVLGITIPASVSQAINPLSIIIFGFLFGTYM
KFKQKYATSMFTLGLLTAMCFFTLYIGCLNSNIEGKVEYLYLIIAISFMGLGELCIA
PLVQEQATTLPKLNLRGVVMGIVMLSLAFSNLAGVAISKFMSVPSVNGKINYLESLI
YKEGFLKVGIFNLMLVIVFLFFFFNFIHKVVTNSSCTKN"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evaluate 0.0 , alnlength 488 , Bacteria ,
Proteobacteria , WP_007548626.1 MULTISPECIES:
oligopeptide:H+ symporter [Wolbachia]"
gene complement(44302..45621)
/locus_tag="wEsol_00828"
CDS complement(44302..45621)
/locus_tag="wEsol_00828"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evaluate 0.0 , alnlength 439 ,
Bacteria , Proteobacteria , WP_010962578.1 MULTISPECIES:
tRNA (N6-isopentenyl
adenosine(37)-C2)-methylthiotransferase MiaB [Wolbachia]"
/cog="MiaB COG0621 437 2-methylthioadenine synthetase"
/pfam="UPF0004 Radical_SAM TRAM"
/tigr="TIGR01574 miaB-methiolase 437 tRNA-i(6)A37
thiotransferase enzyme MiaB"
/product="tRNA
(N6-isopentenyl adenosine(37)-C2)-methylthiotransferase
MiaB"
/translation="MKGLYIKTYGCQMNVYDSVLMENVIKPLGFNVSDAGKADLVIL
NTCHIREKAAEKLYSELGKIHSRLKEMTIVVAGCVAQAEGEEVFRRAPFVDIVVGPQS
IATLPELIVKASRSKGVHINTDFPEVAKFDKLPDECYGNSQGSSAFLAIQEGCDKFCT
FCVVPYTRGAEYSRPVNEIFREALKLVANGANEINLLGQNVNAYHGECEGEVWDLGKL
ISHIAKIEKLERIRYTTSHPRDMHESLYLAHAEEPKLMPFVHLVPVQSGSNKILHAMNR
KHTAAEYLEIIDRFRKLKPEIEFSSDFIVGFPGETEKDFEETMKLVEKVRYAQAYSFK
YSPRPGTPGAERKDQVPEEVKTERLLRLQKLISKQQLFNFQSMVGKTIPVLFSDKKGK
HQNQIIGKSPYMQSVCIDDSSEDKYRDKIVNVKVLEARQSSLLGCAFH"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evaluate 0.0 , alnlength 439 , Bacteria ,
Proteobacteria , WP_010962578.1 MULTISPECIES: tRNA
(N6-isopentenyl adenosine(37)-C2)-methylthiotransferase
MiaB [Wolbachia]"
gene complement(45807..46193)
/locus_tag="wEsol_00829"
CDS complement(45807..46193)
/locus_tag="wEsol_00829"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 85.15625 , hcoverage 100 ,
similarity 100 , identity 100 , evaluate 5.46e-74 ,
alnlength 109 , Bacteria , Proteobacteria ,
WP_197907214.1 hypothetical protein [Wolbachia]

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endosymbiont of Kradibia gibbosae]"
/translation="MTDLTQKKQKARICSDAWLMYNTEIKIPVLPFLSFQCLTLGSSF
LYKFTKSASFYNAPILTKLNALLAIKFPGCQCQATRMTPTFFFLDPSVKHWDDKKRAL
PSWMEASVSYPHDTLTTVIPLLVSGI"
/product="hypothetical protein"
/besthit="qcoverage 85.15625 , hcoverage 100 , similarity
100 , identity 100 , evalue 5.46e-74 , alnlength 109 ,
Bacteria , Proteobacteria , WP_197907214.1 hypothetical
protein [Wolbachia endosymbiont of Kradibia gibbosae]"
gene complement(46190..46618)
/locus_tag="wEsol_00830"
CDS complement(46190..46618)
/locus_tag="wEsol_00830"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 2.49e-92 , alnlength 142 ,
Bacteria , Proteobacteria , WP_010082641.1 MULTISPECIES:
protoporphyrinogen oxidase HemJ [Wolbachia]"
/cog="COG1981 COG1981 149 Predicted membrane protein"
/pfam="UPF0093"
/tigr="TIGR00701 TIGR00701 142 TIGR00701 family protein"
/product="protoporphyrinogen
oxidase HemJ"
/translation="MNYYHWLEAFHVISVIMWMAGMLYLPRLYVYHATVKPGSENDL
LQTMKRLRLRYIINPAMLFSLGLGITLMVIREAYREGWFHVKAFAILLMLIIHMLLAK
YRKNFAMGSNKKSHIYFRVLNEAVTVLIIIVIVIMVVVKPF"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 2.49e-92 , alnlength 142 ,
Bacteria , Proteobacteria , WP_010082641.1 MULTISPECIES:
protoporphyrinogen oxidase HemJ [Wolbachia]"
gene 46674..47654
/locus_tag="wEsol_00831"
CDS 46674..47654
/locus_tag="wEsol_00831"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 6.19e-234 , alnlength 326 ,
Bacteria , Proteobacteria , WP_006279887.1 MULTISPECIES:
pyruvate dehydrogenase (acetyl-transferring) E1 component
subunit alpha [Wolbachia]"
/cog="AcoA COG1071 358 Pyruvate/2-oxoglutarate
dehydrogenase complex, dehydrogenase (E1) component,
eukaryotic type, alpha subunit"
/pfam="E1_dh TPP_enzyme_C DXP_synthase_N Transketolase_N"
/tigr="TIGR03182 PDH_E1_alpha_y 315 pyruvate dehydrogenase
(acetyl-transferring) E1 component, alpha subunit"
/product="pyruvate
dehydrogenase (acetyl-transferring) E1 component subunit
alpha"
/translation="MKAENFTKEQIIGFYRKMLLIRRFEEKAGQLYGMGLIGGFCHLS
IGQEAVAVGTQAASKLGDAFITSYRDHGLMLACDSDPNVVMALGTGKETGCSKGKGS
MHVFDVEKKKFFGGHGIVGAQVPIGTGIAFANKYKKKDNVVFYTFGDGAANQGQVYESF
NMAISLWELPVVYIIENNEYAMGTSVQRSTLVTELYKRGESFGIPGKQVDGMDFFSVYE
ATSEAAEHTRSGKGPILLEMKTYRGRHSMSPATYRLKEEVEDMKQNHDPISLTKKY
MTDNKMASEEECKVIDKEIRDLVKKSEDFAKNSKEPSVDELYTDVYKFVS"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 6.19e-234 , alnlength 326 ,
Bacteria , Proteobacteria , WP_006279887.1 MULTISPECIES:

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pyruvate dehydrogenase (acetyl-transferring) E1 component subunit alpha [Wolbachia]"

gene 48063..48986
/locus_tag="wEsol_00832"

CDS 48063..48986
/locus_tag="wEsol_00832"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 3.94e-216 , alnlength 307 , Bacteria , Proteobacteria , WP_006279888.1 MULTISPECIES: RluA family pseudouridine synthase [Wolbachia]"
/cog="RluA COG0564 289 Pseudouridylate synthases, 23S RNA-specific"
/pfam="S4 PseudoU_synth_2"
/tigr="TIGR00005 rluA_subfam 298 pseudouridine synthase, RluA family"
/product="RluA family pseudouridine synthase"
/translation="MLQSIKTILIEDDNVRLDRYIRRIFFDLKQSVIEKSLRKGLIKV DDCKAKSSDRVNSGQTITLKHLYNIENANSRKYNEKLVNLLRENILYEDEYILAINK PAGVIVQGGVKVKISMSDLLDQIREGETFKIVHRLDRDTSGVIFARNANVARYLMEE FKGRRVKKTYLALTSGIPSKDSGTIDYPLVKKYVSGQEKVVVDENSPQNATTHFSIIA KSKHNVAYLKLQIPITGRTHQLRAHLAHINCPILGDGKYGGKAFIDGIANKIHLHSHS LSLKLPNNKEITITAPITKHIEKSIEALFFD"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 3.94e-216 , alnlength 307 , Bacteria , Proteobacteria , WP_006279888.1 MULTISPECIES: RluA family pseudouridine synthase [Wolbachia]"

gene complement(48994..50256)
/locus_tag="wEsol_00833"

CDS complement(48994..50256)
/locus_tag="wEsol_00833"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 5.26e-294 , alnlength 420 , Bacteria , Proteobacteria , WP_015589043.1 MULTISPECIES: MFS transporter [unclassified Wolbachia]"
/pfam="Pfam-B_3877 MFS_1 Sugar_tr MFS_2 MFS_2 Sugar_tr"
/tigr="TIGR00883 2A0106 400 MFS transporter, metabolite:H+ symporter (MHS) family protein"
/product="MFS transporter"
/translation="MNNIRKAILSGMICNMIVWYELTLFGVLTDTIINVFFPSEDHYL STLKFLGVFAIGFAFRPIGAVIFGYMGDKYGRKTLTSTVILISISSTIMGIIPGYKE IGLLSPVLLVFCRIVQGITAGGETSINTAFTIEHSDKDKNLGFLGSMKPFSGALGTLT CITMIFICKRVTGENYEIWGWKLLFYFCFFLTIGFLTRYILKESLAYKTNKYANNLA HSPLLELVRNYKRPLIISINLGIAQNAIVYAAIMFYNISIKELVILSISVKDLMRIVI QVVFAASAVLFAILSDKVGRKRVMPVLIMLSLIGTCVLPLLSSVNHYVVIITYLLIT IPVGASFGIYGSVICELFPTKVRCTGVSLANNISAGIFGGLSPYICMWLIEKTETKLA AGIYLTACTLISLISVLQIKAKDRKVDW"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 5.26e-294 , alnlength 420 , Bacteria , Proteobacteria , WP_015589043.1 MULTISPECIES: MFS transporter [unclassified Wolbachia]"

gene complement(50318..52120)
/locus_tag="wEsol_00834"

CDS complement(50318..52120)
/locus_tag="wEsol_00834"
/codon_start=1

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/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
99.8 , identity 99.8 , evalue 0.0 , alnlength 600 ,
Bacteria , Proteobacteria , WP_015589044.1 MULTISPECIES:
aspartate--tRNA ligase [unclassified Wolbachia]"
/cog="AspS COG0173 585 Aspartyl-tRNA synthetase"
/pfam="tRNA_anti DUF1463 tRNA-synt_2 tRNA-synt_2b GAD"
/tigr="TIGR00459 aspS_bact 586 aspartate--tRNA ligase"
/product="aspartate--tRNA
ligase"
/translation="MNCYKTHTCNELRKNDVEKEVTLSGWLYRKRDHGNLIFVDLRDF
YGITQLVFNNDKDFDEISNLKLESVITVTGIVEARTEDTVNSSISTGEIEVIVNNLR
VESEVEFHFDDEEIAKEERSILASITGEQEYPENMRFKYRFLDLRREKVRNNIILRSQI
IAELRKLMIERGFLEIQTPILTASSPEGARDYLVP SRLNPGKFYALPQAPQIFKQLLM
VSGFDKYFQIAPCFRDEDARADRS PGEFYQLDLEMSFVTQEDIFDVIESALYKVFQF
SRKSVDKDFPRITYKEAMLKYGSDKPD LRNPLLISDVTEIFRDSGFNIFKSNIERGMV
VRAIPAPKTAEEPRSFFDKKIEHAQKEFGAKGLGYITFDKDG TAKGPIAKFLDENRLN
HIREATNIEPGDSVFFASDKENEAANIAGKVRTLLGSELSFIDDNIFKFCWIIDFPYF
VYDDKSKKIDFFHNPF SMPHGGLKDLEDKNPLDILAYQYDLVCNGIELSSGAIRNNKL
DIMYKAFAIAGYSRGEVDTRFGALVRAFRFGVPPHGGIAPGVDRIVMLLADEPNIREV
ICFPMNQGEDVLMGAPSKVEDKHLRELSLKVIE"
/besthit="qcoverage 100 , hcoverage 100 , similarity 99.8
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Proteobacteria , WP_015589044.1 MULTISPECIES:
aspartate--tRNA ligase [unclassified Wolbachia]"
gene 52317..52748
/locus_tag="wEsol_00835"
CDS 52317..52748
/locus_tag="wEsol_00835"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 6.34e-91 , alnlength 143 ,
Bacteria , Proteobacteria , WP_006279891.1 MULTISPECIES:
hypothetical protein [Wolbachia]"
/translation="MPLTQIILYSVTLLA VAAVFLFLRKIYKNRIRKIIFPRKVFKEE
WEEDRKFNELYQKNKQKELLKQQETLREKQKDVQVYKEDPEIVDIAKPVGKWTKMVM
GNGLMQRFAQLIHREGGQKGFWELFVKAQASTQGKHKGKGR"
/product="hypothetical protein"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 6.34e-91 , alnlength 143 ,
Bacteria , Proteobacteria , WP_006279891.1 MULTISPECIES:
hypothetical protein [Wolbachia]"
gene 52752..53375
/locus_tag="wEsol_00836"
CDS 52752..53375
/locus_tag="wEsol_00836"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 5.54e-148 , alnlength 207 ,
Bacteria , Proteobacteria , WP_015589045.1 MULTISPECIES:
heme ABC exporter ATP-binding protein CcmA [unclassified
Wolbachia]"
/cog="CcmA COG4133 209 ABC-type transport system involved
in cytochrome c biogenesis, ATPase component"
/pfam="T2SE AAA_15 MutS_V AAA_29 AAA_23 SMC_N
Mg_chelatase AAA_17 AAA_18 AAA_16 AAA_21 ABC_tran AAA_15"
/tigr="TIGR01189 ccmA 198 heme ABC exporter, ATP-binding
protein CcmA"

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/product="heme ABC exporter
ATP-binding protein CcmA"
/translation="MLECENLSCTRNNKVLFKNLSFKAELKSKILITGPNGSGKTSLI
RSLSGLLPVSGNIRHCGKDIYDDPKSYISSMVYIGHKNACKDSLTV AQNVEFWAGIR
NTRELIVAAICCLQLQPVLNIRYGELSAGWKRRVALARLLISNANVWLIDEPFCNLDS
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, identity 100 , eval 5.54e-148 , alnlength 207 ,
Bacteria , Proteobacteria , WP_015589045.1 MULTISPECIES:
heme ABC exporter ATP-binding protein CcmA [unclassified
Wolbachia]"
gene 54420..55715
/locus_tag="wEsol_00837"
CDS 54420..55715
/locus_tag="wEsol_00837"
/codon_start=1
/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
99.8 , identity 99.8 , eval 9.95e-284 , alnlength 431 ,
Bacteria , Proteobacteria , WP_006280467.1 MULTISPECIES:
sodium:proton antiporter [Wolbachia]"
/cog="NhaC COG1757 485 Na+/H+ antiporter"
/pfam="Na_H antiporter CitMHS Na_H antiporter CitMHS"
/product="sodium:proton
antiporter"
/translation="MTAFVPLIIFLILYLGSGAYFSFIGTDNPLHQVSPVICLLPALF
FAVSRGTNKIQHNIDTVIKGMGDKNTLTMCLIFLFGAFSAVTQSIGSADTVANLILN
FLPARLLLPGVFLASAFISTAIGTSMGVVALMVPIAVNLA KSGAFGLEIGTATVVGGA
VFGDNLISMISDTTIA SVSSQEASAKDKLKMNSKVALIASIITLIYLAVASNSTKIISI
SNLDYYSIIKIIPYISLIIMGLLEVATLVTITINIIAGVLGITFFDYAIIQFPHDVY
DGFKKVNEIVIFALFIGGLSHIMYKQGQKALHKLIDESNITKTAEFVIVGIASMFTT
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, identity 99.8 , eval 9.95e-284 , alnlength 431 ,
Bacteria , Proteobacteria , WP_006280467.1 MULTISPECIES:
sodium:proton antiporter [Wolbachia]"
gene complement(56604..56945)
/locus_tag="wEsol_00838"
CDS complement(56604..56945)
/locus_tag="wEsol_00838"
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100 , identity 100 , eval 1.53e-79 , alnlength 113 ,
Bacteria , Proteobacteria , AAS13810.1 transposase, IS5
family, OrfB [Wolbachia endosymbiont of Drosophila
melanogaster]"
/cog="COG3293 COG3293 124 Transposase and inactivated
derivatives"
/pfam="DDE_Tnp_1_2 DDE_Tnp_1"
/product="transposase, IS5 family, OrfB"
/translation="MRTKYTKVKKMWADMGYQGRNLKNHIKEEYDIDIEIVKRPPCRF
WVHKDTPPELLPTREQGFKVQPRRWVVERTFAWVNRNRRLSKEYDLLTTSTENFIYLA
MSRVMLKREYA"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , eval 1.53e-79 , alnlength 113 ,
Bacteria , Proteobacteria , AAS13810.1 transposase, IS5
family, OrfB [Wolbachia endosymbiont of Drosophila
melanogaster]"

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gene      complement(57056..57436)
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CDS       complement(57056..57436)
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100 , identity 100 , evalue 1.16e-87 , alnlength 126 ,
Bacteria , Proteobacteria , AOV87106.1 transposase
[Wolbachia endosymbiont of Drosophila incompta]"
          /cog="COG3293 COG3293 124 Transposase and inactivated
derivatives"
          /pfam="DUF4096"
          /product="transposase"
          /translation="MRKKYPTDLSEREWARIEKHFRVSYKKGGRPPKYSKREILEAIF
YVLRGTGCQWRYLPNDFPLWKTVYEQFRQWKKQGIFEKMNYEITKYSRRKIGRNEQPSA
CIVDSQSVKTTEKGGSKAMMEVKK"
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Bacteria , Proteobacteria , AOV87106.1 transposase
[Wolbachia endosymbiont of Drosophila incompta]"
gene      complement(57646..58533)
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CDS       complement(57646..58533)
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100 , identity 100 , evalue 3.36e-211 , alnlength 295 ,
Bacteria , Proteobacteria , WP_155968567.1 MULTISPECIES:
UDP-N-acetylmuramate dehydrogenase [Wolbachia]"
          /cog="MurB COG0812 291 UDP-N-acetylmuramate
dehydrogenase"
          /pfam="FAD_binding_4 MurB_C"
          /tigr="TIGR00179 murB 290
UDP-N-acetylenolpyruvoylglucosamine reductase"
          /product="
UDP-N-acetylmuramate dehydrogenase"
          /translation="MLISLPKVRGIYRYDVLMSKATWLVNVGGRADVLFKPCDIEDLTY
LIKNTLPVSVIGATSNIIVRDSGIRGITVKLGKEFAYIKSKGNNSIVAGGAVLLSNL
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IFKNPKNYRAWELIDKSGCLGLNIGGARISQKHCNFLNLDNATASDLENLGNKVKDA
VKDKFNVELEWEIRVLGSY"
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Bacteria , Proteobacteria , WP_155968567.1 MULTISPECIES:
UDP-N-acetylmuramate dehydrogenase [Wolbachia]"
gene      complement(58524..59402)
          /locus_tag="wEsol_00841"
CDS       complement(58524..59402)
          /locus_tag="wEsol_00841"
          /codon_start=1
          /transl_table=11
          /fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 3.89e-204 , alnlength 292 ,
Bacteria , Proteobacteria , WP_010962666.1 MULTISPECIES:
hydroxymethylbilane synthase [Wolbachia]"
          /cog="HemC COG0181 307 Porphobilinogen deaminase"
          /pfam="Porphobil_deam Porphobil_deamC"

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/tigr="TIGR00212 hemC 293 porphobilinogen deaminase"
/product="
hydroxymethylbilane synthase"
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YANANLAEIGGKGLFIKEIETELLENNIDMAVHSLKDMPAFFSGGLTIPCVLERLSSC
DAFISHKHNSLES LPQQATIATSSIRRKVQLLNVRPDLNIVPLRGNVTRLQNQSF DG
IILAEAGLIRLEKHHLLITEVLPPKVMLS AVGQGAVCIQCRNDVKIIDLLEKINNMS
FIGVKSESRFMKTVNGSCFTPLAALAEYVSENMLHLRCMLASGKNIFYTERTSFIEDA
EKMGM DAGLELKS KCL"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 3.89e-204 , alnlength 292 ,
Bacteria , Proteobacteria , WP_010962666.1 MULTISPECIES:
hydroxymethylbilane synthase [Wolbachia]"

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gene

CDS

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60462..>60654
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60462..>60654
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/codon_start=1
/transl_table=11
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, similarity 100 , identity 100 , evalue 1.23e-38 ,
alnlength 64 , Bacteria , Proteobacteria , WP_155968442.1
MULTISPECIES: hypothetical protein [Wolbachia]"
/translation="MSLNYHNLKEHPRNFRDVTGLKIEEFKVVVEKVRPEWEK VQEQK
KCHGR TSRLPVLEDKILCII"
/product="hypothetical protein"
/besthit="qcoverage 100 , hcoverage 98.4615384615385 ,
similarity 100 , identity 100 , evalue 1.23e-38 ,
alnlength 64 , Bacteria , Proteobacteria , WP_155968442.1
MULTISPECIES: hypothetical protein [Wolbachia]"

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ORIGIN

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181 taaaacgcat aaacaagcgc gtaactgatt cgtccccaat gcgacaaata tgctccagtc
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 1936)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 1936)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage     :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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ORIGIN

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121 tctgttttaa tgcttactgc tatagtgggt ggaattgcaa cattttcagt tggattgtcc
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481 tttttcgtct gattttatag atgatgctat atctttattc cggaattaat gtgcttgaaa
541 gtagtgaaga tgaagaagat attccttcca acagtgatga tagtaaaactt gatgatgatg
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721 aaattgaatc tgaagaagcat aacatgttac gtgcaataat tgaaacatca gtaacattaa
781 aggtgataaa agtatggcgt gatgatttaa gtagtggagc tctcttactg agagaaatta
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DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_40278, whole genome
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ACCESSION  JAQZAU010000070 JAQZAU010000000
VERSION    JAQZAU010000070.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 785)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 785)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date          :: JUN-2019
            Assembly Method        :: FLYE v. 06-2019
            Genome Representation  :: Full
            Expected Final Version :: Yes
            Genome Coverage        :: 100.0x
            Sequencing Technology  :: Illumina HiSeq; PacBio Sequel
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             Rhagoletis cerasi]"

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ORIGIN

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 VERSION JAQZAU010000071.1
 DBLINK BioProject: PRJNA929258
 BioSample: SAMN33142973
 KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
 REFERENCE 1 (bases 1 to 4625)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 4625)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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 /environmental_sample
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 Northfield, MN"
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, identity 100 , evalue 2.74e-74 , alnlength 115 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_155968342.1 MULTISPECIES: IS630 transposase-related
protein [Wolbachia]"

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ORIGIN

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1 gaggttgtcc ggaaactagt aaattcaagc atattccctc tttaacataa ccctactcat
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121 tctattccta ttaacccaag caaaagtcct ttctacaacc catcttcttg gctgtacttt
181 aaacccttgt tctcttgttg gtagtagctc aggtggcgta tctttgtgca cccaaaatct
241 acatggaggc cttttaacaa tttcaatatc tatgtcatat tcttccttta tgtgattcct
301 taaatttctt ccttggtatc ccatgtcagc ccacattttt taacttttagt atattttggt
361 ctcatattgt ttaatgctat ttaataacca tctctatcat tttcgtttagc agcgcctacg
421 taacaaccta gtataaaacc ctgagtgtct gtaattatat gcctttttct accctttact
481 tttttacttc catcatagcc tttgatcccc ctttttctgt agtctttaca gattgactat
541 ctactataca ggcaactcggc tgctcattcc ttcctatttt tcttctacta tattttgtaa
601 tttcataatt cattttctca aaaattccct gcttcttcca ttgcctgaac tgctcataca
661 cagtcttcca tagcggaaaa tcatttggtg aataaccgcca ttgacaccct gtacgcaata
721 catagaaaat tgcttctaata atttctcttt tgctatactt tggcggcctt cctcctttct
781 tgtatgatac tctgaagtgt ttttctatcc ttgccattc cttttcgctt agatctgttg
841 gatacttttt tctcatcttt acccgcactt aaaatttcag atattatagc cttttactta
901 tttccggaca acctcttata gccttttact tatttccgga cacctcttag aggttgtccg
961 gaaactagta aattcaagca tattccctct ttaacataac cctactcata gctagggtata
1021 tgaaattctc agtggatgtt gtgagtaaat catactcctt cgatagcctt ctattcctat
1081 taacccaagc aaaagtcctt tctacaaccc atcttcttgg ctgtacttta aacccttggt
1141 ctcttgttgg tagtagctca ggtggcgat ctttgtgcac ccaaaatcta catggaggcc
1201 ttttaacaat ttcaatatct atgtcatatt cttcctttat gtgattcttt aaatttcttc
1261 cttggtatcc catgtcagcc cacatttttt taacttttagt atattttggt ctcatattgt
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1381 gtataaaacc ctgagtgtct gtaattatat gcctttttct accctttact tttttacttc
1441 catcatagcc tttgatcccc ctttttctgt agtctttaca gattgactat ctactataca
1501 ggcaactcggc tgctcattcc ttcctatttt tcttctacta tattttgtaa tttcataatt
1561 cattttctca aaaattccct gcttcttcca ttgcctgaac tgctcataca cagtcttcca
1621 tagcggaaaa tcatttggtg aataaccgcca ttgacaccct gtacgcaata catagaaaat
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1741 tctgaagtgt ttttctattc ttgcccattc cctttcgctt agatctgttg gatacttttt
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1861 acctcttaga ggttgtccgg aaactagtaa attcaagcat attccctctt taacataacc
1921 ctactcatag ctaggatatat gaaattctca gtggatgttg tgagtaaata atactccttc
1981 gatagccttc tattcctatt aacccaagca aaagtccttt ctacaacca tcttcttgge
2041 tgtactttta acccttggtc tcttggttgg agtagctcag gtggcgatc tttgtgcacc
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2281 ggcctacgtt aacaacctag tataaaaccc tgagtgtctg taattatatg cctttttcta
2341 ccctttactt ttttacttcc atcatagcct ttgatccccc cttttctgta gtctttacag
2401 attgactatc tactatacag gcactcggct gctcattcct tcctattttt cttctactat
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2521 gtcatacac agtcttccat agcggaaaat catttggtta ataccgccat tgacaccctg
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2701 gatctgttgg atactttttt ctcactttta ccccgtaata aaatttcaga tattatagcc
2761 ttttacttat ttccggacaa cctcttagag gttgtccgga aactagtaaa ttcaagcata
2821 ttccctcttt aacataaccc tactcatagc taggtatatg aaattctcag tggatgttgt
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3061 gtcataattc tcctttatgt gattctttta atttcttctt tggatatcca tgtcagccca
3121 cattttttta acttttagtat attttggtct catattgttt aatgctattt taataccatc
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3481 taccgccatt gacaccctgt acgcaataca tagaaaattg cttctaatat ttctcttttg
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3601 gccatttccc tttcgcttag atctgttgga tacttttttt tcatctttac cccgtactaa
3661 aatttcagat attatagcct tttacttatt tccggacaac ctctatagat attttctaaa
3721 atgaatgata aatttccatt atgggtattac caaccaaag ttgtaagtct gtatatttat
3781 gcattaaagg tctgaggcgg cttttgatgg tattccaaca atgctctata ggggttcaaat
3841 ctggtgaata tggttgtaga tagagcaaac ggcacttagc attatctatt aactcctttg
3901 ttttgaggat tttatggaat gtggcattgt ccataactat tgtagtacca tgtggcaatt
3961 taggtaataa catcttctct aacctgtat tgaataacct tttgtcacac ccaccttga
4021 aagtcattgg tgcaataaat ctctttccaa tccacccgcc tattatactg attctctctc
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4141 ggtataacct attatcaact cctgcttcat ctatatataa gatgctggaa tgggtctattt
4201 ttgagatttt atcggtaaat cgctgcctat cttcttgatt gcgctcttga tatagtgtaa
4261 ctttttttta aagtaattct tagctgtttc agcctatacc aaattgaatt tattccaat
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LOCUS      JAQZAU010000072      1031 bp      dna      linear      ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_40541, whole genome
            shotgun sequence.
ACCESSION  JAQZAU010000072 JAQZAU010000000
VERSION    JAQZAU010000072.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis

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Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE 1 (bases 1 to 1031)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL International Journal Molecular Sciences
REFERENCE 2 (bases 1 to 1031)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##
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/isolation_source="galls on Solidago altissima"
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/db_xref="taxon:955"
/environmental_sample
/country="USA: Cowling Arboretum, Carleton College,
Northfield, MN"
/lat_lon="44.48 N 93.13 W"
/altitude="280 m"
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/note="metagenomic"
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/locus_tag="wEsol_00858"
CDS complement(57..440)
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ananassae]"
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Bacteria , Proteobacteria , EAL58175.1 hypothetical
protein WwAna0404 [Wolbachia endosymbiont of Drosophila
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CDS      complement(766..>1031)
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ORIGIN

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1  gtgcagattt gagcagccat tgcagccggt agtacgaaca ttgcttctac cgctgttat
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121 cttttctggt taagtagcca agctctggca ttaaacacag aaagtcttga gataactttt
181 ccaggaactg ttttaaggat tttttgacgt tgttgtaact cacggctttc atcaataatt
241 ttttgtatag tattattgag ttcattctatt tgactattaa agaatccgat agttttttga
301 caacttttctt ttatatgggtc gttttcaggt gcttccagtc tacatTTTTTc ctgagttctc
361 atttgcgtaa tgtcatcacg acgttgacaa agtgcaacca aggttgattg tttttcagaa
421 gtggggagag agagttccat gacgcatatt gagcaagagc ctttgcattc gatttatcgg
481 actttgctaa agttccgtgt gacaagatga agcttttttac tttacgggta ttagctcgat
541 gtacagcgat attcttgtca ataagaaaat gcgataaacc aatttcctgt attttctaaa
601 gttactaaag aattaggtaa gatattctgaa aacttttttaa acaattgttg ccaaccagaa
661 gcattattat caaattcgac aacactcttc tgtgtgtgaa ccgcaataac attttttaaat
721 tttccgatgt caataccaat aaaatTTTtga taagatgtaa ccatattaat aacctcgata
781 gtttattgat ttaagattgt aaacgggtgc atacatatgt cccatgcaac tattcaaacg
841 tatcgaggga tagccttgat ataaacggtt gtcaacgccg cgtcggtcgc acacgcccg
901 tattcctata gtgagtagtt ccctcttgtt tcttttataa catattttta acttacagcc
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LOCUS      JAQZAU010000073          513 bp    dna        linear    ENV 17-MAR-2023
DEFINITION  MAG: Wolbachia pipientis isolate wEsol contig_40849, whole genome
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ACCESSION   JAQZAU010000073  JAQZAU010000000
VERSION     JAQZAU010000073.1
DBLINK      BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS    WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE      Wolbachia pipientis (insect metagenome)
ORGANISM    Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE   1  (bases 1 to 513)

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AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 513)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
 ##Genome-Assembly-Data-END##
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 /isolation_source="galls on Solidago altissima"
 /host="Eurosta solidaginis MN-2018-EFC"
 /db_xref="taxon:955"
 /environmental_sample
 /country="USA: Cowling Arboretum, Carleton College,
 Northfield, MN"
 /lat_lon="44.48 N 93.13 W"
 /altitude="280 m"
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 /note="metagenomic"
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 similarity 100 , identity 100 , evaluate 5.15e-29 ,
 alnlength 54 , Eukaryota , Arthropoda , GFQ64109.1
 mutator family transposase [Trichonephila clavata]"
 gene 291..>513
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 CDS 291..>513
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 /codon_start=1
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 /pfam="Transposase_mut"
 /translation="MNNRRNGRNAKTLRTSAGSFELLTPRDREGSFEPQIVKKRQTNL
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 /cog="COG3328 COG3328 379 Transposase and inactivated
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 /besthit="qcoverage 98.6486486486486 , hcoverage

27.8625954198473 , similarity 100 , identity 100 , eval
6.67e-42 , alnlength 73 , Eukaryota , Arthropoda ,
CAD7421462.1 unnamed protein product, partial [Timema
poppensis]"

ORIGIN

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61 ttgggagtgt taaataaact gtgtcaaacc gaaaaaaaagt aataaattga gataaaaaaa
121 tggaggtttg acaatgagtc agaaagtagt aaacagaact accggtttgg tagattataa
181 agaattagaa acaaatatcc tgtcgtctat acgagaagga agaccgttga caggaagaga
241 tggagcatta acaccgttta taaaaaagtt gctggaggta agcctggaag gtgaataatc
301 gaagaaatgg gaggaatgca aagactttac gtacaagcgc agggtcattt gagcttttga
361 cgccaagaga tagggaagga agtttcgaac caaaaaatag caaaaaaagg caaacaact
421 tacatccaga gcttgaaacg aagattttga gcacatttgc cagtgggatg ggctatagag
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LOCUS JAQZAU010000074 2202 bp dna linear ENV 17-MAR-2023

DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_41869, whole genome
shotgun sequence.

ACCESSION JAQZAU010000074 JAQZAU010000000

VERSION JAQZAU010000074.1

DBLINK BioProject: PRJNA929258

BioSample: SAMN33142973

KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.

SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis

Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 2202)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 2202)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##

Assembly Date :: JUN-2019

Assembly Method :: FLYE v. 06-2019

Genome Representation :: Full

Expected Final Version :: Yes

Genome Coverage :: 100.0x

Sequencing Technology :: Illumina HiSeq; PacBio Sequel

##Genome-Assembly-Data-END##

FEATURES Location/Qualifiers

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/isolation_source="galls on Solidago altissima"

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/db_xref="taxon:955"

/environmental_sample

/country="USA: Cowling Arboretum, Carleton College,
Northfield, MN"

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alnlength 244 , Bacteria , Proteobacteria ,
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[unclassified Wolbachia]"
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stomatin/prohibitin homologs"
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HflC"
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AYAKYKITNPITFYQAVRNESGLVRRLYPVIEAHIRENIGRFSLLNEKRSEVMQL
IQRGVYSEAEKFGIEIIDVRIKRADLPEENSSAIFRRMQTEREKEAKEIRAEGEQAGQ
EVRSKADKLRKREIISSAVKESYEIRGRGYAEATRIYNEAFKVDEEFFNFYRSMSAYSK
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/besthit="qcoverage 100 , hcoverage 84.1379310344828 ,
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alnlength 244 , Bacteria , Proteobacteria ,
WP_015589224.1 MULTISPECIES: protease modulator HflC
[unclassified Wolbachia]"
gene 739..>2202
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CDS 739..>2202
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/fullproduct="qcoverage 100 , hcoverage 98.1891348088531
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488 , Bacteria , Proteobacteria , WP_010962868.1
MULTISPECIES: DegQ family serine endoprotease
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/cog="DegQ COG0265 347 Trypsin-like serine proteases,
typically periplasmic, contain C-terminal PDZ domain"
/pfam="Trypsin_2 Pfam-B_3070 Trypsin Pfam-B_13657 PDZ
PDZ_2 PDZ PDZ_2 GRASP55_65"
/tigr="TIGR02037 degP_htrA_DO 434 peptidase Do"
/product="DegQ family serine
endoprotease"
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[Wolbachia]"

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ORIGIN

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ACCESSION  JAQZAU010000075  JAQZAU010000000
VERSION    JAQZAU010000075.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 43507)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 43507)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,

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1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT ##Genome-Assembly-Data-START##
Assembly Date      :: JUN-2019
Assembly Method    :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage    :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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 Bacteria , Proteobacteria , WP_044471254.1 MULTISPECIES:
 ankyrin repeat domain-containing protein [unclassified
 Wolbachia]"

gene 12796..14628
 /locus_tag="wEsol_00878"

CDS 12796..14628
 /locus_tag="wEsol_00878"
 /codon_start=1
 /transl_table=11
 /fullproduct="qcoverage 100 , hcoverage 100 , similarity
 99.8 , identity 99.5 , evalue 0.0 , alnlength 610 ,
 Bacteria , Proteobacteria , WP_041582652.1 MULTISPECIES:
 phage terminase large subunit family protein
 [unclassified Wolbachia]"
 /cog="COG5525 COG5525 611 Phage terminase, large subunit
 GpA"
 /pfam="Terminase_GpA DUF3268"
 /product="phage terminase
 large subunit family protein"
 /translation="MIYATSFSEGLRPDPQLKVSEWANEYRVLAPTAASEPGKWRT
 ETPYLKEIMDSLSPSSQAEKVVFMMKGAQIGGTEAGNNWIGYIIDQTPGPMLVVQPTVEM
 GKRWSKGRFAPLIESTPCLKSKVKDPRSRDSGNTVQSKEFPGGIVVITGANSSVSLRS
 MPVKYLFLEIDAYPGDSGGEGDPVLLSIARTNTFAHRKIFLVSTPTIHGISRIEKEF
 EATDKRYFFVPCPHCNYYQVLKWSQIKWENNDSRTAHYVCTECSGKIENHQKTEMLDR
 GEWRATNQVHNSKVVIGFHLSSLYSPVGWYSWQQAVEDFLHAKESQQLKVWINTTLGE
 TWVDKGEVPDWKQLFNRRREFFPVGTVPREVVLTAGVDVQKDRLEVEVLAWGKSRESW
 SIDYRVFEGDTGGGEVWGKLSELLNHHFIGQNGLEYMISMMAVDAGYATQEVYNWVRG
 HQGAGRVMVKGVNKALVPLSSPSRVDITVGGQKLKRGIKLWPGVSVILKSELFQLLN
 ILKEEEGKALPGYCHFPYAPYFQQLTAEQLVSKVVKGYTKQEWQKVRERNEVLDCR
 IYARAASIALGIDRWPEKWNLSLEKPESEKPKPKVRQSKWLNEK"
 /besthit="qcoverage 100 , hcoverage 100 , similarity 99.8
 , identity 99.5 , evalue 0.0 , alnlength 610 , Bacteria ,
 Proteobacteria , WP_041582652.1 MULTISPECIES: phage

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terminase large subunit family protein [unclassified
Wolbachia]"
gene      14630..14854
          /locus_tag="wEsol_00879"
CDS       14630..14854
          /locus_tag="wEsol_00879"
          /codon_start=1
          /transl_table=11
          /pfam="gpW"
          /fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 7.41e-42 , alnlength 74 ,
Bacteria , Proteobacteria , WP_007549008.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
          /translation="MYNEEYLIQVEEAIAKKLQSGERVVSIAYGDHVVRVYAEVQINDLL
NLRQRIKAELKVAGMKPKRKIVFSTSKGII"
          /product="hypothetical protein"
          /besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 7.41e-42 , alnlength 74 ,
Bacteria , Proteobacteria , WP_007549008.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
gene      14854..15912
          /locus_tag="wEsol_00880"
CDS       14854..15912
          /locus_tag="wEsol_00880"
          /codon_start=1
          /transl_table=11
          /pfam="DUF1016"
          /fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 100 , evalue 3.55e-253 , alnlength 352 ,
Bacteria;Viruses , Proteobacteria;Uroviricota ,
ACN95473.1 phage uncharacterized protein [Wolbachia sp.
wRi]"
          /translation="MIKIVERNFMTKVIAKEYTEFLEQLKEQIATSRYKAALAVNSKL
IVLYHHIGTEILKRQKEHGWGAKIIDQLSRDLRDAFPDMKGFSIQNLKYMRRFAEEYS
ENEIGQQAVDQLPWGHNIVIMYEVKNKEERFWYIKKSCEHGWSRNILSMQIETNLYKR
EGKAITNFRNNLISPQSDLAQQTLKNPYVFDLFLSLGKKAHEREIEKALVAHIERFLL
LGEGFAFLGRQYHLRVGDRDFYLDLVFYHIKLRICYVVIELKAGKFRPEYTGKMNFYLS
AVDDLLRQPGDNQSIGLILYRSKVGVIAYALRDINKPIGLAEYRITENLPENIKTAL
PTIEELEAELSKVSDQEK"
          /product="phage uncharacterized protein"
          /besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 3.55e-253 , alnlength 352 ,
Bacteria;Viruses , Proteobacteria;Uroviricota ,
ACN95473.1 phage uncharacterized protein [Wolbachia sp.
wRi]"
gene      15912..17330
          /locus_tag="wEsol_00881"
CDS       15912..17330
          /locus_tag="wEsol_00881"
          /codon_start=1
          /transl_table=11
          /fullproduct="qcoverage 99.5762711864407 , hcoverage 100
, similarity 99.1 , identity 96.4 , evalue 0.0 ,
alnlength 470 , Bacteria , Proteobacteria ,
WP_127464160.1 phage portal protein [Wolbachia
endosymbiont of Bemisia tabaci]"
          /cog="COG5511 COG5511 492 Bacteriophage capsid protein"
          /pfam="Phage_portal_2"
          /tigr="TIGR01539 portal_lambda 457 phage portal protein,
lambda family"

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/product="phage portal protein"
/translation="MLLKSFQKLFNPKPIKSSAWDAAGSGRRFFHFQPELGSINNLLS
QNLETLRSRSDMRKPNPYAANIIDTIVSNSIGTGIKPQSKARDGEFRKKVQELWLRW
TDEADSNQVSDFYGLQALVCRSMIEGGEFCFIRLRTRKLEDVRSVPLQLQVLESEHLEN
KTNKTLANGNVIRNGIEFNRLGQREAYYLFREHPGEGSFGEVSRVPANDVLHIYRPLR
PGQIRGEFWLSNILLKLYELDQYDDAELVRKKTAAMFAGFITRLDPEANIMGEGESNE
QGVALSGLEPGTMQLLDPGEDIKFSEPSDVGGSEAFMRQQLRAIAIGTGITYEQLTG
DLTGVDNYSSIRAGLIEFRRCAMLQHNIIVFQFCRPVWSRWLELAVLCGELSIDEKVV
KAAKEEVKWI PQGFDWVDPLKDQQAQQMAVRNGFKSRAEVVSEMGYDVEEIDQEIAED
QKRANSFGLCFDSDVNHKREGR"
/besthit="qcoverage 99.5762711864407 , hcoverage 100 ,
similarity 99.1 , identity 96.4 , evaluate 0.0 , alnlength
470 , Bacteria , Proteobacteria , WP_127464160.1 phage
portal protein [Wolbachia endosymbiont of Bemisia
tabaci]"
gene 17330..18064
/locus_tag="wEsol_00882"
CDS 17330..18064
/locus_tag="wEsol_00882"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/pfam="CLP_protease Peptidase_S49"
/tigr="TIGR00706 SppA_dom 208 signal peptide peptidase
SppA, 36K type"
/translation="MWINKPVMVERRSFELLSLYNSKQPIFKNLKHFHINPKGIAIIR
IYGVLTCKTEAFDHILDMTSYENIHEEIESALGDKSIETILLDIDSPGGEVNGVFDLA
DFIYESRTKKRIIAIANDDAYSAAAYAIASSAEKVVFVSRTSGVGSIGVIAASHIDQSRFD
ERQGIKYTTIFAGSRKNDLNPHEPMTSESLESLQKEVGRLYEMFLQLIARNRGLSMEK
IRSTEAAIFWRESSRDRSCRWSYNIF"
/cog="SppA COG0616 317 Periplasmic serine proteases (ClpP
class)"
/besthit="qcoverage 95.0819672131148 , hcoverage
67.6384839650146 , similarity 97.8 , identity 95.7 ,
evaluate 1.42e-148 , alnlength 232 , Bacteria ,
Proteobacteria , ONI57885.1 hypothetical protein
N499_0447 [Wolbachia pipientis wVitA]"
gene 18099..18350
/locus_tag="wEsol_00883"
CDS 18099..18350
/locus_tag="wEsol_00883"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTTIEESYENCRRILEIIRLCNVSKMPEKIGEFIEQGVSV EQA
REVLMELLAERTKKTEILSAIPRNSQEDLMTQVAKSRCI"
/besthit="qcoverage 100 , hcoverage 24.9249249249249 ,
similarity 97.6 , identity 94.0 , evaluate 3.17e-43 ,
alnlength 83 , Bacteria , Proteobacteria , WP_187297063.1
S49 family peptidase [Wolbachia pipientis]"
gene 18491..18862
/locus_tag="wEsol_00884"
CDS 18491..18862
/locus_tag="wEsol_00884"
/codon_start=1
/transl_table=11
/pfam="HDPD"
/fullproduct="qcoverage 99.1869918699187 , hcoverage
99.1869918699187 , similarity 99.2 , identity 98.4 ,
evaluate 1.48e-75 , alnlength 122 , Bacteria ,

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Proteobacteria , WP_214303461.1 head decoration protein
[Wolbachia endosymbiont of Erebia cassioides]"
/translation="MISITEGNNLGDLLKYEVSNNLYSRDQITVAKGQNLKLGAVVAKK
TEDGFIRVLNPAGTDGTQTAIGAIVSDVNATENAKAVIITRGAILADHAVVWPANITE
EQKAEAIKQLEARGIIRKGA"
/product="head decoration protein"
/besthit="qcoverage 99.1869918699187 , hcoverage
99.1869918699187 , similarity 99.2 , identity 98.4 ,
evaluate 1.48e-75 , alnlength 122 , Bacteria ,
Proteobacteria , WP_214303461.1 head decoration protein
[Wolbachia endosymbiont of Erebia cassioides]"
gene 18901..19905
/locus_tag="wEsol_00885"
CDS 18901..19905
/locus_tag="wEsol_00885"
/codon_start=1
/transl_table=11
/pfam="Phage_cap_E"
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
99.4 , identity 97.9 , evaluate 1.17e-242 , alnlength 334 ,
Bacteria , Proteobacteria , WP_052265017.1 major capsid
protein [Wolbachia endosymbiont of Operophtera brumata]"
/translation="MQNPFTNTAFSMTALTNAINILPINYGRVENLNLFPNRSVFRH
ITIEEHNGVLSLLPTQVPGAPATVGKRGRKRVRTFTIPHIPHDDVVLPEEVQGIRAFG
SESELKALADVVDHLQLMRNKHAITLEHLRMGALKGIILDADGSELLNLYNEFEITP
KVVNFALGTATTDVKKCLEVLRHIEDNLSGEYMTGIHALVSPEFFDALTSKAVKEA
YERWQEGAALRNDMRSGFTFCGITFEEYRGQATDPEGTVRRFIERDTGHCFFVGTAST
FTTYFAPADFNETVNTLGQPLYAKQEPFRFRDRTDLHTQSNPLPMCHRPVLAIVTT
"
/product="major capsid protein"
/besthit="qcoverage 100 , hcoverage 100 , similarity 99.4
, identity 97.9 , evaluate 1.17e-242 , alnlength 334 ,
Bacteria , Proteobacteria , WP_052265017.1 major capsid
protein [Wolbachia endosymbiont of Operophtera brumata]"
gene 20015..20320
/locus_tag="wEsol_00886"
CDS 20015..20320
/locus_tag="wEsol_00886"
/codon_start=1
/transl_table=11
/pfam="Pfam-B_106"
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
100 , identity 94.1 , evaluate 1.91e-63 , alnlength 101 ,
Bacteria , Proteobacteria , WP_019236397.1 hypothetical
protein [Wolbachia pipientis]"
/translation="MQKNIKRLFKDCFAHLGELALYESKNKAYMVQVLKQEPDKLYEI
GEGQFVGETLVLEVSADFVLQPIVGDIFVIGDRKYKVYSPPLQDNSGMVWKIRASGV"
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/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 94.1 , evaluate 1.91e-63 , alnlength 101 ,
Bacteria , Proteobacteria , WP_019236397.1 hypothetical
protein [Wolbachia pipientis]"
gene 20321..20827
/locus_tag="wEsol_00887"
CDS 20321..20827
/locus_tag="wEsol_00887"
/codon_start=1
/transl_table=11
/pfam="Pfam-B_14565 Pfam-B_12992 Minor_tail_Z"
/fullproduct="qcoverage 96.4285714285714 , hcoverage

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98.1818181818182 , similarity 98.1 , identity 94.4 ,
 evalue 7.26e-97 , alnlength 162 , Bacteria ,
 Proteobacteria , WP_141456764.1 phage tail protein
 [Wolbachia endosymbiont of Carposina sasakii]"
 /translation="MRINTGSIIQSIDAERKKVEKATVSALNKTAIWLKSKAAKEISE
 EKRIKLSLIRKRLRIFKAKTSRLEVLIRANLYDIKASAIGKIQKTRRGSKVGKHEFIG
 GFAAVMPKGNSGMFKREGRAALPIKEVKLPLEPEASRIIGNLVNVEVEKVFTKFFERE
 LSYITGSV"
 /product="phage tail protein"
 /besthit="qcoverage 96.4285714285714 , hcoverage
 98.1818181818182 , similarity 98.1 , identity 94.4 ,
 evalue 7.26e-97 , alnlength 162 , Bacteria ,
 Proteobacteria , WP_141456764.1 phage tail protein
 [Wolbachia endosymbiont of Carposina sasakii]"

gene 20824..21300
 /locus_tag="wEsol_00888"

CDS 20824..21300
 /locus_tag="wEsol_00888"
 /codon_start=1
 /transl_table=11
 /pfam="Pfam-B_4030"
 /fullproduct="qcoverage 100 , hcoverage 100 , similarity
 96.8 , identity 88.6 , evalue 3.40e-100 , alnlength 158 ,
 Bacteria , Proteobacteria , WP_047759345.1 hypothetical
 protein [Wolbachia endosymbiont of Armadillidium
 vulgare]"
 /translation="MNFKDLHNAICTTLKKEIPAIQTCEIYPSIRKELVAPAVFVELS
 GFEEKGHDPGTEELALKARFEARIVIDSTIENAAIIVRSLAAEVAKVVDKNTWNVKNVS
 PGEFISAEVDEFRPELDAYLVMMVEVWHTIHVGRSIWKEGKFMPhKIEIGEINVRE"
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 , identity 88.6 , evalue 3.40e-100 , alnlength 158 ,
 Bacteria , Proteobacteria , WP_047759345.1 hypothetical
 protein [Wolbachia endosymbiont of Armadillidium
 vulgare]"

gene 21287..21751
 /locus_tag="wEsol_00889"

CDS 21287..21751
 /locus_tag="wEsol_00889"
 /codon_start=1
 /transl_table=11
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 98.1 , identity 94.2 , evalue 2.32e-96 , alnlength 154 ,
 Bacteria , Proteobacteria , WP_077188260.1 phage
 baseplate assembly protein V [Wolbachia pipientis]"
 /cog="gpV COG4540 184 Phage P2 baseplate assembly protein
 gpV"
 /pfam="Phage_base_V Pfam-B_2532"
 /tigr="TIGR01644 phage_P2_V 192 phage baseplate assembly
 protein V"
 /product="phage baseplate assembly protein
 V"
 /translation="MLENNFAIAELQRKLANIVRIGVVKEIDCEKAKVRVKIGEFLLD
 YLPWITSKAGKDRNWSPPDIDEQVMVFSPLGELSLGVVLGGIYQEKYSAPEDKKEINS
 VKFQDGTRELLYDKEKHHLEIEVVDKITLKAGESSIEMTKSEIKLKADRINLN"
 /besthit="qcoverage 100 , hcoverage 100 , similarity 98.1
 , identity 94.2 , evalue 2.32e-96 , alnlength 154 ,
 Bacteria , Proteobacteria , WP_077188260.1 phage
 baseplate assembly protein V [Wolbachia pipientis]"

gene 21752..22006

CDS

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/locus_tag="wEsol_00890"
21752..22006
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/codon_start=1
/transl_table=11
/product="hypothetical protein"
/pfam="PAAR_motif DUF4150 PAAR_motif"
/translation="MNKSVVRVGDYCVETPHEFCISGSNNVSVNGKPMCRQGDKFSEG
RALTEGSKTVFANGFGAGRVDIVSCGFKVIKGSENVFAG"
/besthit="qcoverage 58.33333333333333 , hcoverage
58.33333333333333 , similarity 93.9 , identity 91.8 ,
evaluate 2.18e-25 , alnlength 49 , Bacteria ,
Proteobacteria , WP_143688962.1 hypothetical protein
[Wolbachia endosymbiont of Laodelphax striatellus]"

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gene

CDS

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22009..22335
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22009..22335
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/transl_table=11
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95.4954954954955 , similarity 98.1 , identity 93.4 ,
evaluate 2.03e-62 , alnlength 106 , Bacteria ,
Proteobacteria , WP_208571808.1 GPW/gp25 family protein
[Wolbachia pipientis]"
/cog="COG3628 COG3628 116 Phage baseplate assembly
protein W"
/pfam="DUF2634 GPW_gp25"
/product="GPW/gp25 family protein"
/translation="MEGMSDKTGKELEGIEHLKQSIIDILTPINSRIMRRDYGSRLF
ELVDKPISRDLTLEIYAATAEALGKWEKRFKLEKVKITEVKEGKVTLDLGLELYVPSGK
NIRFIV"
/besthit="qcoverage 98.1481481481482 , hcoverage
95.4954954954955 , similarity 98.1 , identity 93.4 ,
evaluate 2.03e-62 , alnlength 106 , Bacteria ,
Proteobacteria , WP_208571808.1 GPW/gp25 family protein
[Wolbachia pipientis]"

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gene

CDS

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22338..23132
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22338..23132
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/transl_table=11
/fullproduct="qcoverage 100 , hcoverage 99.2481203007519
, similarity 98.5 , identity 95.1 , evaluate 6.43e-169 ,
alnlength 264 , Bacteria , Proteobacteria ,
WP_211908057.1 baseplate J/gp47 family protein [Wolbachia
endosymbiont of Spodoptera picta]"
/cog="COG3948 COG3948 306 Phage-related baseplate
assembly protein"
/pfam="Baseplate_J"
/product="baseplate J/gp47 family protein"
/translation="MQQTNIIERLNFEEILSRMKEELVKCDASFTALVESDPAMKVLE
VAAWRELLLRQRINESVKSNNLLKFAMGEDLDNLAEFYGVERQKEEDDERFRKRIKAKI
VGSSTCGSKEYRYHALSADSRVKDALVESPIPGKVQISILSTQLSTTGIVSEELLKI
VKKQVTRDDIRVLDTLTLVIGCNITEIDIHSRMSISPVISKEEIKKQFIQKFELAKRL
GWSVTRSWIISNLFVDGVENVELIEPKEDVVVLGNECANLRNLKVE"
/besthit="qcoverage 100 , hcoverage 99.2481203007519 ,
similarity 98.5 , identity 95.1 , evaluate 6.43e-169 ,
alnlength 264 , Bacteria , Proteobacteria ,

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WP_211908057.1 baseplate J/gp47 family protein [Wolbachia endosymbiont of Spodoptera picta]"

gene 23132..24286
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CDS 23132..24286
/locus_tag="wEsol_00893"
/codon_start=1
/transl_table=11
/pfam="Pfam-B_16372 Tail_P2_I"
/fullproduct="qcoverage 99.73958333333333 , hcoverage 99.2227979274611 , similarity 98.7 , identity 96.9 , evaluate 2.31e-277 , alnlength 383 , Bacteria , Proteobacteria , WP_211908058.1 phage tail protein [Wolbachia endosymbiont of Spodoptera picta]"
/translation="MLLPNATKQEQALVDATDYKVDPGCIRGFKFSLKEETLPWLIE EYELGEILRWVKDKRRAIVEGVKFQRLRGTPASLKIALKWANIEDIKIIEEPPGKHFF ELQVGIKEVPNDFFVDVAVELAKLLLPVRSRLMRIFNDYYNAQRFILDESIFGDLSD YSGVKIEKDGPVLSFGRVNFFRSSGPVIRIIENYL RDHYERALSNDIYRLDVAILGET EPHTKNGIYERNHLWYNLKALYPLPQSLLPSIKFAKAQIVLSDSWDLGDINTCFPV SSVEERGKNFVLGSDKLSGQYWNLKHKPILERFSVTHNYKAKNYTDQKVRKYVLAHN VYYKNDLEQKDSIHELENYILVFYPGVLKWHEHRLHRSWKNSQVISLIS"
/product="phage tail protein"
/besthit="qcoverage 99.73958333333333 , hcoverage 99.2227979274611 , similarity 98.7 , identity 96.9 , evaluate 2.31e-277 , alnlength 383 , Bacteria , Proteobacteria , WP_211908058.1 phage tail protein [Wolbachia endosymbiont of Spodoptera picta]"

gene 24454..25182
/locus_tag="wEsol_00894"

CDS 24454..25182
/locus_tag="wEsol_00894"
/codon_start=1
/transl_table=11
/pfam="Pfam-B_10896 Ank_2 Ank_4 Ank_5 Ank Ank_3 Ank_4 Ank_5 Ank Ank_3 Ank_4 Ank_5 Ank Ank_3 Ank_2 Ank_4"
/fullproduct="qcoverage 95.4545454545455 , hcoverage 97.8813559322034 , similarity 99.6 , identity 99.6 , evaluate 2.78e-125 , alnlength 231 , Bacteria , Proteobacteria , WP_141456723.1 ankyrin repeat domain-containing protein [Wolbachia endosymbiont of Carposina sasakii]"
/translation="MKFSEEKRESFSKFFKEVSSNGFKNINKRNEEGETILHQAVEIS DYKTARLLIKKGAEVNARDKNGYTPLHCAVFAKSL ENVKVLLREGAEVNATQYVTGCT PLHSACKIGGAGVEIIKELVKAGAEVNQLNKYGATPMYYIWESEKYRLCDSKESERAS KFLREKGGITKSRELTCYGIERIVEEIIADMLNGSYMP ELKIIIEIEIIRKRDKSLIKEE CENLASKIMSQVNEMIDEVVKRRA"
/product="ankyrin repeat domain-containing protein"
/besthit="qcoverage 95.4545454545455 , hcoverage 97.8813559322034 , similarity 99.6 , identity 99.6 , evaluate 2.78e-125 , alnlength 231 , Bacteria , Proteobacteria , WP_141456723.1 ankyrin repeat domain-containing protein [Wolbachia endosymbiont of Carposina sasakii]"

gene 25221..25673
/locus_tag="wEsol_00895"

CDS 25221..25673
/locus_tag="wEsol_00895"
/codon_start=1
/transl_table=11

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/pfam="Ank_4 Pfam-B_10896 Ank_2 Ank Ank_3 EPSP_synthase
Ank_2 Ank_4 Ank_5 Ank Ank_3 Ank_2 Ank_4 Ank_3 Ank_5 Ank"
/fullproduct="qcoverage 102 , hcoverage 100 , similarity
92.2 , identity 89.5 , evalue 3.59e-48 , alnlength 153 ,
Bacteria , Proteobacteria , WP_141456724.1 ankyrin repeat
domain-containing protein [Wolbachia endosymbiont of
Carposina sasakii]"
/translation="MSKKGKEESLLENSYKNIYARDKNGRTALHYAVEVKTVELLVEK
GANVNAKDIEGYTALHLAVTEKRLEIVRELIKSGADVNAEEYGNKCIPLHLACMVGEK
AIVEELVKAGGEIEQADKFGMTAMDYSKEVTEVLKKETDRIEKLFMKG"
/product="ankyrin repeat domain-containing
protein"
/besthit="qcoverage 102 , hcoverage 100 , similarity 92.2
, identity 89.5 , evalue 3.59e-48 , alnlength 153 ,
Bacteria , Proteobacteria , WP_141456724.1 ankyrin repeat
domain-containing protein [Wolbachia endosymbiont of
Carposina sasakii]"
gene 25678..26118
/locus_tag="wEsol_00896"
CDS 25678..26118
/locus_tag="wEsol_00896"
/codon_start=1
/transl_table=11
/pfam="DUF2924"
/fullproduct="qcoverage 100 , hcoverage 100 , similarity
99.3 , identity 97.3 , evalue 2.77e-91 , alnlength 146 ,
Bacteria , Proteobacteria , MBR9984245.1 DUF2924
domain-containing protein [Wolbachia endosymbiont of
Homalodisca vitripennis]"
/translation="MEEEIEKKVMNLERKPLGELRKTWKKVFGEKAPRYSKKYLIPRL
AYRMQEKAYGEMSRKGTKRLEYLADRLEKKGKRISDCLPVEGTELILERGEETHAVMV
TDKGLIYREEFFTSLSAVAGKIMGMSYNGPLLFGLRDQKGRENV"
/product="DUF2924 domain-containing protein"
/besthit="qcoverage 100 , hcoverage 100 , similarity 99.3
, identity 97.3 , evalue 2.77e-91 , alnlength 146 ,
Bacteria , Proteobacteria , MBR9984245.1 DUF2924
domain-containing protein [Wolbachia endosymbiont of
Homalodisca vitripennis]"
gene 26066..27598
/locus_tag="wEsol_00897"
CDS 26066..27598
/locus_tag="wEsol_00897"
/codon_start=1
/transl_table=11
/pfam="Resolvase Recombinase Zn_ribbon_recom Pfam-B_1335
Pfam-B_16452"
/fullproduct="qcoverage 97.2549019607843 , hcoverage 100
, similarity 98.4 , identity 98.0 , evalue 0.0 ,
alnlength 496 , Bacteria , Proteobacteria ,
WP_141456726.1 recombinase family protein [Wolbachia
endosymbiont of Carposina sasakii]"
/translation="MGRSYLVCVIKREGKMKCGIRCGIYTRKSNEDGLEQKFNSLDAQ
RVACEKYIKSKEGWVALAKRYDDGGFSGKNLERPAIKELFEDVKKGEVDCVVVYTLDR
LSRETKDSIEVTSFFRRHRVNFVAVTQIFDNNTPMGKFVQTVLSGAAQLEREMIVERV
KNKIATSKHEGLWMGGTLPFGYDVKDKELINEKEAKIVKHIFARYLELKSMALARE
LNSQGYHTKSDIFKKATVRRIITNPIYMGKIRHYEKEYEGKHEAIIIEEEKWQKAQELI
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crystallin family protein [Wolbachia endosymbiont of
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shock protein)"
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MULTISPECIES: winged helix-turn-helix domain-containing
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gene 31856..31978
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gene 31975..32391
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gene 32388..32507
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transport system, permease components"
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[Wolbachia endosymbiont of Drosophila ananassae]"

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        [Wolbachia endosymbiont of Rhagoletis cerasi]"
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        [Wolbachia endosymbiont of Rhagoletis cerasi]"

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ORIGIN

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VERSION    JAQZAU010000076.1
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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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REFERENCE  1 (bases 1 to 10890)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 10890)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission

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JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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9421	accataatc	tctcctcatt	actctactgt	taataggagt	ggtcagtata	tcaattattg
9481	attgttttcag	atgttctatt	ccttctaatt	cttttcctgt	tttgaggtcc	atccctttca
9541	tttttagcct	gcaaacacgt	tttcaactgc	ttttattact	ttaaaccac	atgaaactat
9601	atctcctact	cttcccgcctc	caaaccatt	tgcaaacact	gtttttgatc	cttgaaccat
9661	tacttctcct	tcactaaaac	tttctccttg	tctgcacatt	ggcttaccat	ttacaaaaac
9721	attgttacta	ccactaatgc	aaaaatgcgg	tgttacttct	acacaataat	ctcctactcg
9781	tacaaccgat	ttattcattt	aattaagggt	tattctatct	gctttcaggt	ttatttcgct
9841	cttcgtcatc	tctatgctcg	attccccagc	tttcagtgtt	attttgtcta	ctacttcaat
9901	ctctaaatga	tgcttctctt	tatcatataa	caatcttggt	ccatcctgaa	acttcacact
9961	atagtatttt	ctaaaatgaa	tgataaattt	ccattatggg	attaccaacc	aaaagtgtga
10021	agtctgtata	tttatgcatt	aaaggctctga	ggcggtttt	gatgggtattc	caacaatgct
10081	ctatagggtt	caaactctgg	gaatatgttg	gtagatagag	caaacggcat	ctagcattat
10141	ctattaactc	ctttgttttg	ggagttttat	ggaatgtggc	attgtccata	actattgtag

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10201 taccatgtgg caatttaggt aataacatct tctctaacca tgtattgaat acctctttgt
10261 cacacccacc ttgaaagtc attggtgcaa taaatctctt tccaatccac cgcctatta
10321 tactgattct ctctcgtttt cttcctggaa tatctgcata aattttcttt cctattggag
10381 cacgtccata ctctcggtat aacctattat caactcctgc ttcatttata tataagatgc
10441 tggaatggtc tatttttgag attttatcgg taaatcgctg cctatcttct tgattgcgct
10501 cttgatatag tgtaactttt ttttaaagta attcttagct gtttcagcct ataccaaatt
10561 gaatttattc caaatccaag attttgtttc atctctgcca gcgtatgata tggattcttt
10621 ttaacatatt cttcgagtat ttttgggtct atttttcgaa taaagctgcc gtttttcgat
10681 ggccttaggc tttcaccagc ggctttcttt cttaaccagc ggtacagagt tgctattcct
10741 atctccaaaa gctctgccac ctcaaccttt gacttccctt tttctatcat cgatactgcc
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LOCUS      JAQZAU010000077          1926 bp    dna        linear    ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_4280, whole genome
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ACCESSION  JAQZAU010000077  JAQZAU010000000
VERSION    JAQZAU010000077.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 1926)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 1926)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage     :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
            ##Genome-Assembly-Data-END##
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                                 /isolate="wEsol"
                                 /isolation_source="galls on Solidago altissima"
                                 /host="Eurosta solidaginis MN-2018-EFC"
                                 /db_xref="taxon:955"
                                 /environmental_sample
                                 /country="USA: Cowling Arboretum, Carleton College,
                                 Northfield, MN"
                                 /lat_lon="44.48 N 93.13 W"
                                 /altitude="280 m"
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                                 /metagenome_source="insect metagenome"
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 KVAYQKIINDLKKHGIEEVDPLGELFDSNLHQAVVEREDNEKKPGTIVEVLQTGYTIK
 NRLLRPAMVILSKKSADCGSD"
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 shock protein)"
 /besthit="qcoverage 100 , hcoverage 70.2857142857143 ,
 similarity 100 , identity 100 , evaluate 5.49e-80 ,
 alnlength 123 , Bacteria , Proteobacteria , EAL60143.1
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 simulans]"

gene 1259..1846
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 56.9277108433735 , similarity 100 , identity 100 , evaluate
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 [Wolbachia]"

ORIGIN

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1 aagtcggaag agactttttc gaaggtaaag tcaccttacc tgctatttat agcatacaaa
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121 tttagaccaag cattacacta tattaatcac cataatgcca ttcagctttc tatggaaaaa
181 gctagactac tacattaata tggcacaaaa tgatattagt actttttctg attcttttta
241 taaaaattac tttaattgac tttttaaatg cgagcataga aagacaatgt agctggcgct
301 tgatattttc gaattaattg ctatatattt attagattct taagggtaat gatatgtcag
361 atagcagtaa agagaaaaag aagaaagttt gctgatatgg taagtaggca gaaggtgacg
421 accaacaag tgataacat aagcaaactg atgatttaaa tgaagatctc aatacattaa
481 aagaacgtgc agctcagctt gaagatcatt tacgccgtgc tgttgagat aatgaaaacg
541 tcaaacgtat aatgcaaaaag caaattagcg atgcaagtga ctacgcagtc acaaaaacttg
601 cacgtgatat gatcgactcg tgcgacaatt taaaaagagt aatggaaatt ttgaaagacg
661 gtgatcctgt tcatgagggg attaaagtag cttatcaaaa aattataaat gatctaaaaa
721 aacatggaat agaggaagta gatccacttg gtgagctttt tgatagtaat ttacaccaag
781 ctggtgtgga aagagaagac aatgaaaaaa agcctggcac cattgtagaa gtactacaaa
841 ctggttatac tatcaaaaat aggttgctcc gtcctgcaat gggtattctt tctaagaaat
901 ctgctgattg tgggaagcga tagcatgagg taaatgtata atgacaagta ttgtcttttt
961 caggtatcca gccaaagtggc gtactacatt taggtaatta tcttggtgca atcaaacagt
1021 ggatagactt acaggataaa tacaaatctc tttttgtatt gtcgacctac acgcaatcac
1081 agcaaataag cttcccgcga gtgaattaaa aagtaatatt ttcaaaacag cagcagctta
1141 tattgcatgc ggaatagata cagaaaagtc cattattttt agtcagtcca cagttagtgg
1201 tcatgcagaa ctgggctggc tgcttgatg ctatacacca attgggtggc ttaatcgcat
1261 gactcaattt aaagataaag ctggcagcga taaacaaaaa gcctctcttg gattatatag

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1321 ttatccagta cttatggctg cagatatatt gttgtatcaa actaaatacg ttcctgttgg
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1441 ttataagctg gattatttca tcgtacctga aatcttaact ttggattgca catcaaggat
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1561 cattaacctt gatgatacgg atgacttaat tgtcaaaaaa atagaaaaag caaaaaacaga
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1681 ttattcagtg cttagtaatg taaatgcaga aaaagtatgt gaagaagtga acaaacaatga
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1801 tgagaaaatg aatgatcttt taaaaagacc aattccattt acatgaaata ttaaaaaaag
1861 gcacaaagaa agcagcagaa attgcaaccc ataataataa agaaatcaag gatattattg
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LOCUS      JAQZAU010000078      1860 bp      dna      linear      ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_42877, whole genome
            shotgun sequence.
ACCESSION  JAQZAU010000078  JAQZAU010000000
VERSION    JAQZAU010000078.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 1860)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 1860)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage    :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
            ##Genome-Assembly-Data-END##
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                                /isolation_source="galls on Solidago altissima"
                                /host="Eurosta solidaginis MN-2018-EFC"
                                /db_xref="taxon:955"
                                /environmental_sample
                                /country="USA: Cowling Arboretum, Carleton College,
                                Northfield, MN"
                                /lat_lon="44.48 N 93.13 W"
                                /altitude="280 m"
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 /cog="COG3547 COG3547 303 Transposase and inactivated derivatives"
 /pfam="DEDD_Tnp_IS110 FH2 Transposase_20"
 /product="IS110 family transposase"
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 /besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 4.42e-217 , alnlength 315 , Bacteria , Proteobacteria , WP_015588780.1 MULTISPECIES: IS110 family transposase [unclassified Wolbachia]"

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 /pfam="PDDEXK_2 Pfam-B_12708"
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ORIGIN

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121 gctcactagg aatagcgggc gtgcgcgacc gaaaggaaat tggattaca accgttggtgta
181 tcaaggtacg ctagccctat ctctcgatac gtttgaatag ttgcttgga catatatatg
241 caccggttta caatcttaaa ttaactaaaa ctatcgaggt ttattatggt tacatcttat
301 caaaatttta ttggcattga catcgaaaaa tttaaaaaatg tcgttgcaat tcacaaacag
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Northfield, MN"
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Culex quinquefasciatus Pel]"
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similarity 100 , identity 100 , evaluate 3.77e-38 ,
alnlength 65 , Bacteria , Proteobacteria , CAQ55081.1
hypothetical protein WP0973 [Wolbachia endosymbiont of
Culex quinquefasciatus Pel]"
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CDS 360..626
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protein [Wolbachia endosymbiont of Ceratitis capitata]"
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protein [Wolbachia endosymbiont of Ceratitis capitata]"
gene 635..2182
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/fullproduct="qcoverage 100 , hcoverage 100 , similarity
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group II intron reverse transcriptase/maturase
[Wolbachia]"

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YKPSPLKRIYISKSNGKRRPLGIPTIKDRAMQALYLLALEPVAETISDRHSYGFRPKR
SCADATVACHLLLASRNQLQWILEGDIKGCDFNINHEWLMKHIPMEKKILHRWLKAGF
LESKTLYPTTAGTPQGSIIISPILANFTLDGLEQLLESRFGLGSKRRGKIRSGVNVIR
YADDFIISGFTHEVLENEVKPLVSSFLHERGLILSEEKTKITSITTGFDFLGCNVRRY
NKKLIKPSKESIKRLLNKARTLIKANIANNTQAIVIKSLNSLLRGWGNYYHHVCAKKA
FRKIDNEIWHSLWKWAKKRHRPRKGLRWIKNRYFKVMGQRQWVFAAPICKNKPKEIRYL
RLLKLIDIPIRRHVKIRADANPLDLKWKKYFDERVKRTRMLASSFSREGSLLLVSPLK
LMYSEDL"
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reverse transcriptase/maturase"
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Proteobacteria , WP_155968541.1 MULTISPECIES: group II
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gene 2179..2556
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similarity 100 , identity 97.9 , evalue 1.84e-19 ,
alnlength 47 , Bacteria , Proteobacteria , WP_155968895.1
Rpn family recombination-promoting nuclease/putative
transposase [Wolbachia pipientis]"
gene complement(2577..3170)
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CDS complement(2577..3170)
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52.2988505747126 , similarity 96.7 , identity 91.8 ,
evalue 1.06e-110 , alnlength 182 , Bacteria ,
Proteobacteria , WP_174132894.1 IS110 family transposase
[Wolbachia endosymbiont of Atemnus politus]"
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CDS complement(3167..3508)
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/cog="COG3293 COG3293 124 Transposase and inactivated

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derivatives"
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WVHKDTPPELLPTREQGFKVQPRRWVVERTFAWVNRNRRLSKEYDLLTTSTENFIYLA
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family, OrfB [Wolbachia endosymbiont of Drosophila
melanogaster]"
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[Wolbachia endosymbiont of Drosophila incompta]"
/cog="COG3293 COG3293 124 Transposase and inactivated
derivatives"
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[Wolbachia endosymbiont of Drosophila incompta]"
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CDS complement(4027..4986)
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SOURCE     Wolbachia pipientis (insect metagenome)

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ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 5305)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 5305)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
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 Expected Final Version :: Yes
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ORIGIN

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ENV 17-MAR-2023

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 BioSample: SAMN33142973
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 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
 REFERENCE 1 (bases 1 to 1509)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 1509)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
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VERSION    JAQZAU010000082.1
DBLINK     BioProject: PRJNA929258
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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 940)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 940)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method     :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage      :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
            ##Genome-Assembly-Data-END##
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DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_44164, whole genome
shotgun sequence.
ACCESSION JAQZAU010000083 JAQZAU010000000
VERSION JAQZAU010000083.1
DBLINK BioProject: PRJNA929258
BioSample: SAMN33142973
KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE Wolbachia pipientis (insect metagenome)
ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE 1 (bases 1 to 19378)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL International Journal Molecular Sciences
REFERENCE 2 (bases 1 to 19378)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##
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REFERENCE  1 (bases 1 to 861)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 861)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
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COMMENT     ##Genome-Assembly-Data-START##
            Assembly Date           :: JUN-2019
            Assembly Method          :: FLYE v. 06-2019
            Genome Representation     :: Full
            Expected Final Version    :: Yes
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            Sequencing Technology     :: Illumina HiSeq; PacBio Sequel
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ORIGIN

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 VERSION JAQZAU010000085.1
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 BioSample: SAMN33142973
 KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
 REFERENCE 1 (bases 1 to 711)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 711)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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 MgtE intracellular N domain protein [Wolbachia

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ACCESSION  JAQZAU010000086 JAQZAU010000000
VERSION    JAQZAU010000086.1
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
  ORGANISM Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 4103)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL  International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 4103)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Direct Submission
  JOURNAL  Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method     :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes

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Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##

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VERSION    JAQZAU010000087.1
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SOURCE     Wolbachia pipientis (insect metagenome)
  ORGANISM Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 2261)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL  International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 2261)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Direct Submission
  JOURNAL  Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method     :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage      :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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ORIGIN

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VERSION    JAQZAU010000088.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)

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ORGANISM *Wolbachia pipientis*
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 1960)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of *Eurosta solidaginis* to gall-induction
 JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 1960)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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LOCUS      JAQZAU010000089          12854 bp    dna        linear    ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_45501, whole genome
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ACCESSION  JAQZAU010000089  JAQZAU010000000
VERSION    JAQZAU010000089.1
DBLINK     BioProject: PRJNA929258
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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 12854)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 12854)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT     ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method     :: FLYE v. 06-2019
            Genome Representation :: Full

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Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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ORIGIN

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ORGANISM   Wolbachia pipientis
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REFERENCE  1  (bases 1 to 14214)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 14214)
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TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
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ORIGIN

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SOURCE     Wolbachia pipientis (insect metagenome)

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ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 6969)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 6969)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
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Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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ORIGIN

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VERSION    JAQZAU010000092.1
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 7966)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 7966)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT     ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
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SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 3717)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 3717)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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FEATURES

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ORIGIN

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ORIGIN

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VERSION    JAQZAU010000095.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 11528)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 11528)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,

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1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT ##Genome-Assembly-Data-START##
Assembly Date      :: JUN-2019
Assembly Method    :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage    :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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VERSION    JAQZAU010000096.1
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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REFERENCE 1 (bases 1 to 27315)
AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE     Genomic assessment of the contribution of the Wolbachia
          endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL   International Journal Molecular Sciences
REFERENCE 2 (bases 1 to 27315)
AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE     Direct Submission
JOURNAL   Submitted (10-FEB-2023) Biology, San Francisco State University,
          1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT   ##Genome-Assembly-Data-START##
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          Assembly Method    :: FLYE v. 06-2019
          Genome Representation :: Full
          Expected Final Version :: Yes
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 Drosophila simulans wHa]"
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 oxidoreductase 75 kD subunit (chain G)"
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 gene complement(15679..16500)
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CDS complement(16490..17029)
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/pfam="Pep_deformylase"
/tigr="TIGR00079 pept_deformyl 161 peptide deformylase"
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 /pfam="Pfam-B_713 MazG-like"
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 [unclassified Wolbachia]"
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 [Wolbachia endosymbiont of Drosophila simulans wAu]"
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 I,Metallopeptidase family M24"
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 FGYSIVRSYCGHGIGKVFHAPPNVVHFYDQDEDLVLKEGMFFTIEPMINAGKHETLLS
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aminopeptidase,Xaa-Pro aminopeptidase,methionine
aminopeptidase, type I,Metallopeptidase family M24
[Wolbachia endosymbiont of Drosophila simulans wAu]"
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CDS complement(19809..21056)
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MFS transporter [unclassified Wolbachia]"
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/tigr="TIGR00883 2A0106 400 MFS transporter,
metabolite:H+ symporter (MHS) family protein"
/product="MFS transporter"
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gene 21277..22158
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CDS 21277..22158
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[unclassified Wolbachia]"
/cog="COG0275 COG0275 314 Predicted
S-adenosylmethionine-dependent methyltransferase involved
in cell envelope biogenesis"
/pfam="Methyltransf_5 Methyltransf_31"
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S-adenosyl-methyltransferase MraW"
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ARAIVNARKKKTIKTTFELADIVRSVVFGRGSKIDPATRTFQAIRIWVNDDELGELEKG
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Bacteria , Proteobacteria , WP_015588811.1 MULTISPECIES:

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16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH
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CDS       22155..22466
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CDS       complement(23103..23402)
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CDS       23548..24159
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[Wolbachia]"
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Ctc-form"
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protein L25/general stress protein Ctc"
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[unclassified Wolbachia]"
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endosymbiont of Cardiocondyla obscurior]"
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hydroxylase and related FAD-dependent oxidoreductases"
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4-hydroxylase"
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hydroxylase"
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2-octaprenyl-6-methoxyphenyl hydroxylase [Wolbachia
endosymbiont of Cardiocondyla obscurior]"

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gene

tRNA

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ORIGIN

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721 aatatagcta gagcttcagg aatgtttaag tcgtttttta aagcgtctat aaaatcttta
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ACCESSION  JAQZAU010000097  JAQZAU010000000
VERSION    JAQZAU010000097.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 5636)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 5636)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT     ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
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            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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                BioSample: SAMN33142973
KEYWORDS       WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE         Wolbachia pipientis (insect metagenome)
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                Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
                Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE      1 (bases 1 to 31806)
  AUTHORS      Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE        Genomic assessment of the contribution of the Wolbachia
                endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL      International Journal Molecular Sciences
REFERENCE      2 (bases 1 to 31806)
  AUTHORS      Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE        Direct Submission
  JOURNAL      Submitted (10-FEB-2023) Biology, San Francisco State University,
                1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT        ##Genome-Assembly-Data-START##
                Assembly Date          :: JUN-2019
                Assembly Method        :: FLYE v. 06-2019
                Genome Representation  :: Full
                Expected Final Version :: Yes
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                Sequencing Technology  :: Illumina HiSeq; PacBio Sequel
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CDS complement(12808..13566)
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transmembrane protein, LolC/E family"
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YMPLKSAQAFFNYKNSIKNIEVLVDDVTRADKLADAIEKEIGMEAESWQSQQSHYFSA
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VNISALALLLSFLATIAPALQAAAQDPAEILRYE"
 /cog="LolE COG4591 408 ABC-type transport system,
 involved in lipoprotein release, permease component"
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 66.4835164835165 , similarity 99.6 , identity 99.2 ,
 evaluate 6.74e-154 , alnlength 242 , Bacteria ,
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 protein [Wolbachia endosymbiont of Drosophila simulans]"
 gene complement(13569..14039)
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 CDS complement(13569..14039)
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 transmembrane protein, LolC/E family"
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 /cog="LolE COG4591 408 ABC-type transport system,
 involved in lipoprotein release, permease component"
 /besthit="qcoverage 91.6666666666667 , hcoverage
 53.3582089552239 , similarity 100 , identity 99.3 ,
 evaluate 1.71e-87 , alnlength 143 , Eukaryota , Arthropoda
 , GFQ84694.1 lipoprotein-releasing ABC transporter
 permease subunit [Trichonephila clavata]"
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 CDS complement(14106..14195)
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 1.85e-09 , alnlength 28 , Bacteria , Proteobacteria ,
 QEF50864.1 hypothetical protein EA652_1196 [Wolbachia
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 gene complement(14173..15462)
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 CDS complement(14173..15462)
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 99.8 , identity 99.8 , evaluate 1.32e-314 , alnlength 429 ,
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 DFTEKPEHKLSNDHYWNSGIFVFKAKRYIDEIKKSAPNLYNLCFKYFTQPQERFLYLKQ
 RDFAGIEGISIDYLVMEKAKNVAMIEANFDWLDVGTWNSVLELSEKFSKEPVSFQHVI
 REKEPVSTTKSNKNLLGGACKQPNKSLISFIHKVKKVKVIRKEVKPWGFCSIILMSEN
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CDS complement(15575..16813)
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100 , identity 100 , evalue 3.42e-295 , alnlength 412 ,
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FELTNSSVLTKEVKNKEGKVQEVVDEKGRNGELLYTSDDKKLSTHFSEIRDQNGNLEL
DKSLISVPIVFATSLAKVCTKLLTSLPIKLGKYLISEQNPIAKSFGYLLFTPAMAIKN
LVNMGATILKAPILLFVANEEKKYGDAYYTMWKHQLKGCLEEAKSDFNVIKGEERLKP
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CDS complement(17251..17628)
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Bacteria , Proteobacteria , WP_007548462.1 MULTISPECIES:
succinate dehydrogenase, cytochrome b556 subunit
[Wolbachia]"
/cog="SdhC COG2009 132 Succinate dehydrogenase/fumarate
reductase, cytochrome b subunit"
/pfam="Sdh_cyt"
/tigr="TIGR02970 succ_dehyd_cytB 120 succinate
dehydrogenase, cytochrome b556 subunit"
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dehydrogenase, cytochrome b556 subunit"
/translation="MSDRPLSPHLQIYKVQVTSFFSIMHRLTGILLFLLLMILSWYFI
LHVYFPELLIVRYLNALLFTPVAKLAYVLCFISFVYHFLNGIRHLLWDAGLNLEITGV
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Bacteria , Proteobacteria , WP_007548462.1 MULTISPECIES:
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[Wolbachia]"
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protein WPAU_1221 [Wolbachia endosymbiont of Drosophila
simulans wAu]"
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protein WPAU_1221 [Wolbachia endosymbiont of Drosophila
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CDS 19453..20001
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[unclassified Wolbachia]"
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KKDNKPLLEEIDSNWEYLANFERAFNHISDSMPDTTASIYNDLADDDKAPNVLRELAQ
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/cog="COG4649 COG4649 221 Uncharacterized protein
conserved in bacteria"
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similarity 100 , identity 100 , evalue 9.01e-124 ,
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WP_015589452.1 MULTISPECIES: hypothetical protein
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CDS complement(20406..20747)
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/codon_start=1
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100 , identity 100 , evalue 1.53e-79 , alnlength 113 ,
Bacteria , Proteobacteria , AAS13810.1 transposase, IS5
family, OrfB [Wolbachia endosymbiont of Drosophila
melanogaster]"
/cog="COG3293 COG3293 124 Transposase and inactivated
derivatives"
/pfam="DDE_Tnp_1_2 DDE_Tnp_1"
/product="transposase, IS5 family, OrfB"
/translation="MRTKYTKVKKMWADMGYQGRNLKNHIKEEYDIDIEIVKRPPCRF
WVHKDTPPELLPTREQGFKVQPRRWVVERTFAWVNRNRRLSKEYDLLTTSTENFIYLA
MSRVMLKREYA"
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, identity 100 , evalue 1.53e-79 , alnlength 113 ,
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family, OrfB [Wolbachia endosymbiont of Drosophila
melanogaster]"

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CDS       complement(20858..21238)
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99.2 , identity 99.2 , evalue 3.88e-86 , alnlength 126 ,
Bacteria , Proteobacteria , AOV87106.1 transposase
[Wolbachia endosymbiont of Drosophila incompta]"
          /cog="COG3293 COG3293 124 Transposase and inactivated
derivatives"
          /pfam="DUF4096"
          /product="transposase"
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CVLRTGCQWRYLPNDFPLWKTVYEQFRQWKKQGIFEKMNYEITKYSRRKIGRNEQPSA
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Bacteria , Proteobacteria , AOV87106.1 transposase
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gene      complement(21280..21435)
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CDS       complement(21280..21435)
          /locus_tag="wEsol_01123"
          /codon_start=1
          /transl_table=11
          /product="hypothetical protein"
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          /translation="MTFKGGCDKEVFNTWLEKMLLPKLPHGTTIVMDNATFHKTPTK
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44.6601941747573 , similarity 100 , identity 100 , evalue
4.03e-27 , alnlength 46 , Bacteria , Proteobacteria ,
WP_155968470.1 transposase [Wolbachia pipientis]"
gene      complement(21635..21982)
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CDS       complement(21635..21982)
          /locus_tag="wEsol_01124"
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          /transl_table=11
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100 , identity 100 , evalue 2.74e-74 , alnlength 115 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_155968342.1 MULTISPECIES: IS630 transposase-related
protein [Wolbachia]"
          /cog="COG3415 COG3415 138 Transposase and inactivated
derivatives"
          /pfam="HTH_Tnp_IS630 HTH_Tnp_1 HTH_23 HTH_28 HTH_29 HTH_7
CENP-B_N Pfam-B_14738 HTH_8 HTH_17 HTH_24 Pfam-B_2106"
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transposase-related protein"
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KKSYSISRASRR"
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Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_155968342.1 MULTISPECIES: IS630 transposase-related
protein [Wolbachia]"

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Proteobacteria , WP_213863572.1 ankyrin repeat
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gene      22376..24106
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[Wolbachia pipientis]"
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QQGGKHIVKILEETQKDIEALYSAVKSNDYKEVQSLLSKKVNVNSIDSNGKTPLHEAT
ASGHKEIVDALIKAGADVNIADKNGMVPLFKAAFYGHKDATEVLLNSGAKVDVTMESL
LQSMMEYNYNSSHKDVKALLNKGANADAVIDSYGHTLLHWAAREGYTDIAELLFKKGA
NVNIQDNDLWTPPLHFATKNKVFMGYADRPANASAETVKFLIKKGADVNIENEDGNTPF
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TTSAEQGTGVSNGSQPTGSTQNKGGQTSTTSAEQGTDVQDNDVGPVASTEPAQTEEQP
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similarity 100 , identity 99.8 , evaluate 9.67e-212 ,
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WP_155968555.1 ankyrin repeat domain-containing protein
[Wolbachia pipientis]"
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Transket_pyr Transketolase_C"
/tigr="TIGR00232 tktlase_bact 654 transketolase"
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SFAIEQAKKSDKPTMICCKTIIGKFSSRAGTSSAHSGAFSEEDIKQMKREKLNWNYEPF
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Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_010962555.1 MULTISPECIES: 30S ribosomal protein S4
[Wolbachia]"
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proteins"
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protein S4"
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GLVPTIYSAKQLISHKHVTVNDKVVNIS SYRVKPGDIIKIRERAAKIPVVVEAEQKQE
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[Wolbachia]"
gene 27121..27321
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100 , identity 100 , eval ue 3.24e-37 , alnlength 66 ,
Bacteria , Proteobacteria , WP_007552114.1 MULTISPECIES:
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conserved in bacteria"
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Bacteria , Proteobacteria , WP_007552114.1 MULTISPECIES:
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gene 27769..28110
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Bacteria , Proteobacteria , WP_006279619.1 MULTISPECIES:
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/cog="RpmB COG0227 77 Ribosomal protein L28"
/pfam="Ribosomal_L28"
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protein L28"
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ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE 1 (bases 1 to 1112)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL International Journal Molecular Sciences
REFERENCE 2 (bases 1 to 1112)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA
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100 , identity 100 , evaluate 2.85e-152 , alnlength 211 ,
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RKLHVMLNINNKKAI AVKYSNGVYSDHYGACDLLKEVDFQHA I KALYADRACDRHKFY
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ORIGIN

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1 acttaataaa attcctggat tccagtgggc tttgttgcat cgctcaagtg aaaagaactg
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901 aagatcttat attgaagggt ttttctcaag attaaagcaa atattcgga ttagttttag
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LOCUS      JAQZAU010000100      10271 bp      dna      linear      ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_50425, whole genome
            shotgun sequence.
ACCESSION  JAQZAU010000100  JAQZAU010000000
VERSION    JAQZAU010000100.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis

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Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 10271)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 10271)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University, 1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##

Assembly Date :: JUN-2019

Assembly Method :: FLYE v. 06-2019

Genome Representation :: Full

Expected Final Version :: Yes

Genome Coverage :: 100.0x

Sequencing Technology :: Illumina HiSeq; PacBio Sequel

##Genome-Assembly-Data-END##

FEATURES

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/mol_type="genomic DNA"

/submitter_seqid="contig_50425"

/isolate="wEsol"

/isolation_source="galls on Solidago altissima"

/host="Eurosta solidaginis MN-2018-EFC"

/db_xref="taxon:955"

/environmental_sample

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/lat_lon="44.48 N 93.13 W"

/altitude="280 m"

/collection_date="2018-11"

/metagenome_source="insect metagenome"

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CDS 66..347

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gene complement(614..1864)

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CDS complement(614..1864)

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EIEQSGDIDKFIEKAKDDKDPFKLMGFGRVYKKNYDPRARILKGACHEVLSKLEQNNE
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CDS complement(2266..2991)
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1-acyl-sn-glycerol-3-phosphate acyltransferase
[Wolbachia]"
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[Wolbachia]"
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CDS complement(3047..4033)
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Bacteria , Proteobacteria , WP_151808093.1 MULTISPECIES:
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/cog="XerD COG4974 300 Site-specific recombinase XerD"
/pfam="Phage_integr_N Phage_integr_N2 Pfam-B_15351
Phage_integrase Pfam-B_3560 Integrase_1 Pfam-B_6490"
/tigr="TIGR02225 recomb_XerD 290 tyrosine recombinase
XerD"
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recombinase"
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EFLLES GTTLVGVNKTNIKDYVKS LCTQKKYKSSSISRKISAMKNFYKCLFNDGIIDF
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VRDNLISKEKESDWLFPGDKPNKPITRQRVGQLMKELARKCNIDENKISPHVIRHSFA
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Bacteria , Proteobacteria , WP_007549057.1 MULTISPECIES:
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gene complement(4399..5034)
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synthase [Wolbachia endosymbiont of Ceratitidis capitata]"
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initiation"
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inactivator Hda"
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PKSSGKTHLAHIWQSINDAIFINNVNFVSEIRYSDAFILEDVQNIKDEAMLLHCYNM
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PurR regulon"
/pfam="UPF0118"
/tigr="TIGR02872 spore_ytvI 341 sporulation integral
membrane protein YtvI"
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transporter"
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MVITPVVFFYILRDWPLIIEKASKLIPIPYRGKIADYFSKVDFIISNYLKGQVNVCI
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AI-2E family transporter [Wolbachia]"
gene 6492..7631
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CDS 6492..7631
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93.9546599496222 , similarity 100 , identity 99.7 ,
evalue 2.22e-265 , alnlength 373 , Bacteria ,
Proteobacteria , WP_077188604.1 bifunctional
2-C-methyl-D-erythritol 4-phosphate
cytidyltransferase/2-C-methyl-D-erythritol

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2,4-cyclodiphosphate synthase [Wolbachia pipientis]"
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 NPDFVVIHDACRPFVSDVLIDNLVESMINDQYTGVPVPAIEVEDTMSLVNSNFIESTIS
 RGKLRAIQTPQIFNFKELLSCHQSVKEFTDDSSLMVEHKKHVAIIKGEKSNFKLTKE
 DINMAKLLFEPPKFRVAGYDIHKFIKVQNGAESFIKICGVKIEHNMAIEAHS DGDVA
 IHAIVDAILGALGCGDIGEHFPPSSSEWKDCNSSHFLDFAAKKAKEKGYSVSNLDITI
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 Proteobacteria , WP_077188604.1 bifunctional
 2-C-methyl-D-erythritol 4-phosphate
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 2,4-cyclodiphosphate synthase [Wolbachia pipientis]"

gene 7646..7888
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 of Carposina sasakii]"
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 of Carposina sasakii]"

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 28.1553398058252 , similarity 98.3 , identity 94.8 ,
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 GFR24199.1 n5-carboxyaminoimidazole ribonucleotide
 synthase [Trichonephila clavata]"

gene complement(8813..9334)
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9.83e-111 , alnlength 164 , Bacteria , Proteobacteria ,
WP_010082017.1 MULTISPECIES: 5-(carboxyamino)imidazole
ribonucleotide synthase [Wolbachia]"
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CDS complement(9312..9719)
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carboxylase, ATPase subunit"
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carboxylase (NCAIR synthetase)"
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WP_015589405.1 MULTISPECIES: 5-(carboxyamino)imidazole
ribonucleotide synthase [unclassified Wolbachia]"
gene 9816..10220
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Mg2+/Co2+ transport"
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efflux protein ApaG [Wolbachia endosymbiont of Drosophila
sechellia]"

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ORIGIN

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1  tatagtgctg acattagcca actgagaaac agagtTTTTTg accgagactt tggagcaaag
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121 tagagaatTTt ttctggagag gctgtattac aagaatTTTTg ggcaaacttg gtcattgtgca
181 atatattatc gcttcatatg tgtgatgcac aagggccttg gaaccagat caaattactg
241 agtatcgTTt aaatTTTTtca gTTTTatttg gtgtaatgag gcagaaactc tatcaggtac
301 ttattgCGcc aaaaaacttt caagcccttt ttaagtatac gcgctaaagt taaaatccga
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421 ctaatgaaag ttcttaagtt gacgtcattg gctgaacgga tacggaatga caccatcctt
481 ttttctggat tccagactgg aatgacacct ctggacactt ccgtcgtaaa ggaaccagtg
541 tcagctactc ggatgacacc ttttttctac ttagtttggg ttatgcaaga agtctaataga
601 agtgaaaata aatttatTTa ccaaaataga gttgccttg tctacagatc ttagtttctt
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KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.

SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 1500)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 1500)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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VERSION JAQZAU010000102.1
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 BioSample: SAMN33142973
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 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
 REFERENCE 1 (bases 1 to 8920)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 8920)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
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 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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[Wolbachia]"

ORIGIN

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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM    Wolbachia pipientis
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REFERENCE  1  (bases 1 to 17784)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE       Genomic assessment of the contribution of the Wolbachia
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JOURNAL     International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 17784)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE       Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT     ##Genome-Assembly-Data-START##
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            Assembly Method     :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
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CDS

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ORIGIN

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LOCUS      JAQZAU010000104          46040 bp    dna        linear    ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_51892, whole genome
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ACCESSION  JAQZAU010000104  JAQZAU010000000
VERSION    JAQZAU010000104.1
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 46040)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 46040)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

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TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
 ##Genome-Assembly-Data-END##
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Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit Gata
[unclassified Wolbachia]"
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 tRNA (N(6)-L-threonylcarbamoyladenosine(37)-C(2))-
 methylthiotransferase MtaB [unclassified Wolbachia]"
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 EVDDDELMDLIANESRLMPHLHLSLQSGNNLILKRMKRRHNREQVIEFYHKMKSLRPNI
 AFGADIIAGFPTETDEMFDQTDVLLKKINVVYLHAFYPYSERKNTPAARMPQIPENVRK
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 Drosophila simulans wHa]"
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 LETDNDES VIRSEEVTAKIPIKYQELESSPPSVFQVADQKNMWSRIADQAEPTKEKS
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 FDGKIDFQWFSSMSLGYYAGENGKIDFEAAYS IANIEDSNSPPVFDKSASIFAFLNLF
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Pfam-B_1714 Ank_5 Ank Ank_3 Ank_4 Ank_2 Ank_5 Ank Ank_3
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Wolbachia]"
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DVGIIGMPNAGKSKFLTRCSNSDTKVGDPFTTVRPHLGMVKVDDSEVVIADIPGIIT
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gene complement(16637..16861)
/locus_tag="wEsol_01203"
CDS complement(16637..16861)
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100 , identity 100 , evalue 3.25e-45 , alnlength 74 ,
Bacteria , Proteobacteria , WP_015588949.1 MULTISPECIES:
BolA/IbaG family iron-sulfur metabolism protein
[Wolbachia]"
/cog="BolA COG0271 90 Stress-induced morphogen (activity
unknown)"
/pfam="BolA"
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iron-sulfur metabolism protein"
/translation="MTIAIHELIERIIKQSFDPADIKIHDLAGDDDHHLKINSKCFLG
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, identity 100 , evalue 3.25e-45 , alnlength 74 ,
Bacteria , Proteobacteria , WP_015588949.1 MULTISPECIES:
BolA/IbaG family iron-sulfur metabolism protein
[Wolbachia]"

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CDS       17026..17898
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100 , identity 100 , evaluate 1.60e-211 , alnlength 290 ,
Bacteria , Proteobacteria , WP_080717615.1 MULTISPECIES:
P44/Msp2 family outer membrane protein [Wolbachia]"
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GDNITEGVFSFNKKERIEAGYSPKYVPGFAGSAAIGYLFKNMRVEFEGLYSQTNLYDE
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FNNLAGMVNVYRDFNIAKMPFTPYPVGIGAGVTRVKFLGKTRYALAYQAKLGINHQLTA
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outer membrane protein"
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CDS       complement(17913..19235)
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100 , identity 100 , evaluate 0.0 , alnlength 440 ,
Bacteria , Proteobacteria , WP_015588951.1 MULTISPECIES:
NADP-dependent malic enzyme [unclassified Wolbachia]"
          /cog="SfcA COG0281 432 Malic enzyme"
          /pfam="malic malic ELFV_dehydrog Malic_M"
          /product="NADP-dependent
malic enzyme"
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KSMGKDPIIFALANPDPEVRPEFAKSVRPDAIIATGRSDYNNQVNNVMGFPYIFRGAL
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Proteobacteria , WP_015588951.1 MULTISPECIES:
NADP-dependent malic enzyme [unclassified Wolbachia]"
gene      19316..19912
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CDS       19316..19912
          /locus_tag="wEsol_01206"
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evaluate 7.84e-130 , alnlength 197 , Bacteria ,
Proteobacteria , EAL58732.1
CDP-diacylglycerol-glycerol-3-phosphate

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3-phosphatidyltransferase [Wolbachia endosymbiont of
Drosophila ananassae]"
/cog="PgsA COG0558 192 Phosphatidylglycerophosphate
synthase"
/pfam="CDP-OH_P_transf"
/tigr="TIGR00560 pgsA 183
CDP-diacylglycerol--glycerol-3-phosphate
3-phosphatidyltransferase"
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CDP-diacylglycerol-glycerol-3-phosphate
3-phosphatidyltransferase"
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CDP-diacylglycerol-glycerol-3-phosphate
3-phosphatidyltransferase [Wolbachia endosymbiont of
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CDS 20024..20965
/locus_tag="wEsol_01207"
/codon_start=1
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/pfam="DcuC DUF2207"
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ALVIVGMIMGETSSLEAAEDAILFLANAIAFLATLVSYIDKHEKNKKKETEKSDLDEK
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gene 21026..21733
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CDS 21026..21733
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100 , identity 100 , evalue 3.83e-162 , alnlength 235 ,
Bacteria , Proteobacteria , WP_015588954.1 MULTISPECIES:
outer membrane protein assembly factor BamD [unclassified
Wolbachia]"
/cog="ComL COG4105 254 DNA uptake lipoprotein"
/pfam="YfiO TPR_18 Apc3 TPR_11 TPR_2 TPR_1 TPR_16 RPN7"
/tigr="TIGR03302 OM_YfiO 239 outer membrane assembly
lipoprotein YfiO"
/product="outer membrane

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protein assembly factor BamD"
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Wolbachia]"
gene 21794..22534
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CDS 21794..22534
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100 , identity 100 , evalue 9.42e-173 , alnlength 246 ,
Bacteria , Proteobacteria , WP_015588955.1 MULTISPECIES:
YebC/PmpR family DNA-binding transcriptional regulator
[unclassified Wolbachia]"
/cog="COG0217 COG0217 241 Uncharacterized conserved
protein"
/pfam="Transcrip_reg"
/tigr="TIGR01033 TIGR01033 238 DNA-binding regulatory
protein, YebC/PmpR family"
/product="YebC/PmpR family
DNA-binding transcriptional regulator"
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LNPRLSAIFAARKENLPKDKIETAIKNATGNVAGENYEEIIQYEGHGPGSGTALIVHAL
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KLSALVEELEDNDDVQYVEGNFTFVDKL"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
, identity 100 , evalue 9.42e-173 , alnlength 246 ,
Bacteria , Proteobacteria , WP_015588955.1 MULTISPECIES:
YebC/PmpR family DNA-binding transcriptional regulator
[unclassified Wolbachia]"
gene 22641..23468
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CDS 22641..23468
/locus_tag="wEsol_01210"
/codon_start=1
/transl_table=11
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, similarity 100 , identity 99.6 , evalue 4.90e-196 ,
alnlength 275 , Bacteria , Proteobacteria ,
WP_015588956.1 MULTISPECIES: M23 family metallopeptidase
[unclassified Wolbachia]"
/cog="NlpD COG0739 277 Membrane proteins related to
metalloendopeptidases"
/pfam="Peptidase_M23"
/product="M23 family
metallopeptidase"
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FKKDIVPESKLEVLFRLPNNQKTEEKILYASLTINKKAISLYHYKSQDGKERYFNKE
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IEYIGKNGGYGNYIKIKHKNEYSTCYAHISRFSGDIKLGSKVKQGQVIAYVGSTGVAT
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WP_015588956.1 MULTISPECIES: M23 family metallopeptidase
[unclassified Wolbachia]"
gene 23452..24321
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CDS 23452..24321
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99.7 , identity 99.7 , evalue 6.85e-192 , alnlength 289 ,
Bacteria , Proteobacteria , AGJ99770.1 SPFH domain/Band 7
family protein [Wolbachia endosymbiont of Drosophila
simulans wHa]"
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TIALGVAAVSILTFLQGFFINDPNEARVIEFFGHYIGTYFKSGICVTLPFSSKYIVSL
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ASNYPYDSESEESLRKNSDKISDELRSMLQQRLDIAGIEITEARISHLAYSSIEIAQA
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EQDAQPKISLDNN"
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Bacteria , Proteobacteria , AGJ99770.1 SPFH domain/Band 7
family protein [Wolbachia endosymbiont of Drosophila
simulans wHa]"
gene 24489..24764
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100 , identity 100 , evalue 2.28e-55 , alnlength 91 ,
Bacteria , Proteobacteria , WP_006280002.1 MULTISPECIES:
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/cog="COG4095 COG4095 89 Uncharacterized conserved
protein"
/pfam="PQ-loop MtN3_slv"
/product="hypothetical protein"
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Bacteria , Proteobacteria , WP_006280002.1 MULTISPECIES:
hypothetical protein [Wolbachia]"
gene 24745..25245
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CDS 24745..25245
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pyrophosphokinase"
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LGIPRA"
/cog="THI80 COG1564 212 Thiamine pyrophosphokinase"
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similarity 100 , identity 100 , evalue 2.31e-114 ,
alnlength 166 , Bacteria , Proteobacteria ,
WP_070356831.1 thiamine diphosphokinase [Wolbachia
endosymbiont of Drosophila incompta]"
gene 25848..26177
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CDS 25848..26177
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100 , identity 100 , evalue 4.31e-75 , alnlength 109 ,
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transposase [unclassified Wolbachia]"
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gene 26161..26796
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CDS 26161..26796
/locus_tag="wEsol_01215"
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/transl_table=11
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100 , identity 100 , evalue 2.85e-152 , alnlength 211 ,
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transposase [unclassified Wolbachia]"
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Bacteria , Proteobacteria , WP_081600764.1 MULTISPECIES:
transposase [unclassified Wolbachia]"
gene 27798..29201
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CDS 27798..29201
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/transl_table=11
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100 , identity 100 , evalue 0.0 , alnlength 467 ,
Bacteria , Proteobacteria , WP_015588958.1 MULTISPECIES:
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/translation="MTKESLVKTDIVKVEDKKAVRSFFKILGGVADAVRSWIGNISPD

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SDVLKLKNQYRSLNPLESELKNILYTWVDVDLLDLRQITWDSPASLLEKLIKYEAVHK
ISSWGDLDKNRLDSRCLCAFFHYKIPNEPLIFVEVALVDKIADSIQHLLDESVPSPNDP
SNASTAIFYSISNTQAGLSGISLGNFLIKRVVEKLSQEFKSIKTYATLSPIPGFTKWL
KNNLNQDVTLLGKLNKQSSAEILESAAEQKTNVECTNETKQYMLKLCAYYLLKVNS
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decarboxylase"
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Proteobacteria , WP_015588958.1 MULTISPECIES: malonyl-CoA
decarboxylase [unclassified Wolbachia]"
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/cog="LepA COG0481 603 Membrane GTPase LepA"
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LepA_C"
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elongation factor 4"
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ISAKTGLGIKDVLEAIVAKLPAPQGDVNAPLQAILVDSWYD TYLGVVILVRVKNGLVK
KGMKIVMSNNATYQIDNIGIFT PKKVM TGELSAGEVGFITASMKEVADCKVGD TITE
EKRPCSKALPGFKEVHPVVFCSIFPHKTDDFKYLREALEKLHLNDASFTFEAETSNA L
GYGFR CGFLGMLHLEVIQERLEREFDDLDTATAPSVIYRVTTTRS GEVLNIHNPSDMPD
PTKIEIVEEPWITATIMVPDQYLGEILSLCEERRGEQEDLSYIGNTTTALLRYKLPLS
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Proteobacteria , WP_015588959.1 MULTISPECIES: translation
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CDS complement(31762..31935)
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98.2 , identity 98.2 , eval 3.35e-24 , alnlength 57 ,
Bacteria , Proteobacteria , WP_218937023.1 hypothetical
protein [Wolbachia endosymbiont of Carposina sasakii]"
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AIFIIAAAISAAK"
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gene Bacteria , Proteobacteria , WP_218937023.1 hypothetical protein [Wolbachia endosymbiont of Carposina sasakii]"
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CDS complement(31919..32026)
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gene 32052..32456
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CDS 32052..32456
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gene 33183..33563
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/translation="MNPTIKRIFNIFLIVLFISFSHVGSAAADTNTDTTAQVICNIIGYVWGIGGPLMTVVIIGAALLAIFGRMPWPALFALGIFCAVFFGAKTIVIKVMGGIGGTGNTSLMDQCGTGDTKKNYFFLKQT"
/product="TrbC/VirB2 family protein"
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CDS complement(33539..34537)
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100 , identity 100 , evalue 8.46e-235 , alnlength 332 ,
 Bacteria , Proteobacteria , WP_015588962.1 MULTISPECIES:
 pyruvate dehydrogenase complex E1 component subunit beta
 [unclassified Wolbachia]"
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 dehydrogenase complex, dehydrogenase (E1) component,
 eukaryotic type, beta subunit"
 /pfam="Transket_pyr Transketolase_C"
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 synthase"
 /product="pyruvate
 dehydrogenase complex E1 component subunit beta"
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 VERSION JAQZAU010000105.1
 DBLINK BioProject: PRJNA929258
 BioSample: SAMN33142973
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 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
 REFERENCE 1 (bases 1 to 607)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 607)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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ORIGIN

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ACCESSION  JAQZAU010000106  JAQZAU010000000
VERSION    JAQZAU010000106.1
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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 4657)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 4657)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method     :: FLYE v. 06-2019
            Genome Representation :: Full
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Genome Coverage :: 100.0x
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FEATURES

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ORIGIN

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VERSION    JAQZAU010000107.1
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 8641)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia

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endosymbiont of *Eurosta solidaginis* to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 8641)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
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ORIGIN

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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 1834)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 1834)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##

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Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
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 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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VERSION    JAQZAU010000109.1
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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.

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SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 13798)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 13798)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##

FEATURES Location/Qualifiers

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/host="Eurosta solidaginis MN-2018-EFC"
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Northfield, MN"
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CDS complement(<1..1041)
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WP_038198650.1 MULTISPECIES: hypothetical protein
[Wolbachia]"

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81.0444874274662 , similarity 99.8 , identity 99.8 ,
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similarity 98.9 , identity 98.4 , evaluate 2.83e-163 ,
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CDS

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partial [Wolbachia endosymbiont of Muscidifurax
uniraptor]"
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family protein [unclassified Wolbachia]"
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derivatives"
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ORIGIN

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ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
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REFERENCE 1 (bases 1 to 15074)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 15074)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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N-acetyltransferase"
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UDP-N-acetylglucosamine pyrophosphorylase [Wolbachia
endosymbiont of *Drosophila ananassae*]"

ORIGIN

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VERSION    JAQZAU010000112.1
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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 40382)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 40382)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes

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Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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WP_155968342.1 MULTISPECIES: IS630 transposase-related
protein [Wolbachia]"
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CDS 12022..12333
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CDS complement(12458..13072)
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, similarity 100 , identity 100 , eval 1.02e-143 ,
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WP_227738579.1 DUF1016 domain-containing protein
[Wolbachia endosymbiont of Drosophila simulans]"
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RDMNKPIGLAEYRITENLPENIKTALPTIEELEAELSKISDEEK"
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protein"
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CDS complement(13077..13481)
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Bacteria , Proteobacteria , WP_227738580.1 DUF1016
N-terminal domain-containing protein [Wolbachia
endosymbiont of Drosophila simulans]"
/cog="COG4804 COG4804 159 Predicted nuclease of
restriction endonuclease-like fold"
/pfam="DUF1016"
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domain-containing protein"
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CDS complement(14478..14816)
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Pfam-B_17238 Pfam-B_2938"
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outer membrane protein assembly factor BamE [Wolbachia]"
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CDS 14948..15937
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[Wolbachia]"
/cog="NrdF COG0208 348 Ribonucleotide reductase, beta
subunit"
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/tigr="TIGR04171 RNR_1b_NrdF 316
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subunit"
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KTKLSSVEKNLLTQIFRFFTQADIEVNNCYMRHYSNIFKPTEICMMLASFNMETIHI
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CDS 16076..17206
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[unclassified Wolbachia]"
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/pfam="SDF"
/product="
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TYEETIVPLWSFRLPLLLSNFYALACGFVSSIVVSTLLPKKSKELSNKMLDLTLFILK
TFLTPIIPIFVLGLALKMQHDQVLSIIFKDYSIIFIIIASATYLYVFLLYGAANSFKV
TSWIASIGNMIPAFITAMSTMSSNATMPLTLEGSKKNVKQPDIASSVVPITASFHLVG
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Bacteria , Proteobacteria , WP_015588889.1 MULTISPECIES:
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[unclassified Wolbachia]"
gene 17206..17790
/locus_tag="wEsol_01317"
CDS 17206..17790
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100 , identity 100 , evaluate 3.11e-134 , alnlength 194 ,
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complex dimerization subunit type 1 TsaB [unclassified
Wolbachia]"
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TLFNKHNINYDKIDHLAVVVGPGSFTGIRVGISAAQGINLATNKPLYGVSALEVQAYA
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complex dimerization subunit type 1 TsaB [unclassified
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obscurior]"
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NDQNMRMYDSIVRLSKKMGTEILPVVLRCDLLTLQKRIALKRQRKNRRVINVNNVIEK
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CDS       18692..19399
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, similarity 100 , identity 99.6 , evalue 2.71e-169 ,
alnlength 235 , Bacteria , Proteobacteria ,
WP_174516961.1 class II aldolase/adducin family protein
[Wolbachia endosymbiont of Cardiocondyla obscurior]"
          /cog="AraD COG0235 219 Ribulose-5-phosphate 4-epimerase
and related epimerases and aldolases"
          /pfam="Aldolase_II"
          /tigr="TIGR01086 fucA 214 L-fuculose phosphate aldolase"
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protein"
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SIVAVSSSLKDGLLPISQWALHFY NKISYHNYNSLALSDTEGKR LIADLKENFVMLMRN
HGSITCGRSIQEAMFYTYHLEQACKTQCLTLAMNKELSIPSEE ICSKAVKDLLSFESN
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WP_174516961.1 class II aldolase/adducin family protein
[Wolbachia endosymbiont of Cardiocondyla obscurior]"
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100 , identity 100 , evalue 5.41e-20 , alnlength 44 ,
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derivatives"
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Proteobacteria , ONI56748.1 hypothetical protein
N500_0187 [Wolbachia pipientis wUni]"
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CDS complement(19732..20073)
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Bacteria , Proteobacteria , AAS13810.1 transposase, IS5
family, OrfB [Wolbachia endosymbiont of Drosophila
melanogaster]"
/cog="COG3293 COG3293 124 Transposase and inactivated
derivatives"
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CDS complement(20184..20564)
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CDS complement(20606..20761)
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44.6601941747573 , similarity 100 , identity 100 , evalue
4.03e-27 , alnlength 46 , Bacteria , Proteobacteria ,
WP_155968470.1 transposase [Wolbachia pipientis]"
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derivatives"
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protein [Wolbachia]"
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Bacteria , Proteobacteria , WP_141456877.1 MULTISPECIES:
DNA repair protein RecO [unclassified Wolbachia]"
/cog="RecO COG1381 251 Recombinational DNA repair protein
(RecF pathway)"
/pfam="RecO_N RecO_N_2 RecO_C"
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SEPCAVLYDNFRYFIDVIKHNNQSWQSHYLNLELLLLLTQLGFKLDLSKCAVTGVKENL
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, identity 99.6 , evalue 1.57e-168 , alnlength 240 ,
Bacteria , Proteobacteria , WP_141456877.1 MULTISPECIES:
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gene complement(22956..24338)
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CDS complement(22956..24338)
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Bacteria , Proteobacteria , WP_015588886.1 MULTISPECIES:
PleD family two-component system response regulator
[unclassified Wolbachia]"
/cog="PleD COG3706 435 Response regulator containing a
CheY-like receiver domain and a GGDEF domain"
/pfam="Pfam-B_11357 Response_reg Pfam-B_18970
Response_reg GGDEF"
/product="PleD family two-component system response regulator"
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YFKMVNDSFGHSAGDELLKQIQRRISENIRVTDLLARFGGEEFVVVMPDTS DAYTI
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Proteobacteria , WP_015588886.1 MULTISPECIES: PleD family
two-component system response regulator [unclassified
Wolbachia]"
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CDS

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obscurior]"
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dehydrogenase"
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ORIGIN

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SOURCE     Wolbachia pipientis (insect metagenome)
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REFERENCE  1  (bases 1 to 9509)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 9509)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
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COMMENT     ##Genome-Assembly-Data-START##

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Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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FEATURES

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VERSION    JAQZAU010000114.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 800)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 800)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019

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Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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ACCESSION  JAQZAU010000115  JAQZAU010000000
VERSION    JAQZAU010000115.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 6957)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 6957)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage    :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL  International Journal Molecular Sciences
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  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
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            1600 Holloway Ave, San Francisco, CA 94132, USA
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            Assembly Date          :: JUN-2019
            Assembly Method        :: FLYE v. 06-2019
            Genome Representation   :: Full
            Expected Final Version :: Yes
            Genome Coverage        :: 100.0x
            Sequencing Technology  :: Illumina HiSeq; PacBio Sequel
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LOCUS JAQZAU010000117 17868 bp dna linear ENV 17-MAR-2023

DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_55920, whole genome
shotgun sequence.

ACCESSION JAQZAU010000117 JAQZAU010000000

VERSION JAQZAU010000117.1

DBLINK BioProject: PRJNA929258

BioSample: SAMN33142973

KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.

SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis

Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 17868)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 17868)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##

Assembly Date :: JUN-2019

Assembly Method :: FLYE v. 06-2019

Genome Representation :: Full

Expected Final Version :: Yes

Genome Coverage :: 100.0x

Sequencing Technology :: Illumina HiSeq; PacBio Sequel

##Genome-Assembly-Data-END##

FEATURES Location/Qualifiers

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Wolbachia]"
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REFERENCE  1  (bases 1 to 9730)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
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  JOURNAL  International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 9730)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Direct Submission
  JOURNAL  Submitted (10-FEB-2023) Biology, San Francisco State University,
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VERSION    JAQZAU010000119.1
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SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 3029)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences

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REFERENCE 2 (bases 1 to 3029)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University, 1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##

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ORIGIN

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ORGANISM   Wolbachia pipientis
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REFERENCE  1  (bases 1 to 12663)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 12663)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
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            Assembly Method        :: FLYE v. 06-2019
            Genome Representation   :: Full
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VERSION    JAQZAU010000121.1
DBLINK     BioProject: PRJNA929258
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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 24412)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia

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endosymbiont of *Eurosta solidaginis* to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 24412)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University, 1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##

Assembly Date :: JUN-2019

Assembly Method :: FLYE v. 06-2019

Genome Representation :: Full

Expected Final Version :: Yes

Genome Coverage :: 100.0x

Sequencing Technology :: Illumina HiSeq; PacBio Sequel

##Genome-Assembly-Data-END##

FEATURES

Location/Qualifiers

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/db_xref="taxon:955"

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/lat_lon="44.48 N 93.13 W"

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CDS 10392..10739
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protein [Wolbachia]"
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derivatives"
/pfam="HTH_Tnp_IS630 HTH_Tnp_1 HTH_23 HTH_28 HTH_29 HTH_7
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protein [Wolbachia]"
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CDS 10939..11250
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evalue 2.79e-13 , alnlength 35 , Bacteria ,
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protein, partial [Wolbachia endosymbiont of Drosophila
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gene complement(11392..14187)
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CDS complement(11392..14187)
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sasakii]"
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endosymbiont of Carposina sasakii]"
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Wolbachia]"
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[Wolbachia pipientis]"

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CDS 23336..23683

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sp. wRi_2]"

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ORIGIN

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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 927)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

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TITLE Genomic assessment of the contribution of the Wolbachia endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 927)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University, 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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melanogaster]"

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VERSION    JAQZAU010000123.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 6217)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 6217)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method     :: FLYE v. 06-2019

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Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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FEATURES

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synthetase,Prolyl-tRNA synthetase,serine--tRNA
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and T) [Wolbachia endosymbiont of Drosophila simulans
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REFERENCE  1 (bases 1 to 15804)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

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TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 15804)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
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REFERENCE 1 (bases 1 to 16702)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Genomic assessment of the contribution of the Wolbachia endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 16702)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University, 1600 Holloway Ave, San Francisco, CA 94132, USA

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Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
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Cardiocondyla obscurior]"
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MFS_3"
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transporter, Bcr/CflA subfamily"
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transporter"
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WP_007548640.1 MULTISPECIES: peptide chain release factor
1 [Wolbachia]"
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release factor 1"
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, identity 100 , evaluate 1.01e-219 , alnlength 359 ,
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CDS 7928..8521
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[Wolbachia]"
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[Wolbachia]"
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/cog="Dut COG0756 148 dUTPase"
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gene 10392..11009
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CDS 10392..11009
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WP_155969116.1 MULTISPECIES: hypothetical protein
[Wolbachia]"
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CDS complement(11239..11646)
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Bacteria , Proteobacteria , WP_174516160.1 MULTISPECIES:
transposase [unclassified Wolbachia]"
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Bacteria , Proteobacteria , WP_174516160.1 MULTISPECIES:
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CDS complement(11769..11858)
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gene      complement(12874..13302)
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        /tigr="TIGR00114 lumazine-synth 138
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        YidC [unclassified Wolbachia]"
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protease, TIGR02281 family"
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clan AA aspartic protease"
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Wolbachia]"
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Wolbachia]"

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ORIGIN

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VERSION    JAQZAU010000129.1
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 9299)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 9299)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT     ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method     :: FLYE v. 06-2019

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Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##

FEATURES

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CDS	250..552 /locus_tag="wEsol_01516" /codon_start=1 /transl_table=11 /fullproduct="qcoverage 100 , hcoverage 100 , similarity 100 , identity 99.0 , evalue 3.32e-59 , alnlength 100 , Bacteria , Proteobacteria , WP_015588788.1 MULTISPECIES: 50S ribosomal protein L21 [unclassified Wolbachia]" /cog="RplU COG0261 103 Ribosomal protein L21" /pfam="Ribosomal_L21p" /tigr="TIGR00061 L21 101 ribosomal protein L21" /product="50S ribosomal protein L21" /translation="MFAVIETGGKQYLVKEGSIKVEKLEAEKKEVEINKVICISNN GLSYSSNATVKAEMLQQCRGEKIIIFKKKRRKNYRRKTGHRQYITVLRINEISLQK" /besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 99.0 , evalue 3.32e-59 , alnlength 100 , Bacteria , Proteobacteria , WP_015588788.1 MULTISPECIES: 50S ribosomal protein L21 [unclassified Wolbachia]"
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protein"
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100 , identity 100 , evalue 3.07e-197 , alnlength 275 ,
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oxidase, subunit 3"
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Mycoplasmas and B. subtilis)"
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resolvase RuvX"
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ORGANISM   Wolbachia pipientis
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REFERENCE  1 (bases 1 to 10932)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 10932)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
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ACCESSION  JAQZAU010000131  JAQZAU010000000
VERSION    JAQZAU010000131.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 17023)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 17023)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage    :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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FEATURES   Location/Qualifiers
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CDS

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VERSION    JAQZAU010000132.1
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 7520)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 7520)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission

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JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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FEATURES Location/Qualifiers

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ORIGIN

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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
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REFERENCE  1 (bases 1 to 5804)

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AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 5804)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
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SOURCE     Wolbachia pipientis (insect metagenome)

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ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 4152)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 4152)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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ORIGIN

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VERSION    JAQZAU010000135.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
  ORGANISM Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
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  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL  International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 7050)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Direct Submission
  JOURNAL  Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
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            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage    :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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ORIGIN

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VERSION    JAQZAU010000137.1
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SOURCE     Wolbachia pipientis (insect metagenome)
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AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 14517)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
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COMMENT     ##Genome-Assembly-Data-START##
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 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
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 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 4835)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
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ENV 17-MAR-2023

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 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 4396)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
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 1600 Holloway Ave, San Francisco, CA 94132, USA
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CDS       149..814
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        KEIPFSHQLEQKTRQEGINASASATVYTDREIPTSNQSEQKVQQEIIINTST SAPVLQI
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gene      complement(2140..2823)
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[Wolbachia endosymbiont of Pissodes strobi]"

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ORIGIN

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Wolbachia]"
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dehydrogenase/methenyltetrahydrofolate cyclohydrolase
Fold [unclassified Wolbachia]"
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dehydrogenase/methenyltetrahydrofolate cyclohydrolase

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evaluate 9.00e-06 , alnlength 49 , Bacteria ,
Proteobacteria , OAL97015.1 hypothetical protein
TV42_05260 [Wolbachia endosymbiont of Dactylopius
coccus]"

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ORIGIN

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DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_7860, whole genome
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VERSION JAQZAU010000141.1
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KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE Wolbachia pipientis (insect metagenome)
ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE 1 (bases 1 to 1372)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL International Journal Molecular Sciences
REFERENCE 2 (bases 1 to 1372)
AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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ACCESSION  JAQZAU010000142 JAQZAU010000000
VERSION    JAQZAU010000142.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 19308)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 19308)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
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            Sequencing Technology :: Illumina HiSeq; PacBio Sequel

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DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_7865, whole genome
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ACCESSION  JAQZAU010000143  JAQZAU010000000
VERSION    JAQZAU010000143.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973

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KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
 REFERENCE 1 (bases 1 to 1979)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 1979)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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 /db_xref="taxon:955"
 /environmental_sample
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 Northfield, MN"
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ananassae]"

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ORIGIN

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961  cttttttctt  gtgttataat  tgagtcgatt  atctccactt  tttcagaaat  cattggcaaa
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1201 gggttaagcg gatcattcac aataataaag tcaccacctt caccggttaa tggtcctcca
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LOCUS      JAQZAU010000144                650 bp    dna        linear    ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_7919, whole genome
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ACCESSION  JAQZAU010000144  JAQZAU010000000
VERSION    JAQZAU010000144.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 650)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 650)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage    :: 100.0x
            Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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          Nasonia oneida]"

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ORIGIN

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ACCESSION  JAQZAU010000145  JAQZAU010000000
VERSION    JAQZAU010000145.1
DBLINK     BioProject: PRJNA929258
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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 2034)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 2034)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes

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Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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ORIGIN

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DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_11070, whole genome
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 ACCESSION JAQZAU010000146 JAQZAU010000000
 VERSION JAQZAU010000146.1
 DBLINK BioProject: PRJNA929258
 BioSample: SAMN33142973
 KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Wolbachieae; Wolbachia.
 REFERENCE 1 (bases 1 to 4767)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 4767)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
 COMMENT ##Genome-Assembly-Data-START##
 Assembly Date :: JUN-2019
 Assembly Method :: FLYE v. 06-2019
 Genome Representation :: Full
 Expected Final Version :: Yes
 Genome Coverage :: 100.0x
 Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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ORIGIN

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4021 gattaaacga aaaacgactt gacaaactcc gccagctccc ttataatgac aataagggtg
4081 tttatgactc aaaacttggt tttgacctgc aggtcgaatg acaaaaattc gtaaaaaact
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4261 gtaatataga gtcaaaaact gctactcggg gcttcttttg cttttttttc atttggtaaa
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4381 gaattttatc aagtataaaa gttatgttaa aatgcaccat ttatggaaaa ctagatccca
4441 gtgtctgggc actgggatga catcataggg gcaactggat gacacccttt cctagatgga
4501 gataaattac aatgtttgta cagttatggg attgcgcagt ggatgcagtt taacataaaa
4561 agctttgctt tttgaaattt tgggttatac gcaacttcaa cactattagc aggggtaatg
4621 atcatgaata aagaagaagc tttaaaaatt ttggaaacta cagatagcca tgacgttatc
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LOCUS JAQZAU010000147 2076 bp dna linear ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_12111, whole genome

shotgun sequence.

ACCESSION JAQZAU010000147 JAQZAU010000000

VERSION JAQZAU010000147.1

DBLINK BioProject: PRJNA929258
BioSample: SAMN33142973

KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.

SOURCE Wolbachia pipientis (insect metagenome)

ORGANISM Wolbachia pipientis
Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 2076)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia
endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 2076)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2019
Assembly Method :: FLYE v. 06-2019
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
##Genome-Assembly-Data-END##

FEATURES Location/Qualifiers

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/host="Eurosta solidaginis MN-2018-EFC"
/db_xref="taxon:955"
/environmental_sample
/country="USA: Cowling Arboretum, Carleton College,
Northfield, MN"
/lat_lon="44.48 N 93.13 W"
/altitude="280 m"
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CDS 354..770
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Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
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[Wolbachia endosymbiont of Pissodes strobil]"
/translation="MAESIVEKCTEQVSNRFLVLLASQRTDHLNTGASNPVQTVQFK
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        superfamily [Wolbachia pipientis]"
        /cog="MnhF COG2212 89 Multisubunit Na+/H+ antiporter,
        MnhF subunit"
        /pfam="MrpF_PhaF"
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        regulation protein F (MrpF / PhaF) superfamily"
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        superfamily [Wolbachia pipientis]"
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        /codon_start=1
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 LIMNAPDVAITEASVGAGLSTIFTFAALSLIKNHKVNLSHNPITLFILS"
 /cog="COG1563 COG1563 87 Predicted subunit of the
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 [Wolbachia pipientis]"

ORIGIN

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121 ttgatcagcc aaaggatatca caaattaaaa atggtaaaat agatgggttt tcttttagagc
181 gattgttagg atttctaaaa aaacttgatc atgaaataac aatcacgatg acagaaagcc
241 aagaaataaa atctgaggca gaaaaagtaa aacatgaagt tgaatcgcaa tagatacaaa
301 gttgacaact tgttttttgt gatatagtat aaaacttatt aaggtagtat cttatggctg
361 agtctattgt agaaaagtgt acagaacagg taagtaaccg tttcaaattg gttctattgg
421 caagtcaaag aacacatgat ttaaatacag gagcaagtaa tccagttcaa acagttcagt
481 ttaaagacca taaaaacacc atagtttcct tatatgaaat agcagaaaaa caggtaggata
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601 ataatgttta cagcagtaat acaagtaagc tagcgaattt attaaatttt tctgatggtc
661 aatttaacac agatcttgat gcaagtcaag aaagccaaga ttatgaagtg gatggtgaaa
721 tagatgatga aataaatgat caagatggcg atgaagaagt atccgtttag aaatctactg
781 aagttacata gtcttttaaat gcttcacatt gctatctata cactgttggt ctgtatgagt
841 ataatgttgt gccgcatagt gtctaagtca agtgatgtgt acaataagggt tttagcggtc
901 aataatttct caacgcaagt agttgtactc ataacagcaa tatcaatcat tctgaataat
961 ttttttttaa ttgatatagc attggtgtat gctagcggtt gctttatatc aactatagca
1021 ctaatgagat taatgttggt ttaataattt atgataggat ccgttcttat attttttaggc
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1381 aacagttacg gttttttatag tcttctcgcg acatttagtc gtaagtgtgt ttctaagtgt
1441 tgtatttagt tcacttattg cgcttatata cttaattatg aatgcacctg atgttgcaat
1501 tactgaagct tctgttggtg cggggctcag tacgattttt acgtttgcag cactctcctt
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LOCUS JAQZAU010000148 2076 bp dna linear ENV 17-MAR-2023
 DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_1398, whole genome
 shotgun sequence.
 ACCESSION JAQZAU010000148 JAQZAU010000000
 VERSION JAQZAU010000148.1
 DBLINK BioProject: PRJNA929258
 BioSample: SAMN33142973
 KEYWORDS WGS; ENV; Metagenome Assembled Genome; MAG.
 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
 Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;

Anaplasmataceae; Wolbachieae; Wolbachia.

REFERENCE 1 (bases 1 to 2076)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Genomic assessment of the contribution of the Wolbachia endosymbiont of Eurosta solidaginis to gall-induction

JOURNAL International Journal Molecular Sciences

REFERENCE 2 (bases 1 to 2076)

AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University, 1600 Holloway Ave, San Francisco, CA 94132, USA

COMMENT ##Genome-Assembly-Data-START##

Assembly Date :: JUN-2019

Assembly Method :: FLYE v. 06-2019

Genome Representation :: Full

Expected Final Version :: Yes

Genome Coverage :: 100.0x

Sequencing Technology :: Illumina HiSeq; PacBio Sequel

##Genome-Assembly-Data-END##

FEATURES

source Location/Qualifiers

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/isolate="wEsol"

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/host="Eurosta solidaginis MN-2018-EFC"

/db_xref="taxon:955"

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/country="USA: Cowling Arboretum, Carleton College, Northfield, MN"

/lat_lon="44.48 N 93.13 W"

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CDS 908..1510

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domain-containing protein"
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/besthit="qcoverage 100 , hcoverage 100 , similarity 100
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Bacteria , Proteobacteria , WP_010082495.1 MULTISPECIES:
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gene

CDS

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similarity 100 , identity 100 , evaluate 3.15e-70 ,
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[Drosophila ananassae]"

ORIGIN

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661 ataataattac aatatattaa cttaaaatta actctctaata cttaaataagg aacatatggt
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LOCUS      JAQZAU010000149          11607 bp    dna        linear    ENV 17-MAR-2023
DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_20779, whole genome
            shotgun sequence.
ACCESSION  JAQZAU010000149  JAQZAU010000000
VERSION    JAQZAU010000149.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 11607)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 11607)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date          :: JUN-2019
            Assembly Method        :: FLYE v. 06-2019
            Genome Representation  :: Full
            Expected Final Version :: Yes
            Genome Coverage        :: 100.0x
            Sequencing Technology  :: Illumina HiSeq; PacBio Sequel
            ##Genome-Assembly-Data-END##
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                                   /db_xref="taxon:955"
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                                   Northfield, MN"
                                   /lat_lon="44.48 N 93.13 W"
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gibbosae]"
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gene 1194..1670
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CDS 1812..3044
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        of Kradibia gibbosae]"

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ORIGIN

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REFERENCE  1  (bases 1 to 14568)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 14568)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
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ORIGIN

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NADH-binding (51 kD) subunit"
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Wolbachia]"
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Wolbachia]"
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      acyltransferase,putative phosphate acyltransferase,Fatty
      acid/phospholipid biosynthesis enzyme,fatty
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      protein PlsX,Fatty acid synthesis protein"
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      acyltransferase,putative phosphate acyltransferase,Fatty
      acid/phospholipid biosynthesis enzyme,fatty
      acid/phospholipid synthesis protein PlsX,Fatty acid
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component"
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SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 9600)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 9600)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
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            Assembly Method    :: FLYE v. 06-2019
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ACCESSION  JAQZAU010000154 JAQZAU010000000
VERSION    JAQZAU010000154.1
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            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1 (bases 1 to 15051)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 15051)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage     :: 100.0x

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Sequencing Technology :: Illumina HiSeq; PacBio Sequel

##Genome-Assembly-Data-END##

FEATURES

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12175..12390

CDS

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VERSION    JAQZAU010000155.1
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            BioSample: SAMN33142973
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SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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REFERENCE  1 (bases 1 to 62512)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
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JOURNAL    International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 62512)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method    :: FLYE v. 06-2019

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Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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system, ATPase and permease components"
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VVRLDGADVYTWNRENFGNYVGYLPQDIELFNTSVKANIARMRDPNP EEI IKA KIA
GIHELILSLPNGYDTTIGGPGGVTLSSGGQKQLLGLARAFYGH TKLLVLDEPNANLDSN
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secretion system permease/ATPase [Wolbachia]"
gene complement(15064..15855)
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CDS complement(15064..15855)
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Wolbachia]"
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[Wolbachia]"
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/tigr="TIGR00086 smpB 144 SsrA-binding protein"
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protein SmpB"
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Pfam-B_10896 Ank Ank_3 Ank_4 Ank_2 HEM4 Ank Ank_3
Pfam-B_12244 Ank_5 Ank_4 Pfam-B_1714 Ank_4 Ank_5 Ank
Ank_3 Ank_2 Ank Ank_3 Ank_5 Ank_4 Ank_5 Ank_3 Ank Ank_5
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alnlength 647 , Bacteria , Proteobacteria ,
WP_174516988.1 ankyrin repeat domain-containing protein
[Wolbachia endosymbiont of Cardiocondyla obscurior]"
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[Wolbachia endosymbiont of Cardiocondyla obscurior]"
gene 18444..18974
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CDS 18444..18974
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Na+/H+ antiporter subunit E [Wolbachia]"
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MnhE subunit"
/pfam="MNHE"
/tigr="TIGR00942 2a6301s05 144 multicomponent Na+:H+
antiporter"
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subunit E"
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CDS complement(18967..19383)
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100 , identity 100 , evalue 9.15e-93 , alnlength 138 ,
Bacteria , Proteobacteria , WP_006279382.1 MULTISPECIES:
hypothetical protein [Wolbachia]"
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Bacteria , Proteobacteria , WP_006279382.1 MULTISPECIES:
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gene 19688..20248

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CDS	<pre> /locus_tag="wEsol_01759" 19688..20248 /locus_tag="wEsol_01759" /codon_start=1 /transl_table=11 /fullproduct="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evaluate 3.38e-125 , alnlength 186 , Bacteria , Proteobacteria , WP_015589189.1 MULTISPECIES: phosphoribosylglycinamide formyltransferase [unclassified Wolbachia]" /cog="PurN COG0299 200 Folate-dependent phosphoribosylglycinamide formyltransferase PurN" /pfam="Formyl_trans_N" /tigr="TIGR00639 PurN 192 phosphoribosylglycinamide formyltransferase" /product=" phosphoribosylglycinamide formyltransferase" /translation="MKKIKLGILISGRGSNMQALIEACQDQNFSAEVACVITNNSEAA GLKIAEQAGISAFIVKDKPLDAGKIHEILVQHKVDLICLAGFMRILKADFLSKWHNKV INIHPSLLPSFKGLNAQEQALKAGVKITGCTVHYVTPEVDAGAIQAQVVPVLPADDI QSLSERILAKEHKCYVEAVRSIAEDI" /besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evaluate 3.38e-125 , alnlength 186 , Bacteria , Proteobacteria , WP_015589189.1 MULTISPECIES: phosphoribosylglycinamide formyltransferase [unclassified Wolbachia]" </pre>
gene	<pre> complement(20258..21562) </pre>
CDS	<pre> /locus_tag="wEsol_01760" complement(20258..21562) /locus_tag="wEsol_01760" /codon_start=1 /transl_table=11 /fullproduct="qcoverage 99.0783410138249 , hcoverage 97.9498861047836 , similarity 100 , identity 100 , evaluate 7.87e-302 , alnlength 430 , Bacteria , Proteobacteria , WP_015589188.1 MULTISPECIES: insulinase family protein [unclassified Wolbachia]" /cog="PqqL COG0612 438 Predicted Zn-dependent peptidases" /pfam="Peptidase_M16 Peptidase_M16_C" /product="insulinase family protein" /translation="MYFCFFFCLSFNLQASGSLNIEEVTTTRKGFKFLFVENCALPKVS LNISFKDAGYVYENAEKQGLTWFTSLIIQEGAGKNDKDFAKKLEDKGISLNFADLE AFRVSLNTLSDNLEEAIISLLSDTIMRPKVDPEGLNRVFEKAKVNFNNLEKSPYFVAGK ELDTLLFKKHPYSKSVYGTLDTIMNITRDDVLTYYIKRNFADKNIVISVAGCAKKEEII TLLDKYLSKLPSKRSKVRKIPVKNNFGSAESKNIFMDIPQSVILFAQKGIAYEDPNYY NAGVLIDALGGMRLNSILMTELRLQNLGITYGVYASIIISNKHGNIISGFISTDSSTAGK AISAVKDTFSRIKKQGIDEQLFKDAKIGLVNNLVFLSNNTNTATLLDNMQINDRDVN RINNYANIINDVKLEEVNELASSLLEPENLFFVEVGKNAQQQ" /besthit="qcoverage 99.0783410138249 , hcoverage 97.9498861047836 , similarity 100 , identity 100 , evaluate 7.87e-302 , alnlength 430 , Bacteria , Proteobacteria , WP_015589188.1 MULTISPECIES: insulinase family protein [unclassified Wolbachia]" </pre>
gene	<pre> complement(21565..22788) </pre>
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Bacteria , Proteobacteria , WP_015589187.1 insulinase
family protein [Wolbachia endosymbiont of Drosophila
simulans]"
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/pfam="Peptidase_M16 Peptidase_M16_C"
/product="insulinase family protein"
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RFHDNYYHSGNAILLIVGDVELDEVVKLAEEKYGEIKAKPVMRNYPNQDPVHNAGLSV
TLESTEVKEPVLYFRYRVPLFEHINEASAAHLAVEILGGGKSSKLYNDLVLEDDVAVS
VFAYYNSLAFSDGYIDIQVIPKSGVNLDIVERELDNAINNFMSKGITDEELQSSKYRY
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Bacteria , Proteobacteria , WP_015589187.1 insulinase
family protein [Wolbachia endosymbiont of Drosophila
simulans]"
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CDS complement(23018..23494)
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100 , identity 100 , evalue 2.40e-109 , alnlength 158 ,
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/pfam="Peptidase_A8"
/tigr="TIGR00077 lspA 164 signal peptidase II"
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II"
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100 , identity 100 , evalue 1.10e-228 , alnlength 310 ,
Bacteria , Proteobacteria , WP_010082493.1 MULTISPECIES:
riboflavin biosynthesis protein RibF [Wolbachia]"
/cog="RibF COG0196 304 FAD synthase"
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/tigr="TIGR00083 ribF 290 riboflavin biosynthesis protein
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gene 24484..24822
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CDS 24484..24822
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100 , identity 100 , evalue 1.17e-78 , alnlength 112 ,
Bacteria , Proteobacteria , WP_007550037.1 MULTISPECIES:
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Glutaredoxin DUF836 GST_N_3"
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gene 24938..25810
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CDS 24938..25810
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evaluate 3.93e-14 , alnlength 55 , Bacteria ,
Proteobacteria , WP_174515849.1 hypothetical protein,
partial [Wolbachia endosymbiont of Cardiocondyla
obscurior]"
gene 26750..27349
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CDS 26750..27349
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100 , identity 100 , evaluate 7.62e-142 , alnlength 199 ,
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peroxiredoxin [Wolbachia]"
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/tigr="TIGR03137 AhpC 187 peroxiredoxin"
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gene 27336..28274
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CDS 27336..28274
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100 , identity 100 , evaluate 8.60e-218 , alnlength 312 ,
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thioredoxin-disulfide reductase [unclassified Wolbachia]"
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FAD_oxidored Pyr_redox_3 Pyr_redox_3 Pfam-B_7606
K_oxygenase Shikimate_DH NAD_binding_7 Pyr_redox"
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reductase"
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thioredoxin-disulfide reductase"
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Bacteria , Proteobacteria , WP_015589186.1 MULTISPECIES:
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gene 28364..28861
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WP_007550910.1 ankyrin repeat domain-containing protein,
partial [Wolbachia endosymbiont of Drosophila ananassae]"
gene 28931..29881
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CDS 28931..29881
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similarity 100 , identity 99.7 , evaluate 2.07e-203 ,
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domain-containing protein [unclassified Wolbachia]"
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CDS complement(29878..30714)
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recombinase/integrase [unclassified Wolbachia]"
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XerC"
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dehydrogenase complex, dihydrolipoamide dehydrogenase
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FAD_binding_2 Lycopene_cycl Pyr_redox Pyr_redox_3
NAD_binding_8 AlaDh_PNT_C Pyr_redox 3HCDH_N DAO
FAD_binding_3 Mqo HI0933_like Pyr_redox_dim"
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Wolbachia]"
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assembly lipoprotein YfgL"
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beta-propeller repeat protein"
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gene 34315..34566
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CDS 34315..34566
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CDS complement(34791..35543)
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protein [unclassified Wolbachia]"
/cog="COG5449 COG5449 225 Uncharacterized conserved
protein"
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/tigr="TIGR02218 phg_TIGR02218 266 phage conserved
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Wolbachia]"
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complement(38226..39047)
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CDS complement(38226..39047)
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/pfam="Pfam-B_17156 DNA_pol_B_exo1 DNA_pol_B_exo2
RNase_H_2 GvpG"
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LLESLSDFGASARVKMNEVCAAFNLPGKIGVDGSQVMDLYDSGKIQEIRDYCETDVIN
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GTPase Era [Wolbachia]"
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DUF258 PduV-EutP Dynamin_N AIG1 Dynamin_N Gag_p10 KH_2"
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gene complement(40175..41197)
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100 , identity 100 , evalue 1.74e-247 , alnlength 340 ,
Bacteria , Proteobacteria , WP_015589177.1 MULTISPECIES:
cytochrome d ubiquinol oxidase subunit II [unclassified
Wolbachia]"
/cog="AppB COG1294 346 Cytochrome bd-type quinol oxidase,
subunit 2"
/pfam="Cyto_ox_2"
/product="cytochrome d

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ubiquinol oxidase subunit II"
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Wolbachia]"
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100 , identity 100 , evaluate 0.0 , alnlength 480 ,
Bacteria , Proteobacteria , ONI56523.1 cyanide
insensitive terminal oxidase [Wolbachia pipientis wUni]"
/cog="CydA COG1271 457 Cytochrome bd-type quinol oxidase,
subunit 1"
/pfam="Bac_Ubq_Cox"
/product="cyanide insensitive terminal
oxidase"
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100 , identity 100 , evaluate 2.36e-153 , alnlength 206 ,
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/pfam="Sod_Fe_N Sod_Fe_C"
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dismutase"
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Bacteria , Proteobacteria , WP_010962800.1 MULTISPECIES:
insulinase family protein [Wolbachia]"
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Pfam-B_3045"
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protein"
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QNASCTGGEYLEHRKLDQVHLLIGLPSVSRHDDKYHTFQVLDSILGSGMSSRLFQEV
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Bacteria , Proteobacteria , WP_010962800.1 MULTISPECIES:
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gene complement(45461..47233)
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CDS complement(45461..47233)
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WP_015589174.1 MULTISPECIES: hypothetical protein
[unclassified Wolbachia]"
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alnlength 590 , Bacteria , Proteobacteria ,
WP_015589174.1 MULTISPECIES: hypothetical protein
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Wolbachia]"
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          /tigr="TIGR00430 Q_tRNA_tgt 368 queuine
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transglycosylase Tgt"
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ISEIPLHFDLASL"
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Wolbachia]"
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kD subunit"
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          /tigr="TIGR01958 nuoE_fam 148 NADH-quinone
oxidoreductase, E subunit"
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oxidoreductase subunit NuoE"
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similarity 100 , identity 100 , evaluate 8.71e-186 ,
alnlength 267 , Bacteria , Proteobacteria , ONI56529.1
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a CheY-like receiver domain and a winged-helix
DNA-binding domain"
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regulator"
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transcription factor"
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[Wolbachia]"
gene 54582..55064
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CDS 54582..55064
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Wolbachia]"
/cog="PgpA COG1267 160 Phosphatidylglycerophosphatase A
and related proteins"
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gene 55876..57012
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Bacteria , Proteobacteria , WP_010082472.1 MULTISPECIES:
succinate dehydrogenase iron-sulfur subunit [Wolbachia]"
/cog="FrdB COG0479 234 Succinate dehydrogenase/fumarate
reductase, Fe-S protein subunit"
/pfam="Fer2_3 Fer4_9 Fer4_8 Fer4_17 Fer4_9 Fer4_18"
/tigr="TIGR00384 dhsB 222 succinate dehydrogenase and
fumarate reductase iron-sulfur protein"
/product="succinate
dehydrogenase iron-sulfur subunit"
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CDS complement(57891..58343)
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100 , identity 100 , evaluate 9.97e-105 , alnlength 150 ,
Bacteria , Proteobacteria , WP_010082473.1 MULTISPECIES:
rRNA maturation RNase YbeY [Wolbachia]"
/cog="COG0319 COG0319 153 Predicted metal-dependent
hydrolase"
/pfam="UPF0054"
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RNase YbeY"
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protein [Wolbachia pipientis]"
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protein [Wolbachia pipientis]"
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protein"
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/cog="FtsZ COG0206 338 Cell division GTPase"
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gene complement(61109..>62512)
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family Mg chelatase-like AAA ATPase [Wolbachia]"

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endosymbiont of Rhagoletis cerasi]"
 /cog="COG0606 COG0606 490 Predicted ATPase with chaperone activity"
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ORIGIN

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CDS 257..625
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 /besthit="qcoverage 96.7213114754098 , hcoverage 46.09375 , similarity 97.5 , identity 95.8 , evaluate 1.44e-64 , alnlength 118 , Bacteria , Proteobacteria , EAL58124.1 RNA polymerase sigma factor RpoD [Wolbachia endosymbiont of Drosophila ananassae]"

gene 685..1041
 /locus_tag="wEsol_01803"

CDS 685..1041
 /locus_tag="wEsol_01803"
 /codon_start=1
 /transl_table=11
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 /pfam="Sigma70_r3 Sigma70_r4 Sigma70_r4"
 /tigr="TIGR02393 RpoD_Cterm 238 RNA polymerase sigma factor RpoD"
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 /cog="RpoD COG0568 342 DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)"
 /besthit="qcoverage 97.4576271186441 , hcoverage 62.8415300546448 , similarity 94.8 , identity 93.0 , evaluate 6.97e-65 , alnlength 115 , Bacteria , Proteobacteria , EAL60191.1 RNA polymerase sigma factor RpoD [Wolbachia endosymbiont of Drosophila simulans]"

gene 1365..1697
 /locus_tag="wEsol_01804"

CDS 1365..1697
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 /cog="COG3240 COG3240 370 Phospholipase/lecithinase/hemolysin"
 /besthit="qcoverage 97.2727272727273 , hcoverage 69.4805194805195 , similarity 97.2 , identity 94.4 , evaluate 4.29e-69 , alnlength 107 , Eukaryota , Arthropoda , GFQ81579.1 GDSL family lipase [Trichonephila clavata]"

gene complement(2993..3187)
 /locus_tag="wEsol_01805"

CDS complement(2993..3187)
 /locus_tag="wEsol_01805"
 /codon_start=1
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CDS       complement(5410..5931)
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          /codon_start=1
          /transl_table=11
          /product="hypothetical protein"
          /pfam="Lyase_1 FumaraseC_C"
          /tigr="TIGR00979 fumC_II 458 fumarate hydratase, class
II"
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EFEMIVKSEEMVN"
          /cog="FumC COG0114 462 Fumarase"
          /besthit="qcoverage 100 , hcoverage 50.2906976744186 ,
similarity 97.1 , identity 96.5 , evalue 7.72e-108 ,
alnlength 173 , Bacteria , Proteobacteria , EAL58737.1
fumarate hydratase, class II [Wolbachia endosymbiont of
Drosophila ananassae]"
gene      complement(6170..6799)
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CDS       complement(6170..6799)
          /locus_tag="wEsol_01808"
          /codon_start=1
          /transl_table=11
          /product="hypothetical protein"
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          /tigr="TIGR00979 fumC_II 458 fumarate hydratase, class
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LIKALAIIVKLAAARVNMKQGSIDNKVGDAICAAAREVIDGKFNFPLVWVWQTGSGTQ
TNMNMNEVISNRAIEILGGNLGSKSPIHPNDHVNYGQSSNDTFPTAMHIAAAEQINCL
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          /cog="FumC COG0114 462 Fumarase"
          /besthit="qcoverage 95.2153110047847 , hcoverage
42.8879310344828 , similarity 99.0 , identity 99.0 ,
evalue 3.45e-134 , alnlength 199 , Bacteria ,
Proteobacteria , MBV2146228.1 class II fumarate hydratase
[Wolbachia endosymbiont of Pissodes strobi]"
gene      complement(7142..7483)
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CDS       complement(7142..7483)
          /locus_tag="wEsol_01809"
          /codon_start=1
          /transl_table=11
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98.2 , identity 97.3 , evalue 3.93e-73 , alnlength 113 ,
Bacteria , Proteobacteria , MBV2145176.1 hypothetical

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 Bacteria , Proteobacteria , MBV2145176.1 hypothetical
 protein [Wolbachia endosymbiont of *Pissodes strobi*]"
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 37.2670807453416 , similarity 98.3 , identity 90.0 ,
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 partial [Wolbachia endosymbiont of *Operophtera brumata*]"
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 YIKTHMPMWKKKIQV"
 /cog="gcpE COG0821 361 1-hydroxy-2-methyl-2-(e)-butenyl
 4-diphosphate synthase"
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 40.3755868544601 , similarity 98.3 , identity 97.7 ,
 evalue 1.75e-108 , alnlength 172 , Bacteria ,
 Proteobacteria , WP_209472694.1 flavodoxin-dependent
 (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase
 [Wolbachia endosymbiont of *Wiebesia pumilae*]"
 gene complement(8368..8892)
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 CDS complement(8368..8892)
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 /pfam="GcpE"
 /tigr="TIGR00612 ispG_gcpE 357

4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase"
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 LPVRIGVNWGSLNK"
 /cog="gcpE COG0821 361 1-hydroxy-2-methyl-2-(e)-butenyl
 4-diphosphate synthase"
 /besthit="qcoverage 100 , hcoverage 40.8450704225352 ,
 similarity 98.9 , identity 98.3 , evaluate 7.26e-115 ,
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 Proteobacteria;Arthropoda , MBV2145175.1
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 (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase
 [Wolbachia endosymbiont of Pissodes strobi]"

gene complement(8918..9241)
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CDS complement(8918..9241)
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 SEQQEGKKVTSTREKEVSPINVTIKENPSRKTCSHDSIANLDNVDAYSLSGSSSFGSV
 AETVK"
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 alnlength 107 , Bacteria , Proteobacteria , ONI56764.1
 hypothetical protein N500_0157 [Wolbachia pipientis
 wUni]"

gene 9495..10037
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CDS 9495..10037
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 YKSKGFNCQDACTSNIADQIGRFKENIKILLKLIFKGERQHYNPGCSEETLKDYFFFD
 YFHPTAELHHEVGNEVYELI"
 /cog="COG3240 COG3240 370
 Phospholipase/lecithinase/hemolysin"
 /besthit="qcoverage 100.555555555556 , hcoverage
 55.521472392638 , similarity 96.7 , identity 96.1 ,
 evaluate 1.65e-114 , alnlength 181 , Eukaryota , Arthropoda
 , GFY65264.1 hypothetical protein TNIN_37661
 [Trichonephila inaurata madagascariensis]"

gene complement(10386..>11032)
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CDS complement(10386..>11032)
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 94.8275862068966 , similarity 92.3 , identity 91.4 ,
 evaluate 4.90e-92 , alnlength 220 , Eukaryota , Arthropoda
 , GFY65265.1 uncharacterized protein TNIN_37671
 [Trichonephila inaurata madagascariensis]"
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 94.8275862068966 , similarity 92.3 , identity 91.4 ,
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 [Trichonephila inaurata madagascariensis]"

ORIGIN

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  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL  International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 6679)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Direct Submission
  JOURNAL  Submitted (10-FEB-2023) Biology, San Francisco State University,
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ACCESSION  JAQZAU010000158  JAQZAU010000000
VERSION    JAQZAU010000158.1
DBLINK     BioProject: PRJNA929258
            BioSample: SAMN33142973
KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
            Bacteria; Pseudomonadota; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Wolbachieae; Wolbachia.
REFERENCE  1  (bases 1 to 2203)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 2203)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date          :: JUN-2019
            Assembly Method        :: FLYE v. 06-2019
            Genome Representation   :: Full
            Expected Final Version :: Yes
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            Sequencing Technology  :: Illumina HiSeq; PacBio Sequel
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ORIGIN

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DEFINITION MAG: Wolbachia pipientis isolate wEsol contig_58088, whole genome
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 BioSample: SAMN33142973
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 SOURCE Wolbachia pipientis (insect metagenome)
 ORGANISM Wolbachia pipientis
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 Anaplasmataceae; Wolbachieae; Wolbachia.
 REFERENCE 1 (bases 1 to 41299)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Genomic assessment of the contribution of the Wolbachia
 endosymbiont of Eurosta solidaginis to gall-induction
 JOURNAL International Journal Molecular Sciences
 REFERENCE 2 (bases 1 to 41299)
 AUTHORS Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2023) Biology, San Francisco State University,
 1600 Holloway Ave, San Francisco, CA 94132, USA
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and their inactivated homologs"
/pfam="PmbA_TldD"
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TldD"

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NSINLNEETKSLYSRINPINEMDLNSKIKLLNEVNEYVRSKNNCVKQVKITLSGEWQV
VQIIKGDHRLSDIRPLVRFNVLVIVEKDGRTERGSAGHGGRDSYSKFISEKKWKEVAN
QALEQALVNLEAIPTPAGEMTVVLGPGWPGILLHEAVGHGLEGDFNRKKVSAFSNSVG
KQVAASDITVDDGTLPLNRGSISVDDEGTTPPSYNILIEDGILKGYMQDHMNAKLMGV
SPTGNRRRESYKEVIMPRMTNTYMLPGKYTPKEIISSVKKGLYAVNFGGGQVDITSGK
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CDS 4328..4819
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gene 5064..5771
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CDS 5064..5771
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100 , identity 100 , evalue 2.70e-162 , alnlength 235 ,
Bacteria , Proteobacteria , WP_141456650.1 MULTISPECIES:
uroporphyrinogen-III synthase [unclassified Wolbachia]"
/cog="HemD COG1587 248 Uroporphyrinogen-III synthase"
/pfam="HEM4"
/product="
uroporphyrinogen-III synthase"
/translation="MKSILLTRPLLDSFNTRNLRKYGYKVFIIEPVFTIKYLNPDISA
YEFDVVISTSKNSVKALSQICKEDDFPIITVGNSTMQAANKLGFSDIISADSNVDGLI
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Bacteria , Proteobacteria , WP_141456650.1 MULTISPECIES:
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gene 5771..6550
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CDS 5771..6550
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100 , identity 100 , evalue 6.45e-191 , alnlength 259 ,
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exodeoxyribonuclease III [unclassified Wolbachia]"
/cog="XthA COG0708 261 Exonuclease III"
/pfam="Pfam-B_5213 Exo_endo_phos Pfam-B_1244"
/tigr="TIGR00633 xth 255 exodeoxyribonuclease III (xth)"
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VRVGSVYVPNGQSPDSQAFHEYKLKFFDNLIERMSTLLKNEELTIIAGDYNVAPDEIDV
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CDS complement(6587..7609)
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100 , identity 100 , evalue 1.11e-218 , alnlength 340 ,
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KEKIPFLGKDKKEEDEPPLSDEEMVTTFLSKIFFPVLLSTIPMLIFGPTTLGVVLTAI
GTIFAIKGGVEVLFSNNKKGTLYDPSSQDKDDTEKRAKLNGKILEGIDDILKTPVTEV
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KQAGIT"
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Bacteria , Proteobacteria , WP_015589322.1 MULTISPECIES:
hypothetical protein [unclassified Wolbachia]"
gene complement(7660..10236)
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CDS complement(7660..10236)
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100 , identity 100 , evalue 0.0 , alnlength 858 ,
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DNA polymerase I [unclassified Wolbachia]"
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/tigr="TIGR00593 pola 890 DNA polymerase I"
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KYIAHSDYLTIALDAGKKNFRHDLYPEYKANRVTPPEDLTPQFTILREAVEAFNLSYE
EIEGYEADDIIATLAAKYANHQDFKVVVVSSDKDLFQLLNHNILIFDPIKNIYIDEKQ
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VLFNKMGLNKKKKSKSGSYSTNYEVLEALEEEGVEIASKILNWRHLSKLKGTYTDL
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SADYSQIELRLLAHVANVAAFKEAFANGQDIHEITARQVFGVQEIIDEQLRRKAKSINF
GIIYGISPFGLAKRLGITIAEAAEYINYYFSCYPEIKAYMEKAVSIARLHGIVETLFG
RRCFVRDINNTIPYIRQFAERAAINAPLQGTAAADIKRATIQLFDQLKVGKIIILQVHD
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Proteobacteria , WP_015589323.1 MULTISPECIES: DNA
polymerase I [unclassified Wolbachia]"
gene complement(10451..10615)
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CDS complement(10451..10615)
/locus_tag="wEsol_01835"
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100 , identity 100 , evalue 7.44e-31 , alnlength 54 ,
Bacteria , Proteobacteria , WP_081600771.1 MULTISPECIES:
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/cog="Tra5 COG2801 232 Transposase and inactivated
derivatives"
/pfam="rve_3 rve_2"
/product="IS3 family
transposase"
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EIFYNKQRHY"
/besthit="qcoverage 100 , hcoverage 100 , similarity 100
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Bacteria , Proteobacteria , WP_081600771.1 MULTISPECIES:
IS3 family transposase [unclassified Wolbachia]"
gene complement(10605..10769)
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CDS complement(10605..10769)
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derivatives"
/pfam="rve"
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Bacteria , Proteobacteria , WP_153801314.1 MULTISPECIES:
hypothetical protein [Wolbachia]"
gene complement(10769..10978)
/locus_tag="wEsol_01837"
CDS complement(10769..10978)

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97.1 , identity 91.3 , evaluate 5.68e-37 , alnlength 69 ,
Bacteria , Proteobacteria , CDR78719.1 hypothetical
protein WPAU_0327 [Wolbachia endosymbiont of Drosophila
simulans wAu]"
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DYLHQDQGGMAIFGNNNRSIFTHGS"
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, identity 91.3 , evaluate 5.68e-37 , alnlength 69 ,
Bacteria , Proteobacteria , CDR78719.1 hypothetical
protein WPAU_0327 [Wolbachia endosymbiont of Drosophila
simulans wAu]"
gene complement(11225..11509)
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CDS complement(11225..11509)
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100 , identity 100 , evaluate 1.40e-55 , alnlength 94 ,
Bacteria , Proteobacteria , WP_038198869.1 MULTISPECIES:
transposase [Wolbachia]"
/cog="COG2963 COG2963 116 Transposase and inactivated
derivatives"
/pfam="HTH_Tnp_1 HTH_23 HTH_28 Pfam-B_9422"
/product="transposase"
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, identity 100 , evaluate 1.40e-55 , alnlength 94 ,
Bacteria , Proteobacteria , WP_038198869.1 MULTISPECIES:
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gene complement(11742..12548)
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CDS complement(11742..12548)
/locus_tag="wEsol_01839"
/codon_start=1
/transl_table=11
/pfam="NAD_binding_10 RmlD_sub_bind"
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100 , identity 100 , evaluate 5.73e-194 , alnlength 268 ,
Bacteria , Proteobacteria , WP_015589324.1 MULTISPECIES:
SDR family oxidoreductase [unclassified Wolbachia]"
/translation="MHLFCFGYGYVAKFLSKLLNLGWKVSQTSRSKNIQDVILFNVE
KVSQDLLKSATHVLISIPPDGDDVVERYGDCLQNVKWLGYLSATSVYGDHSGNWNVEE
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HFFSRIHVEDISNILFSSMQNIKPGEIYNCADDLPTTQSEVVIYATKLLNVSPPEPIE
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oxidoreductase"
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, identity 100 , evaluate 5.73e-194 , alnlength 268 ,
Bacteria , Proteobacteria , WP_015589324.1 MULTISPECIES:
SDR family oxidoreductase [unclassified Wolbachia]"
gene complement(12554..13198)
/locus_tag="wEsol_01840"

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CDS complement(12554..13198)
 /locus_tag="wEsol_01840"
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 /transl_table=11
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 /cog="COG0400 COG0400 207 Predicted esterase"
 /pfam="Abhydrolase_2 DLH DUF676 FSH1 Abhydrolase_5 Abhydrolase_6 Abhydrolase_1 Esterase Peptidase_S9 Abhydrolase_6"
 /product="dienelactone hydrolase family protein"
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CDS complement(13596..13961)
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 /product="hypothetical protein"
 /besthit="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 1.05e-74 , alnlength 121 , Bacteria , Proteobacteria , WP_064125381.1 MULTISPECIES: hypothetical protein [unclassified Wolbachia]"

gene complement(14083..15750)
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CDS complement(14083..15750)
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Proteobacteria , WP_015589327.1 MULTISPECIES:
aminopeptidase P family protein [unclassified Wolbachia]"
gene complement(15759..16442)
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CDS complement(15759..16442)
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KTKVAANFV"
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5-carboxymethylaminomethyl modification enzyme GidA"
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similarity 99.6 , identity 99.6 , evalue 2.06e-149 ,
alnlength 227 , Bacteria , Proteobacteria ,
WP_006279401.1 tRNA
uridine-5-carboxymethylaminomethyl(34) synthesis enzyme
MnmG, partial [Wolbachia endosymbiont of Muscidifurax
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gene complement(16442..17680)
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CDS complement(16442..17680)
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5-carboxymethylaminomethyl modification enzyme GidA"
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LQGVIIHIGEQATPSGRMGDKSAVELANTLKKYNFKLGRLRTGTPPRLDRGTINWSILQ
EQVGDNPPVPFESYLTEKINQPQVSCFITHNTNETHKIIIRENLHRSASSYLDDVVAPRY
CPSIEVKVKKFAEKSSHQIFLEPEGLNDDTIYPNGISNSLPPIEVQCEMIKSIKLENA
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5-carboxymethylaminomethyl modification enzyme GidA"
/besthit="qcoverage 97.0873786407767 , hcoverage 62.5 ,
similarity 100 , identity 99.8 , evalue 6.27e-282 ,
alnlength 400 , Bacteria , Proteobacteria ,
WP_141456648.1 MULTISPECIES: tRNA
uridine-5-carboxymethylaminomethyl(34) synthesis enzyme
MnmG [unclassified Wolbachia]"
gene complement(18078..18350)
/locus_tag="wEsol_01845"

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CDS complement(18078..18350)
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 /product="hypothetical protein"
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gene 18406..19581
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CDS 18406..19581
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 /cog="MviN COG0728 518 Uncharacterized membrane protein, putative virulence factor"
 /pfam="MVIN Polysacc_synt MatE"
 /tigr="TIGR01695 mviN 506 integral membrane protein MviN"
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gene 19585..22128
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CDS 19585..22128
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 /codon_start=1
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 /fullproduct="qcoverage 100 , hcoverage 100 , similarity 100 , identity 100 , evalue 0.0 , alnlength 847 , Bacteria , Proteobacteria , WP_141456647.1 MULTISPECIES: hypothetical protein [unclassified Wolbachia]"

gene

CDS

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PKSITLFGMKS NKENLLNIINTNASGNTVDIVIKDSQVSFKNDFADIVNIKEVAVKKN
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DNVNGQVSLNGEIKTQGKSFHDWASNLSGDVNLQAQGIEVTNVDFNSFITNLLSSKNK
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80.352644836272 , similarity 100 , identity 100 , eval 7.11e-230 ,
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WP_015589331.1 MULTISPECIES: phage portal protein
[unclassified Wolbachia]"
/cog="COG4695 COG4695 398 Phage-related protein"
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/tigr="TIGR01537 portal_HK97 343 phage portal protein,
HK97 family"
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protein"
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VIAFRAINMIASAASSVPLTLCQLTEQGKS QLKAHPLLKLLYSPNPM TSKSEFIEGIV
TYRLVNGNSYILMVESQNNRKPPTELYLLRPDRVEIVPGRNNVPYNYRYAINNNSYDF
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AIVVKS AKDGS GGSLSQEYQRLKAQINDHYS GPVNAGRPI LLEGGLEWKEMSLSPRD
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CDS 24335..24952
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Wolbachia]"
/cog="LipB COG0321 221 Lipoate-protein ligase B"
/pfam="BPL_LplA_LipB"
/tigr="TIGR00214 lipB 187 lipoyl(octanoyl) transferase"
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transferase LipB"
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CDS 24952..25320
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YLEKLPNDKKERIAQNKSS"
/cog="LdcA COG1619 313 Uncharacterized proteins, homologs
of microcin C7 resistance protein MccF"
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35.1906158357771 , similarity 100 , identity 100 , evalue
4.04e-75 , alnlength 120 , Bacteria , Proteobacteria ,
WP_197907444.1 LD-carboxypeptidase [Wolbachia
endosymbiont of Kradibia gibbosae]"
gene 25392..25976
/locus_tag="wEsol_01852"
CDS 25392..25976
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 WP_015589333.1 MULTISPECIES: LD-carboxypeptidase
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 CDS complement(26320..27138)
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 similarity 99.6 , identity 99.6 , evaluate 2.20e-193 ,
 alnlength 272 , Bacteria , Proteobacteria , EAL59854.1
 phage uncharacterized protein, partial [Wolbachia
 endosymbiont of Drosophila simulans]"
 gene complement(27128..27784)
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 /cog="COG5410 COG5410 305 Uncharacterized protein
 conserved in bacteria"
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 40.8624229979466 , similarity 100 , identity 100 , evaluate
 1.47e-138 , alnlength 199 , Bacteria , Proteobacteria ,
 WP_015589334.1 MULTISPECIES: phage terminase large
 subunit [unclassified Wolbachia]"
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 CDS complement(28575..29372)
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 100 , identity 100 , evaluate 4.05e-197 , alnlength 265 ,
 Bacteria , Proteobacteria , WP_141456644.1 MULTISPECIES:
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 [unclassified Wolbachia]"
 /cog="PurL COG0047 231 Phosphoribosylformylglycinamide
 (FGAM) synthase, glutamine amidotransferase domain"

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/pfam="GATase_5 GATase_3"
/tigr="TIGR01735 FGAM_synt 1307
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, identity 100 , evalue 4.05e-197 , alnlength 265 ,
Bacteria , Proteobacteria , WP_141456644.1 MULTISPECIES:
phosphoribosylformylglycinamide synthase subunit PurQ
[unclassified Wolbachia]"
gene complement(29379..30629)
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CDS complement(29379..30629)
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100 , identity 100 , evalue 4.03e-280 , alnlength 416 ,
Bacteria , Proteobacteria , WP_015589336.1 MULTISPECIES:
phosphate ABC transporter permease PstA [unclassified
Wolbachia]"
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LDWLKEKRRVKKFFNKSLFLKSDSREPENAGILGAFIGSLMTIIVCLALALPIGIMSG
ICLYEFMPKNRLMTNIVEISINNLAAPVSIIFGVVGLTLYLGIFGLPRSSPLVGGMTL
SFMMLPNII IATKNAFANVPITIKDAAAFALGAPHIKVILDHSLPIALPRIIHGTVLAI
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transporter permease PstA"
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phosphate ABC transporter permease PstA [unclassified
Wolbachia]"
gene complement(30713..31090)
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CDS complement(30713..31090)
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100 , identity 100 , evalue 2.25e-80 , alnlength 125 ,
Bacteria , Proteobacteria , WP_006279489.1 MULTISPECIES:
50S ribosomal protein L19 [Wolbachia]"
/cog="RplS COG0335 115 Ribosomal protein L19"
/pfam="Ribosomal_L19"
/tigr="TIGR01024 rplS_bact 114 ribosomal protein L19"
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CDS complement(31074..31784)
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100 , identity 100 , evalue 4.35e-173 , alnlength 236 ,
Bacteria , Proteobacteria , WP_007549279.1 MULTISPECIES:
tRNA (guanosine(37)-N1)-methyltransferase TrmD
[Wolbachia]"
/cog="TrmD COG0336 240
tRNA-(guanine-N1)-methyltransferase"
/pfam="tRNA_m1G_MT"
/tigr="TIGR00088 trmD 233 tRNA
(guanine(37)-N(1))-methyltransferase"
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(guanosine(37)-N1)-methyltransferase TrmD"
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LLEFPHITILCGRFEGIDQRIIDAYTPYELSIGDYILSGGEPAA MVVLDACIRLLPGV
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[Wolbachia]"
gene 31859..32581
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CDS 31859..32581
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100 , identity 100 , evalue 1.06e-166 , alnlength 240 ,
Bacteria , Proteobacteria , WP_015589337.1 MULTISPECIES:
phosphoribosylaminoimidazolesuccinocarboxamide synthase
[unclassified Wolbachia]"
/cog="PurC COG0152 247
Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR)
synthase"
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/tigr="TIGR00081 purC 279
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Bacteria , Proteobacteria , WP_015589337.1 MULTISPECIES:
phosphoribosylaminoimidazolesuccinocarboxamide synthase

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100 , identity 100 , evalue 3.40e-252 , alnlength 345 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_007549277.1 MULTISPECIES:
phosphoribosylformylglycinamide cyclo-ligase
[Wolbachia]"
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synthetase"
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          /tigr="TIGR00878 purM 332
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, identity 100 , evalue 3.40e-252 , alnlength 345 ,
Bacteria;Eukaryota , Proteobacteria;Arthropoda ,
WP_007549277.1 MULTISPECIES:
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[Wolbachia]"
gene      33749..34042
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CDS       33749..34042
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Bacteria , Proteobacteria , WP_006280049.1 MULTISPECIES:
hypothetical protein [Wolbachia]"
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CDS       34048..34401
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4.49e-71 , alnlength 116 , Bacteria , Proteobacteria ,
 WP_158246746.1 MULTISPECIES: hypothetical protein
 [Wolbachia]"
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 [Wolbachia endosymbiont of Drosophila ananassae]"
 /cog="TlyC COG1253 429 Hemolysins and related proteins
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 /tigr="TIGR03520 GldE 408 gliding motility-associated
 protein GldE"
 /product="CBS domain protein"
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 [Wolbachia endosymbiont of Drosophila ananassae]"

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 , similarity 100 , identity 99.7 , evalue 1.40e-241 ,
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 WP_012673335.1 MULTISPECIES: uroporphyrinogen
 decarboxylase [Wolbachia]"
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 decarboxylase"
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 AGGPWTVASYIIIEGSSKTFKSVLNFYPSCLKEIIERITEVTIIYLIKQIEFGADVIQ
 LFDSNAGALSEPLFKEYVIEPTKRIILAIDRFSDFPFIIGFPRSAGNLYKDYCEQTGV
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WP_012673335.1 MULTISPECIES: uroporphyrinogen
decarboxylase [Wolbachia]"
gene 36775..37968
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100 , identity 100 , evalue 2.86e-284 , alnlength 397 ,
Bacteria , Proteobacteria , WP_015589340.1 MULTISPECIES:
pyridoxal phosphate-dependent aminotransferase
[unclassified Wolbachia]"
/cog="COG0436 COG0436 393 Aspartate/tyrosine/aromatic
aminotransferase"
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phosphate-dependent aminotransferase"
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, identity 100 , evalue 2.86e-284 , alnlength 397 ,
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  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
  JOURNAL  International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 11891)
  AUTHORS  Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
  TITLE    Direct Submission
  JOURNAL  Submitted (10-FEB-2023) Biology, San Francisco State University,
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VERSION    JAQZAU010000161.1
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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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REFERENCE  1  (bases 1 to 9624)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL    International Journal Molecular Sciences
REFERENCE  2  (bases 1 to 9624)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT    ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
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            Genome Representation :: Full
            Expected Final Version :: Yes
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KEYWORDS   WGS; ENV; Metagenome Assembled Genome; MAG.
SOURCE     Wolbachia pipientis (insect metagenome)
ORGANISM   Wolbachia pipientis
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REFERENCE  1 (bases 1 to 4254)
AUTHORS    Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Genomic assessment of the contribution of the Wolbachia
            endosymbiont of Eurosta solidaginis to gall-induction
JOURNAL     International Journal Molecular Sciences
REFERENCE  2 (bases 1 to 4254)
AUTHORS     Fiutek,N., Couger,B.M., Roy,S., de la Torre,J.R. and Connor,E.F.
TITLE      Direct Submission
JOURNAL     Submitted (10-FEB-2023) Biology, San Francisco State University,
            1600 Holloway Ave, San Francisco, CA 94132, USA
COMMENT     ##Genome-Assembly-Data-START##
            Assembly Date      :: JUN-2019
            Assembly Method     :: FLYE v. 06-2019

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Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100.0x
Sequencing Technology :: Illumina HiSeq; PacBio Sequel
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FEATURES

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