
[Ext] Inquiry: GenBank MW434135-MW434220

Amy Kistler <amy.kistler@czbiohub.org>
To: gb-admin@ncbi.nlm.nih.gov

Wed, Mar 3, 2021 at 10:52 PM

This annotation is correct and an established property of the previously described segment in certain lineages of this viral taxa.

On Fri, Feb 19, 2021 at 9:11 AM <gb-admin@ncbi.nlm.nih.gov> wrote:

Dear Dr. Kistler:

We are currently processing your GenBank records MW434135-MW434220 and have come across a point that requires your attention.

Each of these sequences have coding regions mostly contained within other coding regions on opposite strands. Please verify that this annotation is correct.

Send your reply to: gb-admin@ncbi.nlm.nih.gov

Appended for your reference are the GenBank flatfiles containing the information we have currently.

Thank you for your attention, and we look forward to hearing from you soon.

Please reply using the current Subject line.

Sincerely,

Linda Frisse, PhD
The GenBank Submissions Staff
Bethesda, Maryland USA

gb-admin@ncbi.nlm.nih.gov (for replies/updates to records in GenBank)
info@ncbi.nlm.nih.gov (for general questions regarding GenBank)

Working GenBank flatfiles:

```
LOCUS    MW434135      849 bp  RNA  linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_002_ALCO genomic sequence.
ACCESSION MW434135
VERSION   MW434135
DBLINK    BioProject: PRJNA605178
          BioSample: SAMN14051442
          Sequence Read Archive: SRR11035376
KEYWORDS  ENV.
SOURCE    Culex narnavirus 1 (mosquito metagenome)
ORGANISM  Culex narnavirus 1
          Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
          Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 849)
AUTHORS  Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
          Logan,P., Ratnasiri,K. and Retallack,H.
TITLE    Single mosquito metatranscriptomics identifies vectors, emerging
          pathogens and reservoirs in one assay
JOURNAL  bioRxiv (2020) In press
REMARK   DOI: 10.1101/2020.02.10.942854
```

REFERENCE 2 (bases 1 to 849)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 354.167098x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..849

/organism="Culex narnavirus 1"
 /mol_type="genomic RNA"
 /isolate="CMS001_002_ALCO"
 /isolation_source="female, blood fed, collected in marsh /
 wildlife refuge / park habitat"
 /host="Culex tarsalis"
 /db_xref="taxon:2562539"
 /environmental_sample
 /country="USA: Alameda County, California"
 /lat_lon="37.55697 N 122.07938 W"
 /collection_date="21-Sep-2017"
 /note="metagenomic; derived from metagenome: mosquito
 metagenome"

CDS 22..828

/codon_start=1
 /product="putative Robin"
 /translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTDNP
 ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLALAVGEPRSAAGV
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 DSPLAQLAVGVGEMDRNRTSAGNYRRRKSISLQPQRTEQNAAPNTRGSECSPKLGHGT
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CDS complement(37..843)

/codon_start=1
 /product="ORF2"
 /translation="MPNRASGRWRNLRLFNLPRLGYRDKCLPLDGQNRTGADGSATPG
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 KGELAAFVEDKADASRRRARFSYHRQGVDSLTAACRSLYGRRCHRSRLSSLGVLRLN
 HASPVSNRGGQSRVISGRCCRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

1 gatccctgt actggacaac gatgggtgac gcaccgtac gtccggagacg acgaggcggc
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 121 gtagccccgc cggcacctcc cactgataac cctgcttgt cccccccggg tactaaccgg
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 241 gcccggccgc taaaggctgc ggcatgccgt caggctgtcg acctggccct ggcgggttga
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 361 cttagcgctc tcgggatgga gcctagctcg agcgggacgg cagaaagtc tgccgc
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 601 ccccaaggaa cagagaaaaa cgccgctccg aacaccgcg gttcggagtg tagccccaaa
 661 ttggggcatg gcacggctgc agtgcaccc cccggaaagg gtcagggtgc agccggcgat
 721 ggcggaaaccg tcggcccg tccgttctg cccatcaagg gggagacatt tgtccctata
 781 cccctgggc agattaaaca ggagccgaag gttccgcatt cgacctgtat ctctgttgg
 841 catccccc

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LOCUS MW434136 847 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_004_ALCO genomic sequence.

ACCESSION MW434136

VERSION MW434136

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051444

Sequence Read Archive: SRR11035293
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 847)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 847)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 664.774026x
Sequencing Technology :: Illumina
##Assembly-Data-END##
FEATURES Location/Qualifiers
source 1..847
/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_004_ALCO"
/isolation_source="female, blood fed, collected in
industrial (waste water treatment plant) habitat"
/host="Culex pipiens"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.7152 N 122.19431 W"
/collection_date="12-Sep-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"
CDS 19..825
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/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPVPTGNP
ALSPPVNNRGCVIEPDKARKSGTQPGPVAAA AVKAAACRQAVDLALAVGEPRSAAGV
CLVFDKGCLQALSLALGMEPSSSGTAGKSAAPARAEAPVSTARAPVRRSTGGGGCAPG
DSPLAQLAVGVGEMDRNRTSAGNYRRRKSISSLQPQRTEQNAAPNTRGSECSPKLGPGT
AAVRPPGRGQGAAGRGGTVGANPVLPIKGETFVPIPPGQAKQEPKFPPST"
CDS complement(34..840)
/codon_start=1
/product="ORF2"
/translation="MPDRASGRWRKLRLLSLPRGYGDKCLPLDGQDRIGADGSATPG
CTLTPSGGSHCSRARPQFGATLRTAGVRSGVLLCPLGERRDRLPASVVTCCRRTVAIHL
SDPNCELGEGGISRRASPTPASRPADWGPRGGDWSLGTGGGRFRSCRPTRARLHPESA
KGELAAFVEDKADASRRRARFSYHRQGQVDSLTAARRSLYGRRCHRSRLSSTLSGLVRLN
HASPVINRGQQSRVTSGRYRRAHACGYRIPTVSCTVRGWWFMTAASSSPT"
ORIGIN
1 atcctgtact ggacaacgat gggtgacgca ccgtcacgtc ggagacgacg aggcggcggt
61 cataaaaccac catccgcgaa cagtgcagg aacagtggga atgcggtacc cgccaggcgta
121 agccccccgg tacctcccac tggtaaccct gctctgtccc ccccggttaa taaccgggga
181 tgcgtgattt agcctgacaa ggcccgaaag agtggaaactc aaccgggacc tgtggcagcg
241 gccccgtaa aggctgcggc gtgcgtcag gctgtcgacc tggccctggc ggtggtagga
301 gaaccgcgtc cggcggtgg cgtctgcctt gtctcgaca aaggctgcc a gctcgccctt
361 agcgctctcg ggtatggagcc tagctcgagt gggacggcag gaaaatctgc cgccggcc
421 cgtgccgagg ctccagtc caccgcgagg gccccagttcc gccggcgtc ac tggcgggggt
481 ggggatcg cgccggaga ttccccctc gcccaactcg cagtgggtt cgagagatg

541 gatcgcaacc gtacgtccgc aggttaactac cgacgcagga agtcgatctc gtctctcccc
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661 gggcctggca cggctgcagt gcgacccccc ggaaggggtc agggtgacgc cgggcgtggc
721 ggaaccgtcg gcgccaatcc tgtccgtccc atcaaggggg agacattgt ccccataccc
781 cctggcagg ctaagcagga gccgaagtt ccgcacatcgta cctgatgctc tgtcggcat
841 ccccccgg

//

LOCUS MW434137 856 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_011_ALCO genomic sequence.

ACCESSION MW434137

VERSION MW434137

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051451

Sequence Read Archive: SRR11035375

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 856)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 856)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 927.621309x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..856

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_011_ALCO"
/isolation_source="female, blood fed, collected in marsh /
wildlife refuge / park habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.55697 N 122.07938 W"
/collection_date="19-Sep-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 22..834

/codon_start=1
/product="putative Robin"
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ALSSLVSNEGVVRPARPGMSGTQPGPLAAAAVKAAACRQAVDLALAVVGEPRSAAGV
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PGDSPLAQLAAGVGETDRTRTPVRNYRRRKSDPWIPQRTEQQAAPSTGGKVCSPNLGH
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CDS complement(37..849)

/codon_start=1
/product="ORF2"
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PNYAPFVTNEGGQSRVTSGGC RRALACGYRISTV RGWWYMTAASSSST"

ORIGIN

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661 cccaaatttgg ggcattggcac ggctgcgtg cgtcccttgg agaaggacag ggtgcagcc
721 gggcgtggcg gaggcgtcg cgcccatcc tcaaggggaa gacacttgg
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//

LOCUS MW434138 867 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_018_ALCO genomic sequence.

ACCESSION MW434138

VERSION MW434138

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051458

Sequence Read Archive: SRR11035307

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 867)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 867)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 73.853165x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..867

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_018_ALCO"
/isolation_source="female, blood fed, collected in marsh /
wildlife refuge / park habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.55697 N 122.07938 W"
/collection_date="27-Sep-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 22..837
/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSDAVSAGVSPVPPTGDP
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CDS complement(37..852)
/codon_start=1
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CTLSSTKRTHCSRAMPRIGATHWTPGVQCGLMCLPGEIGLPAVIAWRTAQPIE
LSDPNCELGEGGISRRASPTACRPADEGLRGREWGPAGGGRGVDPKIRRPSRAGLHF
ENAKGERARFVKDKAHARRRARFSYYRKQVDSLACRSLYGRRSQMVRSFTLAGPA
RLNYASSVINRGGQSRVTSGGYRRANACGYRIPTVSCTRGWWFMTAASSSPT"

ORIGIN

1 gttatcctgt actggacaac gatgggtgac gcaccgtcac gtccggagacg acgaggcggc
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121 gtagccgcg cggtaaaaaactgtgcgatccgtctgt ctccctctgt taataacaga
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241 gccccggccg taaaggctgc ggcattccgc caggctgtcg acctggccct tgccgttaga
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541 ggagagctcg atcggttggg ccgtacgcca gtaagcaatt accggcgcag gaagaccat
601 cccactctcccccacggac agagcatcaa gcccactgg acacccgggg tccagtgt
661 agcccaatt cggggcatgg cacggctgca gtgcgtcctt tagggatagg acagggtgca
721 gccggccgtg gccggagtgtccgtccatccatcgccg ccatcaagggg ggagacactt
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841 tctgttagggc atccactctcccccag

//

LOCUS MW434139 857 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_019_ALCO genomic sequence.

ACCESSION MW434139

VERSION MW434139

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051459

Sequence Read Archive: SRR11035306

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 857)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnayake,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 857)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnayake,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 981.561538x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..857

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_019_ALCO"
/isolation_source="female, blood fed, collected in marsh /
wildlife refuge / park habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.55697 N 122.07938 W"
/collection_date="04-Oct-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 24..836
/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHLPPSANSAGNSGDAVSAGQGPPVPSTDNP
ALSSLVSNEGCVVRPARTGMSGTQPAHAAAALKAAACRQAVDLALAVGEPRSAAGV
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PGDSPLAQLAVVGEMDRIRTPVGNHRRKTVPLIPRTEQQAAPPTWREVCSPKLGH
GTAAVRPPREDRGAAGRGGGVGAHPGRPIKGETFGPIPPGSAKQEPKSLPST"

CDS complement(69..851)
/codon_start=1
/product="ORF2"
/translation="MPRRASGRWQRLRLFCRPRGYGTKCLPLDPARMGADASATPG
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SDPNCKLGEGGISWRASPNCRSADECLRSGCRLGAGRRGVDLLVRRPTRARLQLE
SAKGQLARFKDEAYAGRARRFSNHQCQKIDSLPACRSLNRRQCQVGRLLSSTHTGPCR
PNYAPFVTNEGGQSRVISGGYRRALACGYRISTVSVTVRGWW"

ORIGIN

1 gggttatcct gtactggaca acgatgggtg acgcaccgtc acgtcgaga cgacgaggcg
61 gcggtcattt accaccatcc gcgaacagtg caggaaacag tggagatcg gtatccgcacg
121 gccaaggccc gccgttaccc tccactgata accctgctct gcctccctc gttagtaacg
181 aagggtgcgt agttaggcgt gcaaggaccg gtatgagtgg aactcaaccc gcccacctgg
241 cagcggcggc cgtaaggct gcggcatgcc ggcaggctgt cgatctgcc ctggcagtgg
301 ttggagaacc gcgcctggcg gcccgtac gcctcgctt tgacaaagcg tgccagctgg
361 cccttagcgc tctcgagctg gagccitagca cgggtcgac ggcggaccaa aaggtaacg
421 cgcgcggcgc cgcgcggag gcacctgcat ccactgcgaa ggcactcgcc cgccgatcg
481 caggcggggtt tggggatgc gcgcaggag attccccctt cgcctaactt gcagttgggg
541 tcggagagat ggatcgatc cgacgcggg tggcaacca caggcgcagg aagaccgttc
601 cgttgatccc cgcacggaca gagcaacaag cgcacccctcc aacttggcg gagggtgtta
661 gccccaaatt ggggcattgc acggctgcg tgctcctcc gagagaggac aggggtgcag
721 cccggcgtgg cggaggcgtc ggcgcctatc ctggccggcc catcaagggg gagacattt
781 gtcccatacc ccctggatcg gcaaaacagg agccgaatgc tctgcattcg acctgatgt
841 ctgggggca tcccccg

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LOCUS MW434140 850 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_022_ALCO genomic sequence.

ACCESSION MW434140

VERSION MW434140

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051462

Sequence Read Archive: SRR11035302

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 850)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 850)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2
 Coverage :: 343.213454x
 Sequencing Technology :: Illumina
 ##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..850
 /organism="Culex narnavirus 1"
 /mol_type="genomic RNA"
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 /isolation_source="female, blood fed, collected in marsh /
 wildlife refuge / park habitat"
 /host="Culex erythrothorax"
 /db_xref="taxon:2562539"
 /environmental_sample
 /country="USA: Alameda County, California"
 /lat_lon="37.55697 N 122.07938 W"
 /collection_date="27-Sep-2017"
 /note="metagenomic; derived from metagenome: mosquito
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CDS 17..829
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 PGDSPLAQLAAGVGETDRTRTPVRNYRRKSDPWIPQRTEQQAAPSTGGKVCSPNLGH
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CDS complement(32..844)
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 CTPVLLQRTHCSRAMPQIGATHLPAGGRGCGLLCPLGDPRIALPAPIISYRTGTIRL
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ORIGIN

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 181 cgtagttagg cctgcacggc cggaaatggat tgaaactcaa cccgggtccac tggcagcgcc
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 541 gacggatgt acccgtaacgc cggtaagaaaa ttatcggcgc aggaagagcg atccgtggat
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 661 ttggggcat ggcacggctg cagtgcgttgc ttggagaag gacagggggtg cagccggcg
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LOCUS MW434141 850 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_023_ALCO genomic sequence.

ACCESSION MW434141

VERSION MW434141

DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051463

Sequence Read Archive: SRR11035301
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 850)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 850)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 873.333765x
Sequencing Technology :: Illumina
##Assembly-Data-END##
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/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
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/isolation_source="female, blood fed, collected in marsh
habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.58191 N 122.04838 W"
/collection_date="06-Oct-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"
CDS 17..829
/codon_start=1
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/translation="MGDAPSRRKRRGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP
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RLVFDKACQLALSALELPSTGRADQKVNAAPARAEAPASTAKALVRRSTGGVGCA
PGDSPLAQLAAGVGGETDRTRTPVNRKKSDPWIPQRTEQQAAPSTGGKVCSPNLGH
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CDS complement(32..844)
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/product="ORF2"
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241 ggccgtaaag gctgcggcat gccggcaggc tgcgtatctt gcccgtccag tggttggaga
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721 tggcggaggg tcggccccc atcctggccg gcccataag ggggagacac ttggtccaa
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841 gcatcccccg

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LOCUS MW434142 844 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_028_ALCO genomic sequence.

ACCESSION MW434142

VERSION MW434142

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051468

Sequence Read Archive: SRR11035296

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 844)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 844)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 110.650587x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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/isolation_source="female, blood fed, collected in
industrial (waste water treatment plant) habitat"
/host="Culex tarsalis"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.7152 N 122.19431 W"
/collection_date="12-Sep-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 17..823

/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNNAVPGVSPPAPPTDNP
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CDS complement(32..838)

/codon_start=1
/product="ORF2"
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ORIGIN

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LOCUS MW434143 929 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_029_ALCO genomic sequence.

ACCESSION MW434143

VERSION MW434143

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051469

Sequence Read Archive: SRR11035295

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 929)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 929)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 1383.575117x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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/isolate="CMS001_029_ALCO"

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adjacent to industrial (waste water treatment plant)

habitat"

/host="Culex pipiens"

/db_xref="taxon:2562539"

/environmental_sample

/country="USA: Alameda County, California"

/lat_lon="37.68473 N 121.91341 W"

/collection_date="13-Sep-2017"

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KGELAAFVEDKADASRRRARFSYHRQGVDSLTAACRSLYGRRCHRSRLSSTLPGLVRLN
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ORIGIN

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901 cgacctgtat ctctgttggg catccccccg

//

LOCUS MW434144 850 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_030_ALCO genomic sequence.

ACCESSION MW434144

VERSION MW434144

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051470

Sequence Read Archive: SRR11035294

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 850)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 850)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 581.238034x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..850
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 /mol_type="genomic RNA"
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 /isolation_source="female, blood fed, collected in
 industrial (waste water treatment plant) habitat"
 /host="Culex pipiens"
 /db_xref="taxon:2562539"
 /environmental_sample
 /country="USA: Alameda County, California"
 /lat_lon="37.7152 N 122.19431 W"
 /collection_date="10-Sep-2017"
 /note="metagenomic; derived from metagenome: mosquito
 metagenome"

CDS 22..828
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CDS complement(37..843)
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 KGELAAFVEDKADASRRARFSYHRQGQVDSLTA
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ORIGIN

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LOCUS MW434145 848 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_034_ALCO genomic sequence.

ACCESSION MW434145

VERSION MW434145

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051474

Sequence Read Archive: SRR11035289

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 848)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
 pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 848)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 857.38262x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

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/mol_type="genomic RNA"
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/isolation_source="female, blood fed, collected in marsh /
wildlife refuge / park habitat"
/host="Culex tarsalis"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.55697 N 122.07938 W"
/collection_date="11-Sep-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 21..827
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DSPLAQLAVGVGEMDRNRTSAGNYRRRSISSLPQRTEQNAAPNTRGSECSPKLGHGT
AAVRPPGRGQGAAGRGGTVGASPVLPIKGETFVPIPPGQVKQEPKVPPST"

CDS complement(36..842)
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/product="ORF2"
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CTLTPSGGSHCSRAMPQFGATLRTAGVRSGVLLCPLGERDRDLPASVTCRRTVAIHL
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HASPVSNRGQSRVISGRCRANACGYRIPTVSCTVRGWWFMTAACSFPT"

ORIGIN

1 ctatccgtta ctggacaacg atgggtgacg caccgtcacg tcggaaacga cgaggcggcg
61 gtcataaacc accatccgcg aacagtgcag gaaacagtgg gaatgcggta cccgcaggcg
121 ttagcccccc ggcacccccc actgataacc ctgtctgtc cccccccgtt actaaccggg
181 gatgcgttat tgaggctgac aaggccgaa agagtggAAC tcaaccggga cctgtggcag
241 cggcggccgt aaaggctgac gcattccgtc aggctgtca cctggccctg gcggttgt
301 gagaaccgcg ctccggcgct ggctctgcc ttgtcttcga caaaggctgc cagctgccc
361 ttagcgctct cggatggag ctagctcga gcgggacggc agggaaatct gccgcgccc
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481 gtggggatgc cgcgcggga gatccccccc tcgccccact cgcagtggg gtggagaga
541 tggatcgcaa ccgtacgtcg gcaggtaact accgacgcacg gaagtgcata tcgtctctcc
601 cccagcggac agagaaaaac gccgtcccgaa acacccgcgg ttccggatgt agccccaat
661 tggggcatgg cacggctgca gtgcgacccc ccggaaagggg tcagggtgca gccggcggt
721 gcggaaacctt cggcggccagt cctgtctgtc ccatcaagggg ggagacattt gtccccatac
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841 atcccccg

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LOCUS MW434146 852 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_035_ALCO genomic sequence.
ACCESSION MW434146
VERSION MW434146

DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051475
 Sequence Read Archive: SRR11035288
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
 Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 852)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
 pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 852)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
 499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
 Assembly Method :: IDSeq pipeline v. 3.2
 Coverage :: 414.313548x
 Sequencing Technology :: Illumina
 ##Assembly-Data-END##
FEATURES Location/Qualifiers
 source 1..852
 /organism="Culex narnavirus 1"
 /mol_type="genomic RNA"
 /isolate="CMS001_035_ALCO"
 /isolation_source="female, blood fed, collected in marsh /
 wildlife refuge / park habitat"
 /host="Culex erythrothorax"
 /db_xref="taxon:2562539"
 /environmental_sample
 /country="USA: Alameda County, California"
 /lat_lon="37.55697 N 122.07938 W"
 /collection_date="11-Sep-2017"
 /note="metagenomic; derived from metagenome: mosquito
 metagenome"
 CDS 19..831
 /codon_start=1
 /product="putative Robin"
 /translation="MGDAPSRRKRRGGSHLPPSANSAGNSGDAVSAGQGPPVPSTDNP
 ALSSLVSNEGCVVRPARTGMSGTQPAHAAA
 VKAACRQAVDLALAVVGEPRSAAGV
 RLVFDKACQLALSALEPSTGR
 TADQKVNAAPARA
 EVPA
 STAKALVRRSTGGVGCA
 PGDSPLAQLAVGVGEMDRTRPVGNHRRRKTVPLIPR
 TEQQAAPPTWREVCSPKLGH
 GTAAVRPPREDRGAAGRGGVGAHPGRPIKG
 ETLGPKPPGSAKQE
 PKSPPST"
 CDS complement(64..846)
 /codon_start=1
 /product="ORF2"
 /translation="MPRRASGRWRRLLFCRPRGF
 GT
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 MGADASATPG
 CTPVLSRRTHRSRAMPQFGATHLPPSWRCGL
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 TGPIHL
 SDPNCKLGE
 GGGISWRASP
 NPACRSADECL
 RSGCRNL
 GAGRRGV
 DLLVRRP
 TRARLQLE
 SAKGQLAR
 FK
 DEAYAGRR
 ARFSNH
 CQGK
 IDSLP
 ACRSLY
 GRR
 CQV
 GRLS
 STHTG
 PCR
 PNYAP
 FVT
 NEGG
 QSR
 VISGG
 YRR
 ALAC
 GYR
 ISTV
 C
 T
 RG
 WW"
ORIGIN
 1 atccgtact ggacaacgat gggtgacgca ccgtcacgtc gaaaacgacg cggcggcagt
 61 catttaccac catccgcgaa cagtcgacca aacagtggag atgcggatc cgcaggccaa
 121 gccccggcgg taccctccac tgataaccct gctctgtccct ccctcgtag taacgaagg
 181 tgcgtagtta ggcctgcgaa gaccggatg agtggaaactc aacccggccca cctggcagcg
 241 gccccggtaa aggctgcggc atgcccggcag gctgtcgatc ttgcccggc agtggttgga
 301 gaaccgcgcg cggcggccgg cgtacgcctc gtcttgaca aagcgtgcca gctggccctt
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421 ccggcccccgcc cgaggttcc tgcatccact gcgaaggcac tcgtccgccc atcgacaggc
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661 aaattggggc atggcacggc tgccgtcgct cctccgagag aggcacagggg tgcagccggg
721 cgtggcggag gcgtccggc ccatcctggc cgcccatca agggggagac acttggtccc
781 aaacccctcg ggtccgaaa acaggagccg aagtctccgc catcgacctg atgctctcg
841 gggcatcccc ca

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LOCUS MW434147 844 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_036_ALCO genomic sequence.

ACCESSION MW434147

VERSION MW434147

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051476

Sequence Read Archive: SRR11035287

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 844)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 844)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 209.842243x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..844

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_036_ALCO"
/isolation_source="female, blood fed, collected in marsh /
wildlife refuge / park habitat"
/host="Culex tarsalis"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.55697 N 122.07938 W"
/collection_date="11-Sep-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 17..823

/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPGVSPPAPPTDNP
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAA AVKAAACRQAVDLALAVVGEPRSAAGV
CLVFDKGCLALSALGMEPSSSGTAGKSAAPARAEAPVSTARAPVRRSTGGGGCAPG
DSPLAQLAVGVGEMDRNRTSAGNYRRRKSISSLPQRTEQNAAPNTRGSECSPKLGHGT
AAVRPPGRGQGAAGRGGTVGASPVLPIKGETFVPIPPGQIKQEPKVPPST"

CDS complement(32..838)

/codon_start=1
/product="ORF2"

/translation="MPNRASGRWRNLRLLFNLPRGYRDKCLPLDGQNRTGADGSATPG
CTLTPSGGSHCSRAMPQFGATLRTAGVRSGVLLCPLGERRDRLPASVVTCRRTVAIHL
SDPNCELGEGGISRRASPTPASRPADWGPRGGDWLSGTGRRGRLSCRPARARLHPESA
KGELAAFVEDKADASRRARFSYHRQGVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN
HASPVSNRGQSRVISGRCRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

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121 cccgcccggca cctcccaactg ataacctgc tctgtcccccc ccgggttacta accggggatg
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241 ggccgtaaag gctgcggcat gccgtcaggc tgtgacactg cccctggcg tggtaggaga
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541 tcgcaaccgt acgtcggcag gtaactaccg acgcaggaag tcgatctcg tctccccc
601 gcggacagag caaaacgcgc ctccgaacac cccgggttcg gagtgtagcc ccaaattggg
661 gcatggcagc gctgcagtgc gaccccccgg aagggggtcag ggtgcagccg ggcgtggccg
721 aaccgtcgcc gccagtcctg ttctgccc catgggggag acatttgcc ctatacccc
781 tgggcagatt aaacaggagc cgaaggttcc gccatcgacc tgatgctcg ttggcatcc
841 ccca

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LOCUS MW434148 843 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_037_ALCO genomic sequence.

ACCESSION MW434148

VERSION MW434148

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051477

Sequence Read Archive: SRR11035286

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 843)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 843)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 300.668407x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..843

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_037_ALCO"
/isolation_source="female, blood fed, collected in marsh /
wildlife refuge / park habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.55697 N 122.07938 W"
/collection_date="18-Aug-2017"

/note="metagenomic; derived from metagenome: mosquito metagenome"

CDS 17..829
/codon_start=1
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/translation="MGDAPSRRNRRGGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP
ALSSLVSNEGCVVRPARPGMSGTQPGPLAAAVKAAACRQAVDLALAVVGEPRSAAGV
RLVFDKACQLALSALELPSTGRTADQKVNAAPARAEAPASTAKALVRRSTGGVGCA
PGDSPLAQLAAGVGGETDRTRTPVSNYRRRKSDPWIPQRTEQQAAPSTGGKVCSPNLGH
GTAAVCPLERGAAGRGGVGAHPGRPIKGETLGPKPPGSAKQEPKSPPST"

ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg aatcgacgag gcggcggtca
61 tataccacca tccgcgaaca gtgcaggaaa cagtggagat gcggtagcccg caggccaagg
121 cccgccccca ccctccactg gtaaccctgc tctgtccctc ctcgttagta acgaagggtg
181 ctagtttagg cctgcacggc ccggaatgag tggaactcaa ccgggtccac tggcagcgcc
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661 ttggggcat ggcacggctg cagtgtgtcc ttggagaag gacaggggtg cagccggcg
721 tggcggagggc gtcggccccc atccgtggccg gcccatcaag ggggagacac ttggcccaa
781 accccctggg tcggcaaaac aggagccgaa gtctccgcca tcgacctgat gctctgcggg
841 gcg

//

LOCUS MW434149 841 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_038_ALCO genomic sequence.

ACCESSION MW434149

VERSION MW434149

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051478
Sequence Read Archive: SRR11035285

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricetes; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 841)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 841)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 53.701571x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..841
/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_038_ALCO"
/isolation_source="female, blood fed, collected in marsh
habitat"
/host="Culex tarsalis"

/db_xref="taxon:2562539"
 /environmental_sample
 /country="USA: Alameda County, California"
 /lat_lon="37.58391 N 122.09238 W"
 /collection_date="24-Aug-2017"
 /note="metagenomic; derived from metagenome: mosquito
 metagenome"

CDS 17..823
 /codon_start=1
 /product="putative Robin"
 /translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAPAVGSPPAPPTDNP
 ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAAVKAACRQAVDLALAVGEPRSAAGV
 CLVFDKGCLALSALGMEPSSSGTAGKTAAPARAEAPVSTARAPVRRSTGGGGCALG
 DSPLAQLAVGVGEMDRHRTSAGNYRRRKSISSLQPQTEQNAAPNTQGSECSPKLGHGT
 AAVRPPGRGQGAAGRGGTVGASPVLPIKRETFVPIPMSGQIKQEPKVPPST"

CDS complement(32..838)
 /codon_start=1
 /product="ORF2"
 /translation="MPNRASGRWRNLRLFYLPREGDKCLPLDGQNRTGADGSATPG
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 SDPNCELGEGGISQRASPTPASRPADWGPRGGDWSLGTGGRSGFTRCPARARLHPESA
 KGELAAFVEDKADASRRRARFSYHRQGVDSLTTARRSLYGRRCHRSRLSSTLSGLVRLN
 HASPVSNRGGQSRVISGRCRRAHACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN
 1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg agacgcagag gcggcggtca
 61 taaaccacca tccgcgaaca gtgcaggaaa cagtggaaat gcggtacccg caggcgtgag
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 241 ggccgtaaag gctgcggcgt gccgtcaggc tgcgacccctg gcccggcgg tggtaggaga
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 661 gcatggcacg gctgcagtgc gaccccccgg aagggttcg ggtgcagccg ggcgtggcgg
 721 aaccgtcggc gccagtccgt ttctgcccattt caagagggag acatttgcc ccataccctc
 781 tggcagata aaacaggagc cgaaggttcc gccatcgacc tgcgtctg ttggcattcc
 841 c

//

LOCUS MW434150 851 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_040_ALCO genomic sequence.
ACCESSION MW434150
VERSION MW434150
DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051480
 Sequence Read Archive: SRR11035283

KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
 Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 851)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
 pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 851)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
 499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##
 Assembly Method :: IDSeq pipeline v. 3.2
 Coverage :: 411.014212x
 Sequencing Technology :: Illumina
 ##Assembly-Data-END##
 FEATURES Location/Qualifiers
 source 1..851
 /organism="Culex narnavirus 1"
 /mol_type="genomic RNA"
 /isolate="CMS001_040_ALCO"
 /isolation_source="female, blood fed, collected in undeveloped habitat"
 /host="Culex pipiens"
 /db_xref="taxon:2562539"
 /environmental_sample
 /country="USA: Alameda County, California"
 /lat_lon="37.49949 N 121.93378 W"
 /collection_date="31-Aug-2017"
 /note="metagenomic; derived from metagenome: mosquito metagenome"
 CDS 24..830
 /codon_start=1
 /product="putative Robin"
 /translation="MGDAPSRRRRGGGQKPPSANSAGDSREAVSAGASPPMPPTGNP
 ALSSSVNNRGCYEPDRARKSGTQPGPATAAASKAAVCRQAVDLALTIVGEPRSVAGV
 RLVFDKACQLTCSALGMEPSTSGAASKLAAPARAEAPISTVRAPVRRSTGGGGCALG
 DSPLAQLAVGVGEMDRVRTTAGNYRRRHTVSSFPQRTEHKAVPDTHGPECSPKLGHGT
 AAVRPPGRGQGAAGRGAIGTHPALPIKEETLGPKPPQIKREPKVPPST"
 CDS complement(39..845)
 /codon_start=1
 /product="ORF2"
 /translation="MPYRASGRWRNLRLPLYLPERRFGTKCLLDGQSGMGADSSATPG
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 SDPNCELGEGGVSQRASPTPASRPADWSPHGGDWGLGAGGRGKLACRSARARLHPERA
 TGELARLVKDEAYACHGARFSYHRQGQVDSLTTDCSLRGRRCRGSRLSSTLGPVRLI
 HASSVINRGQQRVTSRGHRRACACGYRFPTVSCTVRGWWFLTAASSSPT"
 ORIGIN
 1 gggttatcct gtactggaca acgatgggtg acgcaccgtc acgtcgaga cgacgaggcg
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 181 gaggatgcgt gtatgagcct gacagggccc gaaagagtg aactcaacc ggacccgcga
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 421 ccgcggcgcg cgagggccca atccaccc tgaggcgtcc agtccgcgg tcgactggcg
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 721 gtggcggagc tatccgcacc catccgcctc tgccatcaa ggaggagaca ctggtccca
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 841 ggcattcccc g
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 LOCUS MW434151 857 bp RNA linear ENV 18-FEB-2021
 DEFINITION Culex narnavirus 1 isolate CMS001_041_ALCO genomic sequence.
 ACCESSION MW434151
 VERSION MW434151
 DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051481
 Sequence Read Archive: SRR11035281
 KEYWORDS ENV.
 SOURCE Culex narnavirus 1 (mosquito metagenome)
 ORGANISM Culex narnavirus 1
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
 Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 857)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 857)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 296.325641x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..857

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_041_ALCO"
/isolation_source="female, blood fed, collected in
undeveloped habitat"
/host="Culex pipiens"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.49949 N 121.93378 W"
/collection_date="31-Aug-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 17..823

/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNNAVPGVSPPAPPTGNP
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DSPLAQLAVGVGEMDRHRTSAGNYRRKSISLPLQRTEQNAAPNTQGSECSPKLGP
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CDS complement(32..838)

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ORIGIN

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301 accgcgctcg gccgtggcg tctgcctgt ctgcacaaa ggctgccagc tcgccccttag
361 cgctctcggt atggagccca gcccggcg gacggcggtt aaaacccgtg ccccccccg
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661 gcctggcacg gtcgcagtgc gaccccccgg aaggggtcg ggtgcagccg ggcgtggccg
721 aaccgtcgcc gccaacctg ttctgcccattt caagaggag acattcgcc ccataccctc
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LOCUS MW434152 845 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_042_ALCO genomic sequence.
ACCESSION MW434152
VERSION MW434152
DBLINK BioProject: PRJNA605178
BioSample: SAMN14051482
Sequence Read Archive: SRR11035280
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenaviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 845)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 845)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 333.809896x
Sequencing Technology :: Illumina
##Assembly-Data-END##
FEATURES Location/Qualifiers
source 1..845
/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_042_ALCO"
/isolation_source="female, blood fed, collected in golf
course habitat"
/host="Culex tarsalis"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.66126 N 122.13335 W"
/collection_date="25-Aug-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"
CDS 17..823
/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPGVSPPAPPTDNP
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CLVFDKGCLALSALGMEPSSSGTAGKSAAPARAEAPVSTARAPVRRSTGGGGCAPG
DSPLAQLAVGVGEMDRNRTSAGNYRRRKSISSLPQRTEQNAAPNTRGSECSPKLGHGT
AAVRPPGRGQGAAGRGGTVGASPVLPIKGETLVPPIPPGQIKQEPEVPPST"
CDS complement(32..838)
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/product="ORF2"
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HASPVSNRGQSRVISGRCRANACGYRIPTVSCTVRGWWFMTAASSSPT"
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121 cccgccccca cctcccaactg ataaccctgc tctgtccctcc ccgggttacta accggggatg
181 cgtgatttag cctgacaagg cccgaaagag tgaactcaa ccgggacctg tgccagccgc
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661 gcacggcagc gctgcagtgc gaccccccgg aaggggtcg ggtcagcc ggcgtggcgg
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841 cccca

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LOCUS MW434153 846 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_044_ALCO genomic sequence.

ACCESSION MW434153

VERSION MW434153

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051484
Sequence Read Archive: SRR11035278

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 846)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 846)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 71.460338x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..846
/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
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/isolation_source="female, blood fed, collected in golf
course habitat"
/host="Culex pipiens"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat lon="37.66126 N 122.13335 W"
/collection_date="25-Aug-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 22..828
/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGHKPPSANSAGNSGNAVPAGVSPPAPPTDNP
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAAVKAAACRQAVDLALAVGEPRSAAGV
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DSPLAQLAVGVGEMDRNRTSAGNYRRRKSISLPLQRTEQNAAPNTRGSECSPKLGPGT
AAVRPPGRGQGAAGRGGTVGANPVLPIKGETFVPIPPGQVKQEPRFPPST"
CDS complement(37..843)
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HASPVSNRGQSRVISGRCCRANACGYRIPTVSCTRGWWFMTAASSSPT"
ORIGIN
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181 ggatgcgtga ttgagcctga caaggcccga aagagtggaa ctcaaccggg acctgtggca
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661 ttggggctcg gcacggctgc agtgcgaccc cccggaaggg gtcagggtgc agccggcgt
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841 catccc
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LOCUS MW434154 933 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_045_ALCO genomic sequence.
ACCESSION MW434154
VERSION MW434154
DBLINK BioProject: PRJNA605178
BioSample: SAMN14051485
Sequence Read Archive: SRR11035277
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricetes; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 933)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 933)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 99.811916x
Sequencing Technology :: Illumina
##Assembly-Data-END##
FEATURES Location/Qualifiers
source 1..933
/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_045_ALCO"
/isolation_source="female, blood fed, collected in marsh /
wildlife refuge / park habitat"
/host="Culex erythrothorax"

/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.55697 N 122.07938 W"
/collection_date="03-Aug-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 101..913
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/translation="MGDAPSRRRRGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP
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RLVFDKACQLALSALELPSTGRTADQKVNAAPARAEPASTAKALVRRSTGGVGGCA
PGDSPLAQLAAGVGETDRTRTPVSNYRRRKSDPWIPQRTEQQAAPSTGGKVCSPNLGH
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CDS complement(116..928)
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SDPSCKLGEGGISWRASPNCRSADECLRSGCRLGAGRRGVDLLVRRPTRARLQLE
SAKGQLARFKDEAYAGRRARFSNHCQGKIDSLPACRSLYGRRCQWTRLSSTHSGPCR
PNYAPFVTNEGGQSRVTSGGCRRALACGYRISTVRGWWYMTAASSSPT"

ORIGIN

1 cagctcgaaa gcggttcca acttgcatt cattcctgaa ggtttcctag cttccaaatc
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121 tcggagacga cgaggccgcg gtcataacc accatccgcg aacagtgcac gaaacagtgg
181 agatcggtt cccgcaggcc aaggcccgc ggcacctcc actggtaacc ctgtctgtc
241 ctccctcggt agtaacgaag ggtgcgttgt taggcctgca cggcccgaa tgagtggAAC
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601 ccaactgtca gctgggtcgtc gagagacggc tcgtaccgt acgcccgtaa gcaattatcg
661 ggcgcaggaaag agcgatccgt ggatccccca gcccggacagag caacaagccg caccccccac
721 cggcggaaag gtgttagcc ccaattttggg gcatggcactc gtcgtgc gtcctttgg
781 gaaggacagg ggtgcagccg ggcgtggccg aggcgtccgc gcccattctg gcccggccat
841 caagggggag acacttggtc ccaaaaccccccc tgggtcggca aaacaggagc cgaagtctcc
901 gccatcgacc tgatgtctg cggggcatcc ccc

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LOCUS MW434155 853 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_047_ALCO genomic sequence.

ACCESSION MW434155

VERSION MW434155

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051487

Sequence Read Archive: SRR11035275

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 853)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 853)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,

499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 311.988402x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..853

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
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/isolation_source="female, blood fed, collected in marsh /
wildlife refuge / park habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.55697 N 122.07938 W"
/collection_date="03-Aug-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 22..834

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/product="putative Robin"
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CDS complement(37..849)

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/product="ORF2"
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SAKGQLARFKDEAYAGRRARFSNHCQGKIDSLPACRSLYGRRCQWTRLSSTHSGPCR
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ORIGIN

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721 gggcgtggcg gaggcgtcg cgcccatctt ggcggccca tcaaggggaa gacacttgc
781 cccaaacccc ctgggtcgcc aaaacaggag ccgaagttc cgcacatcgac ctgtatgcct
841 gccccccatc ccc

//

LOCUS MW434156 840 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_048_ALCO genomic sequence.

ACCESSION MW434156

VERSION MW434156

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051488

Sequence Read Archive: SRR11035274

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 840)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 840)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 152.897772x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..840

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_048_ALCO"
/isolation_source="female, blood fed, collected in marsh /
wildlife refuge / park habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.55697 N 122.07938 W"
/collection_date="03-Aug-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 17..>840

/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRKRRGGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP
ALSSLVSNEGCVVRPARPGMSGTQPGSLAAAALKAAACRQAVDLALAVVGEPRSAAGV
RLVFDKACQLALSALELPSTGRADQKVNAAPARAEVPAKALVRRSTGGGGCA
PGDSPLAQLAVGVGETDRIRTPVSYRRRKSDPWIPRRTEQQAAPPTWREVCSPLGH
GTAAVCPPREDRGAAGRGGVGAHPGRPIKGETLGPKPPGSAKQEPKSPPSTRCSAG"

ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcga aaacgacgag gcggcggtca
61 tataccacca tccgcgaaca gtgcaggaaa cagtggagat gcgggtcccc caggccaagg
121 cccgcggca ccctccactg gtaacctgc tctgtccctc ctgcgttaga acgaagggtg
181 cgtagttagg cctgcacggc ccggaaatgg tagaactcaa ccgggcttc tggcagcggc
241 ggccgtaaag gctgcagcat gcccgcaggc tgcgcattt gcccgtggcag tggttggaga
301 accgcgcctcg gcccgcggcg tacgcctcg ttggacaaaa gcgtgccgc tgcccttag
361 cgctctcgag ctggagccta gcacgggtcg gacggcggac caaaagggtca acgcccgcacc
421 ggcgcgcgc gagggtccctg catccactgc gaaggcactc gtccgcgcgt cgacaggcg
481 ggggtggggga tgcgcgcgc gagattcccc cctcgcccaa ctgcgttg gggtcggaga
541 gacggatcg atccgtacgc cgtagttag ctatcgccgc aggaagagcg atccgtggat
601 ccccgacgg acagagcaac aagccgcacc tccaacttgg cgggagggtgt gtggcccaa
661 attggggcat ggcacggctg cagtgtgtcc tccgagagag gacagggggtg cagccggcgc
721 tggcggaggc gtcggcgcgc atccgtggcgc gcccataag ggggagacac ttggcccaa
781 accccctggg tcggcaaaac aggagccaa gtctccgcgc gtcgtcgccc

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LOCUS MW434157 854 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_051_ALCO genomic sequence.

ACCESSION MW434157

VERSION MW434157

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051491

Sequence Read Archive: SRR11035270

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 854)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 854)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 462.212355x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..854

/organism="Culex narnavirus 1"

/mol_type="genomic RNA"

/isolate="CMS001_051_ALCO"

/isolation_source="female, blood fed, collected in marsh
habitat"

/host="Culex tarsalis"

/db_xref="taxon:2562539"

/environmental_sample

/country="USA: Alameda County, California"

/lat_lon="37.50608 N 121.99857 W"

/collection_date="17-Oct-2017"

/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 27..833

/codon_start=1

/product="putative Robin"

/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTDNP
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLAGLAVVGEPRSAAGV
CLVFDKGCLQLALSALGMEPSSSGTAGRSAAPARAEAPVSTARAPVRRSTGGGGCAPG
DSPLAQLAVGVGEMDRNRTSTGNCRRKSISSLQPQRTEQHAAPNTRGSECSPKLGHGT
AAVRPPGRGQGAAGRGGTVGASPVLPIKGETFVPIPPGQVKQEPKVPPST"

CDS complement(42..848)

/codon_start=1

/product="ORF2"

/translation="MPNRASGRWRNLRLFNLPGYGDKCLPLDGQDRTGADGSATPG
CTLTPSGGSHCSRAMPQFGATLRTAGVRSGVLLCPLGERRDRLPASAVTCRRTVAIHL
SDPNCELGEGGISRRASPTPASRPADWGPRGGDWSLGTGGGRRSSCRPARARLHTESA
KGELAAFVEDKADASRRRARFSYHRQGQVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

1 ggggggttat cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg agacgacgag
61 gcggcggtca taaaccacca tccgcgaaca gtgcaggaaa cagtggaat gcggtacccg
121 caggcgtag cccgccccca cctcccactg ataaccctgc tctgtcccc ccggttacta
181 accggggatg cgtgattgag cctgacaaagg cccgaaagag tggaactcaa ccgggacctg
241 tggcagcggc gggcgtaaag gctgcggcat gccgtcaggc tgtgcacctg gcccggccg
301 tggtaggaga accgcgctcg gccgctggcg tctgccttg ctccgacaaa ggctgccagc
361 tcggcccttag cgctctcggt atggaggcta gctcgacgg gacggcagga agatctgc
421 cgcccgcccg tgccgaggct ccagtctcca ccgcgaggggc cccagtcgc cggctcactg
481 gcgggggtgg gggatgcgcg ccgggagatt cccccctcgc ccaactgcga gttggggtcg
541 gagagatgga tcgcaaccgt acgtcgacag gtaactgcga acgcaggaag tcgatctcg

601 ctctccccca gcggacagag caacacgccc ctccgaacac ccgcgggtcg gagtgttagcc
661 ccaaattggg gcatggcacr gctgcagtgc gaccccccgg aaggggtcag ggtgcagccg
721 ggcgtggcgg aaccgtggc gcgcgtccgt tcctgccccat caagggggag acatttgc
781 ccataccccc tgggcaggaa acaggagc cgaagggtcc gccatcgacc tgatgctctg
841 ttggcattcc cccg

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LOCUS MW434158 849 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_052_ALCO genomic sequence.

ACCESSION MW434158

VERSION MW434158

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051492
Sequence Read Archive: SRR11035269

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 849)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 849)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 315.13342x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..849
/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_052_ALCO"
/isolation_source="female, blood fed, collected in marsh /
wildlife refuge / park habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.55697 N 122.07938 W"
/collection_date="21-Sep-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 17..829
/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRERRGGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP
ALSSLVSNEGCVVRPARPGMSGTQPGPLAAAVKAAACRQAVDLALAVVGEPRSAAGV
RLVFDKACQLALSALELEPSTGRTADQKVNAAPARAEAPASTAKALVRRSTGGVGGCA
PGDSPLAQLAAGVGETDRTRTPVRNYRRRKSDPWIPQRTEQQAAPSTGGKVCSPNLGH
GTAAVRPLEKDRGAAGRGGVGAHPGRPIKGETLGPKPPGSAKQEPKSPPST"

CDS complement(32..844)
/codon_start=1
/product="ORF2"
/translation="MPRRASGRWRLRLFCRPRGFGTKLPLDPARMGADASATPG
CTPVLLQRTHCSRAMPQIGATHLPAGGRGCGLLCPLGDPRIALPAPIISYRRGTIRL
SDPSCKLGEGGISWRASPNPACRSADECLRSGCRLGAGRRGVDLLVRRPTRARLQE

SAKGQLARFKDEAYAGRRARFSNHCQGKIDSLPACRSLYGRRCQWTRLSSTHSGPCR
PNYAPFVTNEGGQSRVTSGGCRRALACGYRISTVSRGWWYMTAASSFST"

ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcga gaacgacgag gcggcggtca
61 tataccacca tccgcgaaca gtgcaggaaa cagtggagat gcggtacccg caggccaagg
121 cccgcccggca ccctccactg gtaacctgc tctgtcctc tcgttagta acgaagggtg
181 ctagttagg cctgcacggc ccggaatgag tggaactcaa ccgggtccac tggcagccgc
241 ggccgtaaag gctgcggcat gccggcaggc tgcgatctt gcccggcag tggttggaga
301 accgcgtcg gcggccggcg tacgcctcg tttgacaaa gctgcccagc tggcccttag
361 cgctctcgag ctggagccta gcacgggtcg gacggcggac caaaagggtca acgcccgc
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481 ggtggggga tgccgcggcag gagattcccc ctcgcggcaa ctgcgctg gggtcggaga
541 gacggatcgatcccgtaacgc cggtaaagaaa ttatcggcgc aggaagagcg atccgtggat
601 cccccagcgg acagagcaac aagccgcacc ttccaccggc gggaaagggtgt gtggcccaa
661 ttggggcat ggcacggctg cagtgcgtcc ttggagaag gacagggggtg cagccggcg
721 tggcggaggc gtcggcggcc atccctggccg gccatcaag ggggagacac ttggtcccaa
781 accccctggg tcggcaaaac aggagccaa gtcctccgca tcgacctgat gctctgcggg
841 gcatcccc

//

LOCUS MW434159 844 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_054_ALCO genomic sequence.

ACCESSION MW434159

VERSION MW434159

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051494

Sequence Read Archive: SRR11035267

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 844)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 844)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 88.254237x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..844

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_054_ALCO"
/isolation_source="female, blood fed, collected in marsh /
wildlife refuge / park habitat"
/host="Culex pipiens"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.63083 N 122.14267 W"
/collection_date="10-Feb-2016"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 17..823

/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPVPTGNP
ALSPPVSNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLALAVGEPRSAAGV
CLVFDKGCLQALSLALGMESSPSGTAGKTAAPARAEAPVSTARAPVRRSTGGGGCALG
DSPLAQLAVGVGEMDRHRTSAGNYRRRKSISSLQPQTEQNAAPNTQGSECSPELGP
AAVRPPGGGQGAAGRGGTVGANPVLPIKRETFVPKPSQIKQEPKVPPST"

CDS complement(32..838)
/codon_start=1
/product="ORF2"
/translation="MPDRASGRWRNFRLFNLPFGDECLPLDGQNRIADGSATPG
CTLTPAGGSCHCSRARPQFGATLTLGVRSGVLLCPGLERRDRLPAPVACRTVSIHL
SDPNCELGEGGISQRASPTPASRPADWGPGRGGDWLSLTGGRSGFTRPARARLHPESA
KGELAALVKDKADASRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN
HASPVRNRGGQSRVTSGRYRRANACGYRIPTVSCTVRGWWFVTAASSP"

ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg agacgacgag gcggcggtca
61 caaacccacca tccgcgaaca gtgcaggaaa cagtggaaat gcggtaaccgg caggcgtag
121 cccgccccgtta cctcccaactg gtaaccctgc tctgtcccccc cccgttcta accggggatg
181 cgtgatttag cctgacaagg cccgaaagag tgaactcaa ccgggacctg tggcagccgc
241 ggccgtaaag gctgcggcat gccgtcaggc tgcgtacccgc gcccggcg tgtaggaga
301 accgcgcctcg gcggctggcg tctgcctgt ctggacaag ggctgccagc tcgcccattag
361 cgctctcggg atggagtcta gcccggcg gacggcggtt aaaaccgctg cggccggcc
421 tgccgaggct ccagtctcca cccgcggggc cccagtcgcg cggcgtactg ggggggtgg
481 gggatgcgcg ctggagatt ccccccgc ccaactcgca gttgggtcg gagatgga
541 tcgacaccgt acgtcgccag gcaactaccg gcgcaggaaat tcgatctcg ctctccca
601 gcggacagag caaaaacgcgcg ctccgaacac ccagggttcg gagtgtagcc cgaattggg
661 gcctggcgcg gtcgcgtgc gaccccccgg cgggggtcag ggtgcagcc ggcgtggcg
721 aaccgtcgcc gccaatctgt ttctggccat caagaggag acattcgcc ccaaaccctc
781 tggcagatt aaacaggagc cgaaagtcc gccatcgacc tgatgctcg tcggcattcc
841 cccg

//

LOCUS MW434160 847 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_058_ALCO genomic sequence.

ACCESSION MW434160

VERSION MW434160

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051498
Sequence Read Archive: SRR11035263

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 847)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 847)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 63.862338x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..847
/organism="Culex narnavirus 1"

/mol_type="genomic RNA"
/isolate="CMS001_058_ALCO"
/isolation_source="female, blood fed, collected in
marsh/swamp habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: Alameda County, California"
/lat_lon="37.557 N 122.0794 W"
/collection_date="21-Sep-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 23..835
/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRKRRGGSHKPPSANSAGNSGDAVSAGQGPPVPSTGNP
ALSSLVSNEGCVVRPARTGMSGTQPAHAAAVKAAACRQAVDLALAVGEPRSAAGV
RLVFDKACQLALSALEEPSTGRADQKVNAAPARAEVPASTAKALVRRSTGGVGCA
PGDSPLAQLAVGVGEMDRTRTPVGNHRRRKTVPLIPRTEQQAAPPTWREVCSPKLGH
GTAAVRPPREDRGAAGRGGGVGANPGRPIKGTLGPKPPGSAKQEPKSPPST"

ORIGIN

1 ggttatcccg tactggacaa cgtatgggtga cgccaccgtca cgtcgaaaac gacgaggcgg
61 cagtctaaaa ccaccatccg cgaacagtgc aggaaacagt ggagatgcgg tatccgcagg
121 ccaaggcccc ccgttacccct ccactggtaa cctgtctcg tcctccctcg ttagtaacga
181 agggtcgtta gttagccgtt caaggaccgg tatgagtggaa actcaaccgg cccacccgg
241 agccgcggcc gttaaaggctg cggcatggc gcaggctgtc gatctggccc tggcagtgg
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481 aggcgggggtt gggggatgcg cggcaggaga ttccccctc gccaacttg cagttgggg
541 cggagagatg gatcggaccc gtacgccagt gggcaaccac cggcgcagga agaccgtcc
601 gttgatcccc cgacggacag agcaacaaggc cgccacctcca acttggcggg aggtgttag
661 ccccaaattt gggcatggca cggctcggtt ggcgcctcc agagaggaca ggggtgcacg
721 cggcgtggc ggaggcgtcg gcccataatcc tgccggccc atcaaggggg agacacttgg
781 tcccaaaccctt cctgggtcgg caaaacagga gccaaggatct cggccatcgaa cctgatgctc
841 tgccgggg

//

LOCUS MW434161 844 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_059_ALCO genomic sequence.

ACCESSION MW434161

VERSION MW434161

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051499

Sequence Read Archive: SRR11035262

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 844)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 844)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 271.877445x

Sequencing Technology :: Illumina
 ##Assembly-Data-END##
FEATURES Location/Qualifiers
 source 1..844
 /organism="Culex narnavirus 1"
 /mol_type="genomic RNA"
 /isolate="CMS001_059_ALCO"
 /isolation_source="female, blood fed, collected in
 industrial (waste water treatment plant) habitat"
 /host="Culex pipiens"
 /db_xref="taxon:2562539"
 /environmental_sample
 /country="USA: Alameda County, California"
 /lat lon="37.6683 N 122.15915 W"
 /collection_date="24-Oct-2017"
 /note="metagenomic; derived from metagenome: mosquito
 metagenome"
 CDS 17..823
 /codon_start=1
 /product="putative Robin"
 /translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTDNP
 ALSSPVNRCGVIEPDKARKSGTQPGPMAAAAVKAAACRQAVDLALAVVGEPRSAAGV
 CLVFDKGQCQLALSALGMEPSPSGTAGKTAAPARAEAPVSTARAPVRRSTGGGGCALG
 DSPLAQLAVGVGEMDRHRTSAGNYRRKSISSLPQRTEQNAAPNTQGSECSPKLGP GT
 AAVRPPGRGQGAAGRGGTVGANPVLPKRETVPVIPSGQIKQEPKVPPST"
 CDS complement(32..838)
 /codon_start=1
 /product="ORF2"
 /translation="MPDRASGRWRNFRLFYLPRGYGDECLPLDGQNRIADGSATPG
 CTLTPSRGSHCSRARPQFGATLRTLGVRSGVLLCPLGERDRDRLPAPVACRRTVSIHL
 SDPNCELGEGGISQRASPTPASRPADWGRGGDWLSLTGGRSGFTRCPAWARLHPESA
 KGELAAFVEDKADASRRARFSYHRQQVQDSLTA CRSLYGRRCHRSRLSSTLSGLVRLN
 HASPVSNRGGSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"
ORIGIN
 1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg agacgacgag gcccggta
 61 taaaccacca tcgcgaaca gtgcaggaaa cagtggaat gcggtaccc caggcgtag
 121 cccgccccca cctcccaactg ataaccctgc tctgtccctcc ccggttacta accggggatg
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 241 ggccgtaaag gctgcggcat gccgtcaggc tgcgcacccg gcccctggcgg tggtaggaga
 301 accgcgcctcg gccgcggcg tctgcctgt ctgcacaaa ggctgccagc tcgccttag
 361 cgctctcgcc atggaggcta gccaagcgg gacagcgggt aaaaccgcgt cggcccccgc
 421 tgccgaggct ccagtctcca ccgcgaggcc cccagtcgc cggcgcactg gccccgggtgg
 481 gggatgcgcg ctggagatt ccccccgc ccaactcgca gttggggtcg gagatgga
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 661 gcctggcacg gctgcagtgc gaccccccggg aagggttcg ggtgcagccg ggcgtggccg
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 841 cccca
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LOCUS MW434162 845 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_001a_SAND genomic sequence.
ACCESSION MW434162
VERSION MW434162
DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051501
 Sequence Read Archive: SRR11035259
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
 Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 845)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 845)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 1740.710938x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..845
/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS002_001a_SAND"
/isolation_source="female, blood fed, collected in park/cemetery/golf course habitat"
/host="Culex quinquefasciatus"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: San Diego County, California"
/lat_lon="32.7962659 N 116.9594824 W"
/collection_date="15-Nov-2017"
/note="metagenomic; derived from metagenome: mosquito metagenome"

CDS 19..825
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/product="putative Robin"
/translation="MGDAPSRRKRRGGGHIPPSANSAGNSGNAVPAGVSPPVPTGNP
ALSPPVTNRGCVIEPGKARKSGTQPGPVAAA
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CLVFDKGCLQALSA
LGMEPSPSGTAGKTAAPARAEAPVSTARAPVRRSTGGGGCALG
DSPLAQLAVGVGEMDRYRTL
LAGNYRRRKSISSLPQRTEQNAAPNTQGSECSPKLGPGT
AAVRPPGRGQGAAGRGGTVGANPVLPIKRET
FVPIP
SGQIKQEPKVPPST"

CDS complement(34..840)
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/product="ORF2"
/translation="MPDRASGRWRNFRLLNLP
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GVR
SGILL
CPLG
ERRD
RDP
APV
VAC
QRT
VSIHL
SDPN
CEL
GEG
GIS
QR
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PTP
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GLARLN
HAS
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CTV
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ASS
FPT"

ORIGIN

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241 gcggccgtaa aggctgcggc ttgcgtcag gctgtcgacc tggccctggc ggtggtagga
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841 ccccg

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LOCUS MW434163 853 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_022a_SAND genomic sequence.

ACCESSION MW434163
VERSION MW434163
DBLINK BioProject: PRJNA605178

BioSample: SAMN14051521
Sequence Read Archive: SRR11035237

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenaviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 853)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 853)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 389.385309x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..853

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS002_022a_SAND"
/isolation_source="female, unfed, collected in undeveloped
habitat"
/host="Culex quinquefasciatus"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: San Diego County, California"
/lat_lon="32.552783 N 117.0559469 W"
/collection_date="27-Dec-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 27..833

/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGDSGNAPAGVSPPAPPTGNP
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CLVFDKGCLQLSALGMEPSSSGTAGKSAAPARAEPVSTARAPVRRSTGGGRGCAPG
DSPLAQLAVGVGEMDRDRTSAGNYRRRKSISLSPQRTEQKAAPNSRGSECSPKLGPGT
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CDS complement(42..848)

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/product="ORF2"
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ORIGIN

1 caggggttat cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg agacgacgag
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121 caggcgtag cccgcggca cctcccactg gtaaccctgc tctgtcccccc ccggttacta
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661 ccaaattggg gcctggcacg gctgcagtgc gaccccccgg aagggggtcag ggtgcagccg
721 ggcgtggccg aaccgtcgcc gccaatcccg tcctgcccatt caagggggag acatggtcc
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841 ttggccatcc ccc

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LOCUS MW434164 930 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002_023a_SAND genomic sequence.

ACCESSION MW434164

VERSION MW434164

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051522
Sequence Read Archive: SRR11035236

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 930)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 930)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 1606.478312x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..930
/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS002_023a_SAND"
/isolation_source="female, unfed, collected in
commerical/industrial/transportation habitat"
/host="Culex quinquefasciatus"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: San Diego County, California"
/lat lon="32.5928337 N 117.0575668 W"
/collection_date="27-Dec-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 102..908
/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNNAVPGVSPPAPPTGNP
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLALAVGEPRSAAGV
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CDS complement(117..923)

/codon_start=1
/product="ORF2"
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KGELAAVEDKANASRRARFSYHRQGVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN
HASPVSNRGGQSRVTSGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

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301 ctcaccggg acctgtggca gcggcggccg taaaggctgc ggcacccgt caggctgtcg
361 acctggccct ggccgtggta ggagaaccgc gtcggccggc tggcggttgc ctgtcttcg
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661 ggaagtcgat ctgcgtctc cccagccggc cagagaaaa tgccgtccgg aacaccccg
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781 gtcagggtgc agccggccgt ggcggaaaccgc tcggccggccaa tcctgtccctg cccatcaagg
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901 cgacctgtat ctctgttggg catccccccg

//

LOCUS MW434165 844 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002_027a_WVAL genomic sequence.

ACCESSION MW434165

VERSION MW434165

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051534
Sequence Read Archive: SRR11035223

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 844)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 844)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 580.211213x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

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/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS002_027a_WVAL"
/isolation_source="unknown sex, unfed, collected in
residential habitat"
/host="Culex quinquefasciatus"
/db_xref="taxon:2562539"
/environmental_sample

/country="USA: West Valley, California"
/lat_lon="34.150853 N 117.642917 W"
/collection_date="15-Nov-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 17..823
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/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGDSGNAPAVGSPPAPPTGNP
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DSPLAQLAVGVGEMDRNRTSAGNYRRRKSISLPLQRTEQNAAPNTCGSECSPKLGPGT
AAVRPPGRGQGAAGRGGTVGANPVLPIKGETFVPIPPIPGQVKQEPRFPPST"

CDS complement(32..838)
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/product="ORF2"
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ORIGIN

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661 gcctggcacg gtcgactgc gaccccccgg aagggttcg ggtgcagccg ggcgtggcg
721 aaccgtcgcc gccaatctg tctgccccat caagggggag acatttgcc ccatacccccc
781 tggcagggtt aaacaggagc cgaggttcc gccatcgacc tgcgtctg tggcgtatcc
841 cccg

//

LOCUS MW434166 867 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_027b_WVAL genomic sequence.

ACCESSION MW434166

VERSION MW434166

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051535

Sequence Read Archive: SRR11035222

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 867)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 867)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 3470.868354x
 Sequencing Technology :: Illumina
 ##Assembly-Data-END##
FEATURES Location/Qualifiers
 source 1..867
 /organism="Culex narnavirus 1"
 /mol_type="genomic RNA"
 /isolate="CMS002_027b_WVAL"
 /isolation_source="unknown sex, unfed, collected in residential habitat"
 /host="Culex pipiens"
 /db_xref="taxon:2562539"
 /environmental_sample
 /country="USA: West Valley, California"
 /lat lon="34.150853 N 117.642917 W"
 /collection_date="15-Nov-2017"
 /note="metagenomic; derived from metagenome: mosquito metagenome"
 CDS 26..832
 /codon_start=1
 /product="putative Robin"
 /translation="MGDVPSRRRRGGGHKPPSANSAGNSGNAPAVGVSPPAPPTDNP
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 DSPLAQLAVGVGEMDRNRTSAGNYRRKSISLPLQRTEQNAAPNTRGSECSPKLGPGT
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 CDS complement(41..847)
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 /product="ORF2"
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 181 cggggatgc gtgatttgcgct ctgacaaggc ccgaaagagt ggaactcaac cgggacctgt
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 661 caaatgggg cctggcacgg ctgcgttgcg acccccgga aggggtcagg gtgcaggcc
 721 gcgtggcgga accgtccgc ccaatccgtt ctcgtccatc aagggggaga catttgtcc
 781 cataccccctt gggcaggta agcaggagcc gaggttccg ccatcgacct gatgctctgt
 841 tgggcatccc ccctcgccca actcgca
//
LOCUS MW434167 618 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_028a_WVAL genomic sequence.
ACCESSION MW434167
VERSION MW434167
DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051536
 Sequence Read Archive: SRR11035221
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
 Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 618)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,

Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 618)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M., Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub, 499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 3.253235x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..618

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS002_028a_WVAL"
/isolation_source="unknown sex, unfed, collected in marsh/swamp habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: West Valley, California"
/lat_lon="33.935 N 117.655833 W"
/collection_date="15-Nov-2017"
/note="metagenomic; derived from metagenome: mosquito metagenome"

CDS 17..>618

/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGDAVSAGVSPPVPTGDP
ALSSSVNNRGCVIEPGRPGKSETRPGHLAAAALKAAACRQAVDLALAVGEPRSAAGV
RLVFDKACSLALSALDMGPSTGGTADLRINAAPARAEAPLSTAKALVRRSTGGGGCA
PGDSPLAQLAVVGELDRSGRTPVSNYRRRTDPTLPQRT"

ORIGIN

1 cctgtactgg acagcgatgg gtgacgcacc gtcacgtcgg agacgcagag gcggcggtca
61 taaaccacca tccgcgaaca gtgcaggaaa cagtggggat gcggtatccg caggcgtag
121 cccggcgta cccccactg gtgaccctgc tctgtcctcc tctgttaata acagaggatg
181 cgtgattgag cctggcaggc cggcaagag tggaaactcgaa ccggggccatt tggcagcggc
241 ggccgtaaag gctgcggcat gccgcaggc tgccgttgcggttgcgc tcggcccttag
301 accgcgctcg gcggcggcg tgccgttgcggttgcgc tcggcccttag
361 cgctctcgat atggggccta gcacgggagg gacggcggtatcttagatca acgcccgc
421 cggccgcgc gaggccccac tctctaccgc gaaggccctc gtccgcgggttgcgc
481 ggggtggggta tgccgcggg gagatcccc cctcgcccaa ctgcagtttgggtcgaga
541 gctcgatcggtcgccgtatcccgatca caattaccgg cgccaggagga ccgatccac
601 tctccccccatcgacaga

//

LOCUS MW434168 957 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002_028e_WVAL genomic sequence.

ACCESSION MW434168

VERSION MW434168

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051540
Sequence Read Archive: SRR11035217

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 957)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,

Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 957)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M., Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub, 499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 2547.032955x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..957

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS002_028e_WVAL"
/isolation_source="unknown sex, unfed, collected in marsh/swamp habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: West Valley, California"
/lat_lon="33.935 N 117.655833 W"
/collection_date="15-Nov-2017"
/note="metagenomic; derived from metagenome: mosquito metagenome"

CDS 89..904

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/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGDAVSAGVCPPVPTGDP
ALSSSVNNRGCVVEPGRPKGSETRPDHAAA
VKAACRQAVDLALAVVGEPRSAAGV
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RSTGGGGCA
PGDSPLAQLAVGVGELDRSGRTPVSSYRRRKTDPTLPQRTEHQ
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HGTAAVRPPGRGQGAAGRGGVVGAHPARPIKGETLGP
KPPGTQEPKTPPST"

CDS complement(104..919)

/codon_start=1
/product="ORF2"
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CTLSSSRTHCSRAMPQIGATHWTPGVQCGLMLCPLGESIGI
LPAPVTAYRRTARPIE
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GPGAGGGRGVDPKIRRPSRAGPHI
ESAKGERARFVEDKAHARRRARFSYYRK
GQVDSLAA
CRSLYGRRCQMVRSSFTLAGPA
RLNYASSVINRGGQSRVTSGGYRRANACGYRI
PTVSCTVRGWWFMTAASSSPT"

ORIGIN

1 ccccactgg taccctgctc tgtcctcc tcgttaataac agaggatgcg tagttgagcc
61 tggcggggtt atccgtact ggacaacgat gggtagcgc ca ccgtcacgtc ggcgacgacg
121 aggccggcgtt cataaaccac catccgcga cagtgcagga aacagtgggg atcggtatc
181 cgcaggcgtt tgccccccgg tacccccc ac ttggtagccct gctctgtc ctctgtta
241 taacagagga tgcgttagtg agcctggcag gcccggcaag aytgaaactc gaccggacca
301 ttggcagcg gccggccgtaa aggctgcgcg atgcccggc gctgtcgacc tggccctgc
361 ggttagtagga gaaccgcgtt cggccggccgg cgtgcgcctt gcttcgaca aagctgc
421 gctgcgcctt agcgcctcg atatggggcc cagcacggga gggacggcgg atcttcgat
481 caacgcgcgc cccgcgcgcg ccggggcccc actcttacc gcgaaggccc tcgtccgc
541 gtcgacaggg ggggggtgggg gatgcgcgc gggagattcc cccctgc
601 tggggtcgaa gagctcgatc ggtcggccg tacggccgtt agcagtacc ggcgc
661 gaccgatccc actctccccc agcggacaga gcatcaagcc gcaactggaca cccgggg
721 agtgtgttagc cccaaattgg ggcattggc ac ggcgc
781 ggggtcagcc gggcgtggcg gagtcgtcgg cgcccatct gctcggccca tcaagg
841 gacactgtt cccaaacccc ctggccgat taagcaggag cggaa
901 ctgatgctt gtagggcattt ccccaacgacg ggcgc
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LOCUS MW434169 860 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_029c_WVAL genomic sequence.
ACCESSION MW434169
VERSION MW434169
DBLINK BioProject: PRJNA605178
BioSample: SAMN14051543
Sequence Read Archive: SRR11035372
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 860)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 860)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 501.581098x
Sequencing Technology :: Illumina
##Assembly-Data-END##
FEATURES Location/Qualifiers
source 1..860
/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS002_029c_WVAL"
/isolation_source="unknown sex, unfed, collected in
residential habitat"
/host="Culex tarsalis"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: West Valley, California"
/lat_lon="33.925833 N 117.659722 W"
/collection_date="15-Nov-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"
CDS 18..824
/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGHKPPSANSAGNSNAVPGVSPPAPPTDNP
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAAVKAAACRQAVDLAGLAVVGEPRSAAGV
CLVFDKGCLALSLGMEPSSGTAGKSAAPARAEAPVSTARAPVRRSTGGGGCAPG
DSPLAQLAVGVGEMDRNRTSAGNYRRRSISSLQPQRTEQNAAPNTRGSECSPKLGHGT
AAVRPPGRGQGAAGRGGTVGASPVLPIKGETFVPIPPGQIKQEPKVPPST"
CDS complement(33..839)
/codon_start=1
/product="ORF2"
/translation="MPNRASGRWRNLRLFNLPRGYRDKCLPLDGQNRTGADGSATPG
CTLTPSGGSHCSRAMPQFGATLRTAGVRSVGVLCPGLERRDRLPASVVTCRRTVAIHL
SDPNCELGEGGISRRASPTPASRPADWGPRGGDWLSLTGGGRFRSCRPARARLHPESA
KGELAAFVEDKADASRRARFSYHRQGQVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSSP"
ORIGIN
1 tcctgtactg gacaacgtatggtgacgcac cgtcacgtcg gagacgacga ggccggcggtc
61 ataaaccacc atccgcaac agtgcaggaa acagtggaa tgccgtaccc gcaggcgta
121 gccccccgc acctccact gataaccctg ctctgtcccc cccggttact aaccggggat

181 gcgtgattga gcctgacaag gcccggaaaga gtggactca accgggacct gtggcagcg
241 cggccgtaaa ggctgcccgc tgccgtcagg ctgtcgacct gcccctggcg gtggtaggag
301 aaccgcgtc ggcggctggc gtctgcctg tcttcgacaa aggtgcggcag ctgcggcc
361 gcgctctcg gatggagcct agtgcggcgg ggcacggcagg aaaatctgcc ggcggccccc
421 gtggcggaggc tccagtcacc accggcggaggc ccccgatcggc ccggcgtcact ggcgggggt
481 ggggatgcgc gcccggagat tccccctcg cccaactcgc agtggggtc ggagagatgg
541 atcgcaaccg tacgtcgccgca ggttaactacc gacgcggcggaa gtcgatctcg totctcccc
601 agcggacaga gcaaaacgc gctccgaaca cccgcgggtc ggagtgttagc cccaaattgg
661 ggcgtggcac ggctgcggcgt cgaccccccga gaaggggtca gggtgccggc gggcgtggcg
721 gaaccgtcg cgccaggfcct gttctgcca tcaagggggta gacatttgc cctatacccc
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841 ccccccctcgc ccaactcgc
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LOCUS MW434170 873 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_029d_WVAL genomic sequence.
ACCESSION MW434170
VERSION MW434170
DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051544
 Sequence Read Archive: SRR11035371
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
 Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 873)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
 pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 873)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
 499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
 Assembly Method :: IDSeq pipeline v. 3.2
 Coverage :: 2483.567839x
 Sequencing Technology :: Illumina
##Assembly-Data-END##
FEATURES Location/Qualifiers
source 1..873
 /organism="Culex narnavirus 1"
 /mol_type="genomic RNA"
 /isolate="CMS002_029d_WVAL"
 /isolation_source="unknown sex, unfed, collected in
 residential habitat"
 /host="Culex tarsalis"
 /db_xref="taxon:2562539"
 /environmental_sample
 /country="USA: West Valley, California"
 /lat_lon="33.925833 N 117.659722 W"
 /collection_date="15-Nov-2017"
 /note="metagenomic; derived from metagenome: mosquito
 metagenome"
CDS 26..832
 /codon_start=1
 /product="putative Robin"
 /translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTDNP
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLALAVVGEPRSAAGV
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DSPLAQLAVGVGEMDRNRTSAGNYRRRSISLPRTEQNAAPNTRGSECSPKLGHGT

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CDS complement(41..847)
/codon_start=1
/product="ORF2"
/translation="MPNRASGRWRNLRLFNLPGYRDKCLPLDGQNRTGADGSATPG
CTLTPSGGSRAMPQFGATLRTAGVRSGVLLCPPGERDRDRLPASVVTCCRRTVAIHL
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KGELAAFVEDKADASRRARFSYHRQGVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN
HASPVSNRGGSQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

1 cggggttatc ctgtactgga caacgatggg tgacgcaccg tcacgtcgga gacgacgagg
61 cggcggtcat aaaccacccat ccgcgaacag tgaggaaac agtggaaatg cggtaccgc
121 aggccgttagc ccgcggcac ctcccaactgta taaccctgt ctgtcccccc cggttactaa
181 ccggggatgc gtgattgagc ctgacaaggc ccgaaagagt ggaactcaac cgggactgt
241 ggcagcggcg gccgtaaagg ctgcggcatg ccgtcaggct gtgcacctgg ccctggcggt
301 ggttaggagaa ccgcgtcgcc cggcggcggt ctgcctgtc ttgcacaaag gtcgcagact
361 cgcgccttagc gctctcgga tggaggctag ctgcaggcgg acggcaggaa aatctgccgc
421 gcccgcctgt gccgaggctc caatctccac cgcgcggcc ccagtccgc ggtcgactgg
481 cgggggtggg ggatgcgcgc cggcggattc cccctcgcc caactcgca gttgggtcg
541 agagatggat cgcacccgt cgtccggcagg taactaccga cgcaggaaat cgtatctcg
601 tctccccccg cggacagagc aaaacgcgc tccgaacacc cgcggccgg agttagcccc
661 caaatgggg catggcacgg ctgcagtgcg acccccccga aggggtcagg gtgcagccgg
721 gcgtggcgga accgtccgcg ccagtcctgt tctgcctatc aagggggaga caattgtccc
781 tataccctt gggcagatta aacagagacc gaaggtccg ccatcgacct gatgctctgt
841 tggcatccc ccctcgccca actcgccgtt ggg

//

LOCUS MW434171 843 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002_031a_COAV genomic sequence.

ACCESSION MW434171

VERSION MW434171

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051546
Sequence Read Archive: SRR11035369

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 843)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 843)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 10.262402x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..843
/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS002_031a_COAV"
/isolation_source="female, unfed, collected in marsh;
undeveloped habitat"
/host="Culex tarsalis"
/db_xref="taxon:2562539"

/environmental_sample
/country="USA: Coachella Valley, California"
/lat_lon="33.516797 N 116.082468 W"
/collection_date="07-Nov-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 17..823
/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAPAVGVSPPAPPTDNP
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DSPLAQLAVGVGEMDRHRTPAGNYRRRKSISSLQPQRTEQNAAPNTQGSECSPKLGHGT
AAVRPPGRGQGAAGRGGTVGASPVLPIKRETFVPIPQIKQEPKVPPST"

CDS complement(32..838)
/codon_start=1
/product="ORF2"
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CTLPSGGSHCSRAMPQFGATLRTLGVRSVGVLCPGLERRDRLPAPVTCRRTVSIHL
SDPNCELGEGGISQRASPTPASRPADWGPGRGGDWLSGTGRRSGFTRCPARARLHPESA
KGELAAFVEDKADASRRRARFSYHRQGVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN
HASPVSNRGGSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAAASSP"

ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg agacgacgag gcggcggtca
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121 cccgcggca cctcccactg ataaccctgc tctgtcccccc cccgttacta accggggatg
181 cgtgatttag cctgacaagg cccgaaagag tgaactcaa ccgggacctg tggcagccgc
241 ggccgtaaag gctgcggcat gccgtcaggc tgcgacactg gcccggcg tgtaggaga
301 accgcgcctg gcggctggcg tctgcctgt ctgcacaaa ggctgccagc tcgccttag
361 cgctctcggg atggagccta gtcgagccg gacagcgggt aaaaccgctg cgcccgcccg
421 tgccgaggct ccagtctcca ccgcgaggcc cccagtccgc cggcgtactg gcgggggtgg
481 gggatgcgcg ctggagatt ccccccgc ccaactcgca gttgggtcg gagagatgga
541 tcgacaccgt acggccggcag gtaactaccg ggcgcaggaaat tcgatctcg ctctcccca
601 gcggacagag caaaacgcgg ctccgaacac ccagggttcg gagtgtagcc ccaaattggg
661 gcatggcacg gtcgcaatgc gaccccccgg aagggttcg ggtgcagccg ggcgtggtgg
721 aaccgtcggc gccagtctg ttctgcccattt caagaggag acattcgcc ccataccctc
781 tggcagata aaacaggagc cgaaggttcc gccatcgacc tgcgtctg ttggcattcc
841 ccc

//

LOCUS MW434172 858 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_046a_WVAL genomic sequence.

ACCESSION MW434172

VERSION MW434172

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051570

Sequence Read Archive: SRR11035343

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 858)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 858)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2
 Coverage :: 1681.380282x
 Sequencing Technology :: Illumina
 ##Assembly-Data-END##
FEATURES Location/Qualifiers
 source 1..858
 /organism="Culex narnavirus 1"
 /mol_type="genomic RNA"
 /isolate="CMS002_046a_WVAL"
 /isolation_source="unknown sex, unfed, collected in residential habitat"
 /host="Culex quinquefasciatus"
 /db_xref="taxon:2562539"
 /environmental_sample
 /country="USA: West Valley, California"
 /lat_lon="33.9725 N 117.714444 W"
 /collection_date="29-Nov-2017"
 /note="metagenomic; derived from metagenome: mosquito metagenome"
 CDS 24..830
 /codon_start=1
 /product="putative Robin"
 /translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTGNP
 ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAACRQAVDLALAVGEPRSAAGV
 CLVFDKGCLQALSLALGMEPSSSGTAGKPAAPARAEPSTARAPVRRSTGGGRGCAPG
 DSPLAQLAVGVGEMDRNRTSAGNYRRRKSISLPLQRTEQNAAPNTRGSECSPKLGP GT
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 CDS complement(39..845)
 /codon_start=1
 /product="ORF2"
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ORIGIN
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 661 aattggggcc tggcacggct gcagtgcac ccccccggaaag gggtcagggt gcagccggc
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LOCUS MW434173 866 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_046b_WVAL genomic sequence.
ACCESSION MW434173
VERSION MW434173
DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051571
 Sequence Read Archive: SRR11035341
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
 Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 866)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 866)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 1949.740177x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..866

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS002_046b_WVAL"
/isolation_source="unknown sex, unfed, collected in
residential habitat"
/host="Culex quinquefasciatus"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: West Valley, California"
/lat_lon="33.9725 N 117.714444 W"
/collection_date="29-Nov-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 18..824

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/translation="MGDAPSRRKRRGGGHKPPSANSAGNSGNAPAVGSPPVPTGNP
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLALAVGEPRSAAGV
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CDS complement(33..839)

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ORIGIN

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LOCUS MW434174 864 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_047a_WVAL genomic sequence.
ACCESSION MW434174
VERSION MW434174
DBLINK BioProject: PRJNA605178
BioSample: SAMN14051572
Sequence Read Archive: SRR11035340
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 864)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 864)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 437.84244x
Sequencing Technology :: Illumina
##Assembly-Data-END##
FEATURES Location/Qualifiers
source 1..864
/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS002_047a_WVAL"
/isolation_source="unknown sex, unfed, collected in
marsh/swamp habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: West Valley, California"
/lat_lon="33.93778 N 117.633056 W"
/collection_date="29-Nov-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"
CDS 17..832
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/translation="MGDAPSRRRRGGGHKPPSANSAGNSGDAVSAGVSPPVPTGDP
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CDS complement(32..847)
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//

LOCUS MW434175 874 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002_047f_WVAL genomic sequence.

ACCESSION MW434175

VERSION MW434175

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051577
Sequence Read Archive: SRR11035335

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricetes; Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 874)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M., Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 874)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M., Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub, 499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 562.268507x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..874
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/isolate="CMS002_047f_WVAL"
/isolation_source="unknown sex, unfed, collected in marsh/swamp habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
/country="USA: West Valley, California"
/lat_lon="33.93778 N 117.633056 W"
/collection_date="29-Nov-2017"
/note="metagenomic; derived from metagenome: mosquito metagenome"

CDS 27..842
/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGDAVSAGVSPPVPTGDP
ALSSSVNNRGCVVEPGRPKGSETRPDHAAAAGKAAACRQAVDLALAIVVGEPRSAAGV
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CDS HGTAAVRPPARGQGAAGRGGVVGAGHPARPIKGETLGPKPPGPIKQEPKTPPST"
complement(42..857)
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ORIGIN

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721 gtgcagccgg gcgtggcggat gtcgtcgccccc atccatctgc tcggccatc aaaaaaaaa
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LOCUS MW434176 899 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002_047j_WVAL genomic sequence.

ACCESSION MW434176

VERSION MW434176

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051581
Sequence Read Archive: SRR11035330

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 899)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 899)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 2069.181265x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

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/mol_type="genomic RNA"
/isolate="CMS002_047j_WVAL"
/isolation_source="unknown sex, unfed, collected in
marsh/swamp habitat"
/host="Culex erythrothorax"
/db_xref="taxon:2562539"

/environmental_sample
/country="USA: West Valley, California"
/lat_lon="33.93778 N 117.633056 W"
/collection_date="29-Nov-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 51..866
/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGDAVSAGVSPPVPTGDP
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PGDSPLAQLAVGVGELDRSGRTPVSNYRRRKTDPTLPQRTEHQAALDTRGPVCSPNSG
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CDS complement(66..881)
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RLNYASSVINRGGQSRVTSGGYRRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

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721 tgcgtccccc tgcgagggga cagggtgcag cggccgcgtgg cggagtcgtc ggcgcgc
781 ctgctcgcc catcaagggg gagacacttg gtcccaaacc ccctggccgc attaaggcagg
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//

LOCUS MW434177 860 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_053a_PLCR genomic sequence.

ACCESSION MW434177

VERSION MW434177

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051585

Sequence Read Archive: SRR11035326

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 860)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 860)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2
 Coverage :: 793.02682x
 Sequencing Technology :: Illumina
 ##Assembly-Data-END##
FEATURES Location/Qualifiers
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 /organism="Culex narnavirus 1"
 /mol_type="genomic RNA"
 /isolate="CMS002_053a_PLCR"
 /isolation_source="unknown sex, unfed, collected in agriculture & residential habitat"
 /host="Culex erythrothorax"
 /db_xref="taxon:2562539"
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 /collection_date="21-Nov-2017"
 /note="metagenomic; derived from metagenome: mosquito metagenome"
 CDS 27..839
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 TADQKVNAAPARA
 EVPA
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 PGDSPLAQLAVGVGETDRTRTPV
 NYRRKSDPWIPRRTEQQ
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 CDS complement(42..854)
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 FSNHC
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 PACRSL
 NGRR
 CQW
 TRL
 SSTHTG
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 QSRT
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 RALAC
 GYR
 ISTV
 RGWW
 YMTA
 ASSS
 ST"
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LOCUS MW434178 3150 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_002_ALCO genomic sequence.
ACCESSION MW434178
VERSION MW434178
DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051442
 Sequence Read Archive: SRR11035376
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
 Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 3150)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3150)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 193.138301x
Sequencing Technology :: Illumina
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FEATURES Location/Qualifiers

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LOCUS MW434179

3148 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_004_ALCO genomic sequence.
ACCESSION MW434179
VERSION MW434179
DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051444
 Sequence Read Archive: SRR11035293
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
 Wolframviraes; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 3148)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
 pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3148)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
 499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
 Assembly Method :: IDSeq pipeline v. 3.2
 Coverage :: 123.031911x
 Sequencing Technology :: Illumina
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DEFINITION Culex narnavirus 1 isolate CMS001_011_ALCO genomic sequence.
ACCESSION MW434180
VERSION MW434180
DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051451
 Sequence Read Archive: SRR11035375
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
 Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 3151)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
 pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3151)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
 499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
 Assembly Method :: IDSeq pipeline v. 3.2
 Coverage :: 188.837671x
 Sequencing Technology :: Illumina
##Assembly-Data-END##
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LOCUS MW434181 3147 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_018_ALCO genomic sequence.

ACCESSION MW434181

VERSION MW434181

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051458

Sequence Read Archive: SRR11035307

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3147)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3147)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 31.853094x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434182 3132 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_019_ALCO genomic sequence.

ACCESSION MW434182

VERSION MW434182

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051459

Sequence Read Archive: SRR11035306

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3132)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnayake,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3132)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnayake,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 162.359411x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434183 3123 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_022_ALCO genomic sequence.

ACCESSION MW434183

VERSION MW434183

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051462

Sequence Read Archive: SRR11035302

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3123)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3123)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,

Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 37.561392x
Sequencing Technology :: Illumina
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LOCUS MW434184 3140 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_023_ALCO genomic sequence.
ACCESSION MW434184
VERSION MW434184
DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051463
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KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3140)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3140)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 197.935684x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434185 3130 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_028_ALCO genomic sequence.

ACCESSION MW434185

VERSION MW434185

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051468
Sequence Read Archive: SRR11035296

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenaviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3130)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3130)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 28.188012x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434186 3151 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_029_ALCO genomic sequence.

ACCESSION MW434186

VERSION MW434186

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051469
Sequence Read Archive: SRR11035295

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3151)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3151)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 424.830514x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434187 3154 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_030_ALCO genomic sequence.

ACCESSION MW434187

VERSION MW434187

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051470
Sequence Read Archive: SRR11035294

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3154)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3154)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 116.249919x
Sequencing Technology :: Illumina
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FEATURES Location/Qualifiers

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LOCUS MW434188 3150 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_034_ALCO genomic sequence.

ACCESSION MW434188

VERSION MW434188

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051474

Sequence Read Archive: SRR11035289

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenaviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3150)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3150)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 270.617963x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434189 3154 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_035_ALCO genomic sequence.

ACCESSION MW434189

VERSION MW434189

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051475

Sequence Read Archive: SRR11035288

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3154)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3154)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
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FEATURES Location/Qualifiers

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LOCUS MW434190 3134 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_036_ALCO genomic sequence.
ACCESSION MW434190
VERSION MW434190

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051476
Sequence Read Archive: SRR11035287
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 3134)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3134)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
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LOCUS MW434191 3152 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_037_ALCO genomic sequence.

ACCESSION MW434191

VERSION MW434191

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051477
Sequence Read Archive: SRR11035286

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3152)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3152)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 73.860813x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

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wildlife refuge / park habitat"
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CDS complement(43..2889)
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CDS 55..3144

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LOCUS MW434192 3138 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_038_ALCO genomic sequence.

ACCESSION MW434192

VERSION MW434192

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051478

Sequence Read Archive: SRR11035285

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3138)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3138)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 60.482849x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
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REFERENCE 1 (bases 1 to 3145)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3145)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
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DEFINITION Culex narnavirus 1 isolate CMS001_041_ALCO genomic sequence.

ACCESSION MW434194

VERSION MW434194

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051481

Sequence Read Archive: SRR11035281

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricetes; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3137)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3137)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 114.780719x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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CDS complement(42..3068)

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CDS 54..>3137

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ORIGIN

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LOCUS MW434195 3148 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_042_ALCO genomic sequence.

ACCESSION MW434195

VERSION MW434195

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051482

Sequence Read Archive: SRR11035280

KEYWORDS ENV

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3148)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3148)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 206.454575x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..3148

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CDS complement(42..3068)

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//
LOCUS MW434196 3184 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_044_ALCO genomic sequence.
ACCESSION MW434196
VERSION MW434196
DBLINK BioProject: PRJNA605178
BioSample: SAMN14051484
Sequence Read Archive: SRR11035278
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenaviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 3184)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3184)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 44.723206x
Sequencing Technology :: Illumina
##Assembly-Data-END##
FEATURES Location/Qualifiers
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course habitat"
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DEFINITION Culex narnavirus 1 isolate CMS001_045_ALCO genomic sequence.
ACCESSION MW434197
VERSION MW434197
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BioSample: SAMN14051485
Sequence Read Archive: SRR11035277
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 3144)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3144)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 29.941311x
Sequencing Technology :: Illumina
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DEFINITION Culex narnavirus 1 isolate CMS001_047_ALCO genomic sequence.

ACCESSION MW434198

VERSION MW434198

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BioSample: SAMN14051487

Sequence Read Archive: SRR11035275

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3151)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3151)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 50.828887x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434199 3112 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_048_ALCO genomic sequence.

ACCESSION MW434199

VERSION MW434199

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051488

Sequence Read Archive: SRR11035274

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3112)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,

Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3112)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,

Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 21.71631x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434200 3158 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_051_ALCO genomic sequence.
ACCESSION MW434200
VERSION MW434200
DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051491
 Sequence Read Archive: SRR11035270
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
 Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 3158)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
 pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3158)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 114.15482x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434201 3143 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_052_ALCO genomic sequence.
ACCESSION MW434201
VERSION MW434201
DBLINK BioProject: PRJNA605178
BioSample: SAMN14051492

Sequence Read Archive: SRR11035269

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3143)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3143)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 64.833986x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434202 3107 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_054_ALCO genomic sequence.

ACCESSION MW434202

VERSION MW434202

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051494

Sequence Read Archive: SRR11035267

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3107)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3107)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 26.888119x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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DEFINITION Culex narnavirus 1 isolate CMS001_058_ALCO genomic sequence.
ACCESSION MW434203
VERSION MW434203
DBLINK BioProject: PRJNA605178
 BioSample: SAMN14051498
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KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
 Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 3140)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
 pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3140)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
 Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
 499 Illinois St, San Francisco, CA 94158, USA
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DEFINITION Culex narnavirus 1 isolate CMS001_059_ALCO genomic sequence.

ACCESSION MW434204

VERSION MW434204

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051499

Sequence Read Archive: SRR11035262

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3154)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3154)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 48.444264x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434205 3148 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002_001a_SAND genomic sequence.

ACCESSION MW434205

VERSION MW434205

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051501

Sequence Read Archive: SRR11035259

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3148)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3148)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##
 Assembly Method :: IDSeq pipeline v. 3.2
 Coverage :: 328.765549x
 Sequencing Technology :: Illumina
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LOCUS MW434206 3164 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_022a_SAND genomic sequence.
ACCESSION MW434206
VERSION MW434206
DBLINK BioProject: PRJNA605178
BioSample: SAMN14051521
Sequence Read Archive: SRR11035237
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 3164)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3164)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 273.961451x
Sequencing Technology :: Illumina
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LOCUS MW434207 3164 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_023a_SAND genomic sequence.
ACCESSION MW434207
VERSION MW434207
DBLINK BioProject: PRJNA605178
BioSample: SAMN14051522
Sequence Read Archive: SRR11035236
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenaviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 3164)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3164)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 582.525105x
Sequencing Technology :: Illumina
##Assembly-Data-END##
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LOCUS MW434208 3148 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002_027a_WVAL genomic sequence.

ACCESSION MW434208

VERSION MW434208

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051534
Sequence Read Archive: SRR11035223

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricetes; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3148)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3148)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 255.684142x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434209 3161 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_027b_WVAL genomic sequence.

ACCESSION MW434209

VERSION MW434209

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051535

Sequence Read Archive: SRR11035222

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3161)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3161)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 1200.155966x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434210 3160 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_028d_WVAL genomic sequence.

ACCESSION MW434210

VERSION MW434210

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051539

Sequence Read Archive: SRR11035218

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3160)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3160)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ###Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 703.74927x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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DEFINITION Culex narnavirus 1 isolate CMS002_028e_WVAL genomic sequence.
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VERSION MW434211
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BioSample: SAMN14051540
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KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 3158)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3158)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 1037.473872x

Sequencing Technology :: Illumina

##Assembly-Data-END##

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DEFINITION Culex narnavirus 1 isolate CMS002_029c_WVAL genomic sequence.

ACCESSION MW434212

VERSION MW434212

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BioSample: SAMN14051543
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SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
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REFERENCE 1 (bases 1 to 3148)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3148)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
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REFERENCE 1 (bases 1 to 3160)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3160)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
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LOCUS MW434214 3148 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002_046a_WVAL genomic sequence.

ACCESSION MW434214

VERSION MW434214

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051570

Sequence Read Archive: SRR11035343

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3148)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3148)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 495.439596x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434215 3152 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_046b_WVAL genomic sequence.
ACCESSION MW434215
VERSION MW434215
DBLINK BioProject: PRJNA605178
BioSample: SAMN14051571
Sequence Read Archive: SRR11035341
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 3152)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3152)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 757.424065x
Sequencing Technology :: Illumina
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LOCUS MW434216 3154 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_047a_WVAL genomic sequence.

ACCESSION MW434216

VERSION MW434216

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051572

Sequence Read Archive: SRR11035340

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3154)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3154)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 138.320442x
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LOCUS MW434217 3159 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002_047f_WVAL genomic sequence.

ACCESSION MW434217

VERSION MW434217

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051577

Sequence Read Archive: SRR11035335

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3159)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3159)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 111.901363x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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DEFINITION Culex narnavirus 1 isolate CMS002_047j_WVAL genomic sequence.
ACCESSION MW434218
VERSION MW434218
DBLINK BioProject: PRJNA605178
BioSample: SAMN14051581
Sequence Read Archive: SRR11035330
KEYWORDS ENV.
SOURCE Culex narnavirus 1 (mosquito metagenome)
ORGANISM Culex narnavirus 1
Viruses; Riboviria; Orthornavirae; Lenaviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.
REFERENCE 1 (bases 1 to 3164)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay
JOURNAL bioRxiv (2020) In press
REMARK DOI: 10.1101/2020.02.10.942854
REFERENCE 2 (bases 1 to 3164)
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA
COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 625.481697x
Sequencing Technology :: Illumina
##Assembly-Data-END##
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LOCUS MW434219 3137 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002_051a_PLCR genomic sequence.

ACCESSION MW434219

VERSION MW434219

DBLINK BioProject: PRJNA605178
BioSample: SAMN14051584
Sequence Read Archive: SRR11035327

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3137)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Single mosquito metatranscriptomics identifies vectors, emerging
pathogens and reservoirs in one assay

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REFERENCE 2 (bases 1 to 3137)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
Logan,P., Ratnasiri,K. and Retallack,H.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 140.784641x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434220 3158 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_053a_PLCR genomic sequence.

ACCESSION MW434220

VERSION MW434220

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BioSample: SAMN14051585

Sequence Read Archive: SRR11035326

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3158)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,
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499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 354.941577x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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Amy Kistler PhD, MPH
Group Leader, Infectious Diseases
Chan Zuckerberg Biohub
499 Illinois St
4th Floor
San Francisco CA 94158

Phone: 415-310-0701
Email: amy.kistler@czbiohub.org