
[Ext] Inquiry: GenBank MW434135-MW434220

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

Fri, Feb 19, 2021 at 9:11 AM

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
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAVKAACRQAVDLALAVGEPRSAAGV
CLVFDKGQLALSALGMEPSSGTAGKSAAPARAEAPVSTARAPVRRSTGGGGCAPG
DSPLAQLAVGVGEMDRNRTSAGNYRRKSISLQPQTEQNAAPNTRGSECSPKLGHGT
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CDS complement(37..843)

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SDPNCELGEGGISRRASPTPASRPADWGPRGGDWSLGTGGRGRLSCRPARARLHPESA
KGELAAFVEDKADASRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSLGVLRLN
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAACSSPT"

ORIGIN

1 gatctcgt actggacaac gatgggtgac gcaccgtac gtcggagacg acgaggccgc
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121 gtagccccgc cggcacctcc cactgataac cctgctctgt cccccccgt tactaaccgg
181 ggatgcgtga ttgagcgtga caaggccga aagaatggaa ctcaaccggg acctgtggca
241 gcccggccgc taaaggctgc ggcatccgt caggctgtcg acctggccct ggcggtgtta
301 ggagaaccgc gtcggccgc tggcgtctgc ctggcttcg acaaaggctg ccagctcgccc
361 cttagcgctc tcggatggaa gcctagctcg agcggacgg caggaaatgc tgccgcgccc
421 gcccgtccgc aggctccagt ctccaccgcg agggcccgag tccgcggcgtc gactggccgg
481 ggtggggat ggcgcgggg agattcccc ctcgcacaac tcgcgttgg ggtcggagag
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601 ccccaacggaa cagagaaaaa cgccgctccg aacaccgcg gtcggagtg tagccccaaa
661 ttggggcatg gcacggctgc agtgcgaccc cccggaaagggt gcagggtgc agccggcg
721 ggcggaaaccg tcggcgcagg tcctgttctg cccatcaagg gggagacatt tgccctata
781 cccctgggc agattaaaca ggagccgaag gttccgcatt cgacctgtatg ctctgttggg
841 catccccca

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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

/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPVPTGNP
ALSPPVNNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLAGLAVGEPRSAAGV
CLVFDKGQLALSLALGMEPSSSGTAGKSAAAPARAEPVSTARAPVRRSTGGGGCAPG
DSPLAQLAVGVGEMDRNRTSAGNYRRKSISLPLQRTEQNAAPNTRGSECSPKLGPGT
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CDS complement(34..840)

/codon_start=1
/product="ORF2"
/translation="MPDRASGRWRKLRLLSLPRGYGDKCLPLDGQDRIGADGSATPG
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SDPNCELGEGLSRRASPTPASRPADWGPRGGDWLSGTGGRGRFSCRTRARLHPESA
KGELAAFVEDKADASRRARFSYHRQGVDSLTTARRSLYGRRCHRSRLSSTLGLVRLN
HASPVINRGGQSRVTSGRYRRAHACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

1 atcctgtact ggacaacgat gggtgacgca ccgtcacgtc ggagacgcg aggccggcggt
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121 agcccccccg tacctcccac tggtaacct gctctgtccc ccccggtta taaccgggga
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301 gaaccgcgcgct cggccgcgtgg cgtctgcctt gtctgcaca aaggctgcca gctcgccctt
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421 cgtgccgagg ctccagtctc cacccgcgagg gccccagtc gcccgtcgc tggccgggggt
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661 gggcctggca cggctgcagt gcgacccccc ggaagggttc agggcgcgc cggccgtggc
721 ggaaccgtcg gcgccaaatcc tgtccgtcccc atcaaggggg agacatttg ccccatcccc

781 cctgggcagg ctaagcagga gccgaagttt ccgcacatcgatgtgttgtcggcat
841 cccccc
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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"
/translation="MGDAPSRRRRGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP
ALSSLVSNEGCVVRPARPGMSGTQPGPLAAA
VKAACRQAVDLALAVVGEPRSAAGV
RLVFDKACQLALSALELEPSTGRTADQKVNAAPARA
EAPASTAKALVRRSTGGVGGCA
PGDSPLAQLAAGVGETDRTRTPVNYRRKSDPWIPQRTEQQAAP
STGGKVCSPNLGH
GTAAVRPLEKDRGAAGRGGVGAHPGRPIKGETLGP
KPPGSAKQEPKSPPST"
CDS complement(37..849)
/codon_start=1
/product="ORF2"
/translation="MPRRASGRWRRLLFCRPRGF
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ARMGADASATPG
CTPVLLQRT
HCSRAMPQIGATHLPAGGRCGL
LCPLDGP
RIALPAPIISYRRTGTIRL
SDPSCKLGEGGISWRASP
NPACRSA
DECLRGCRGLGAGRRGV
DLLVRRP
TRARLQLE
SAKGQLARFVK
DEAYAGRR
RARFSNH
CQGKIDSLP
ACRS
LYGR
RCQW
TRLSS
THSGPCR
PNYAPFVT
NEGGQSRV
TSGGC
RRA
LACGY
RISTV
RGWWY
MTA
ASSSST"
ORIGIN

1 gttatccgt actggacaac gatgggtgac gcaccgtac gtcgaagacg acgaggcggc
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661 cccaaattgg ggcatggcac ggctcgatg cgtccttgg agaaggacag gggcagcc
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841 gcggggcatac ccccgaa

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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="MGDAPSRRRRGGGHKPPSANSAGNSGDAVSAGVSPVPPTGDP"

ALSSVNNRGCVVEPGRPGKSETRPDHLAAAALKAAACRQAVDLALAVVGEPRSAAGV
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PGDSPAQLAVVGELDRRLGRTPVSNYRRRKTDPTLPQRTEHQAAALDTRGPVCSPNSG
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CDS complement(37..852)
/codon_start=1
/product="ORF2"
/translation="MPYRASGRWRSLLNRPRGFGTKCLPLDGPSRMGADDSATPG
CTLSSTKRTHCSRAMPRIGATHWTPGVQCGLMLCPLGESGIGLPAPVIAYWRTAQPIE
LSDPNCELGEGGISRRASPTPACRPADEGLRGREWGPAGGRGVDPKIRRPSRAGLHF
ENAKGERARFVKDKAHARRRARFSYYRKQVDSLACRSLYGRRSQMVRSSFTLAGPA
RLNYASSVINRGGQSRVTSGGYRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

1 gttatccgt actggacaac gatgggtgac gcaccgtcac gtcggagacg acgaggcgcc
61 ggtcataaac caccatccgc gaacagtca ggaacacagtggatgcggatccgcaggc
121 gttagcccgc cggtaccccc cactggtagc cctgctctgt cttccctctgt taataacaga
181 ggatgcgttag ttgagccctgg caggccccggc aagagtggaaa ctgcaccggccattinggt
241 gcggcggccgc taaaggctgc ggcacccgc caggctgtcg acctgtccct tgccgttagta
301 ggagaaccgc gctcggcggc gggcgtgcgc ctgtcttg acaaaggctgt ctcgctcgcc
361 cttagcgttc tcgaaatggc gcccagcagc ggagggacgg cgatcttag gatcaacgccc
421 gcggccggccgc cccactctt accgcgaagg ccctcgatcccgccgc
481 gcgggggtgt ggggatgcgc gcccggagat tccccctcg cccaactcgc agtgggggtc
541 ggagagctcg atcggttggg cctgtacgc gtaagcaatt accggcgcag gaagacccat
601 cccactctcc cccagcggac agagcatcaa gcccacttgg accaccgggg tccagtgtgt
661 agccccaatt cggggcatgg cacggctgc gtcgcgtc ttggtagagg acagggtgca
721 gccgggcgtg cggaggtgt cggcggccat cctgtcgcc ccatcaagggg ggagacactt
781 ggtccaaac cccctggggcc gattaagcag gagccgaaga ctccgcacatc gacgtatgc
841 tctgttagggc atccactt ccccaag

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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., 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 :: 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
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CDS complement(69..851)
 /codon_start=1
 /product="ORF2"
 /translation="MPRRASGRWQRLRLLCRPRGYGTKCLPLDPARMGADASATPG
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 SAKGQLARFKVDEAYAGRARRFSNHCGKIDSPLACRSLSNGRRCQVGRLLSHTGPCR
 PNYAPFVTNEGGQSRVISGGYRRALACGYRISTVSRGWW"

ORIGIN

1 gggttatcct gtactggaca acgatgggtg acgcaccgtc acgtccggaga cgacgaggcg
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 121 gccaaggccc gccggtaccc tccactgata accctgcgtc gtcctccctc gtagtaacg
 181 aagggtgcgt agttaggcct gcaaggaccg gtatgagtgg aactcaaccg gcccacccgtgg
 241 cagcggccgc cgttaaggct gccgcattgcc ggcaggctgt cgtatccgtcc ctggcagtgg
 301 ttggagaacc gcgcctggcg gccggcgatc gcctcgctt tgacaaagcg tgccagctgg
 361 cccttagcgc tctcgagctg gagcctagca cgggtcggac ggcggaccaa aaggtaacg
 421 cccgcggccgc cccgcggcag gcacctgcat ccactgcgaa ggcacctgc cccgcgtcga
 481 caggcgggggt tggggatgc gcgcaggag attccccct cgcggcaattt gcagttgggg
 541 tcggagagat ggatcggtc cgcacccgg tggccaacca caggcgcagg aagaccgttc
 601 cgttgatccc cgcacggaca gagcaacaag cgcacccctcc aacttggcg gagggtgtta
 661 gccccaaatt ggggcatggc acggctgcag tgcgtccctc gagagaggac aggggtgcag
 721 cccggcgtgg cggaggcgtc ggcgcggccatc ctggcggcc catcaagggg gagacatttt
 781 gtcccatacc ccctgggtcg gcaaaacagg agccgaagtc tctccatcg acctgatgt
 841 ctgcggggca tcccccg

//

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"

/isolate="CMS001_022_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 17..829

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/product="putative Robin"

/translation="MGDAPSRRRRGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP
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RLVFDKACQLASALEPSTGRADQKVNAAPARAEPASTAKALVRRSTGGVGCGA
PGDSPLAQLAAGVGETDRTRTPVRNYRRRKSDPWIPQRTEQQAAPSTGGKVCSPNLGH
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CDS complement(32..844)

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SAKGQLARFKVDEAYAGRRARFSNHCGKIDSPLACRSLYGRRCQWTRLSSTHSGPCR
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ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcga agacgacgag gcggcggtca
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121 cccgcggca ccctccactg gtaacctgc tctgtcctcc ctgcgttagta acgaagggtg
181 cgttgttagg cctgcacggc ccggaatgag ttgaaactcaa ccgggtccac tggcagcggc
241 ggcgtaaag gctgcggcat gcccgcggc tacgcctcg tttgacaaa gcgtgccagc tggcccttag
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361 cgctctcgag ctggagccta gcacggctcg gacggcggac caaaagggtca acgcccgcgg
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481 ggtggggga tgccgcgcag gagattcccc ctcgcggccaa ctgcgcgtg gggcggaga
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721 tggcggagggc gtcggcgccc atcctggccg gcccataag ggggagacac ttggcccaa
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841 gcatcccccg

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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##

FEATURES Location/Qualifiers

source 1..850

/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_023_ALCO"
/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

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/product="putative Robin"
/translation="MGDAPSRRKRRGGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP
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PGDSPAQLAAGVGETDRTRTPVRNYRRRKSDPWIPQRTEQQAAPSTGGKVCSPNLGH
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CDS complement(32..844)

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/product="ORF2"
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SDPSCKLGEGGISWRASPNCRSADECLRSGCRGLGAGRRGVDLLVRPTRARLQLE
SAKGQLARFKVDEAYAGRARRFSNHCQGKIDSLPACRSLYGRRCQWTRLSTHSGPCR
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ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcga aaacgacgag gcggcggtca
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601 ccccccagcg acagagcaac aagccgcacc ttccacccgc gggaaagggtgt gtggcccaa
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841 gcatcccccc
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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
source 1..844
/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_028_ALCO"
/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
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLAGLAVGEPRSAAGV
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DSPLAQLAVGVGEMDRHRTSAGNYRRKSISLPLQRTEQNAAPNTQGSECSPKLGHGT
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CDS complement(32..838)
/codon_start=1
/product="ORF2"
/translation="MPNRASGRWRNLRLFYLPGRGYGDKCLPLDGQNRTGADGSATPG
CTLTPSGGSHCSRAMPQFGATLRTLGVRSVLLCPLGERRDRLPAPVVTCRRTVSIHL
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KGELAAVEDKADASRRRARFSYHRQQVDSLTAACRSILYGRRCHRSRLSSTLSGLVRLN
HASPVSNRGQSRVISGRCRRANACGYRIPTSVCTRGWWFMTAAASSPT"
ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg agacgacgag gcggcggtca
61 taaaccacca tccgcgaaca gtgcaggaaa cagtggaat gcggtacccg caggcgtag
121 cccgccccca cctcccactg ataacctgc tctgtcccccc ccggftacta accggggatg
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721 aaccgtcggc gccagtcctg ttctgccc cat caagaggag acattgtcc ccataccctc
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841 ccct

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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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/organism="Culex narnavirus 1"
/mol_type="genomic RNA"
/isolate="CMS001_029_ALCO"
/isolation_source="female, blood fed, collected in park /
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"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 102..908

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/product="putative Robin"

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DSPLAQLAVGVGEMDRNRTSAGNYRRRKSISSLPQRTEQNAAPNTRGSECSPKLGPGT
AAVRPPGRQQGAAGRGGTVGANPVLPIKGETFVPIPPGQIKQEPKFPPT"
CDS complement(117..923)
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/product="ORF2"
/translation="MPNRASGRWRKLRLFNLPGYRDKCLPLDGQNRIAGGSATPG
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SDPNCELGEGGISRRASPTPASRPADWSPRGGDWSLGTGGGRFRSCRTRARLHPESA
KGELAAFVEDKADASRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSTLPGLVRLN
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"
ORIGIN
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841 gggagacatt tgcctata cccctgggc agattaaaca ggagccgaag ttccgccat
901 cgacctgtat ctctgttggg catcccccg
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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
/organism="Culex narnavirus 1"
/mol_type="genomic RNA"

/isolate="CMS001_030_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="10-Sep-2017"
 /note="metagenomic; derived from metagenome: mosquito
 metagenome"

CDS 22..828

/codon_start=1
 /product="putative Robin"
 /translation="MGDAPSRRERRGGGHKPPSANSAGNSGNAVPAGVSPPVPTGNP
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 CLVFDKGCLALSALGMEPSSGTAGKTAAPVRAEAPVSTARAPVRRSTGGGGCALG
 DSPLAQLAVGVGEMDRHRTSAGNYRRRKSISSLPQRTEQNAAPNTQGSECSPELGP
 AAVRPPERGQGAAGRGGTVGANPVLPIKRETFVPKPSGQIKQEPKFPPST"

CDS complement(37..843)

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 /product="ORF2"
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 KGELAAVEDKADASRRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN
 HASPVINRGGSRVTSGRYRRANACGYRIPTVSCTVRGWWFMTAASSFPT"

ORIGIN

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 241 gcccggccgc taaaggctgc ggcatgccgt caggctgtcg acctgtggccct ggcgggtggta
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 721 ggcggaaaccgc tcggcccaa tcctgtctg cccatcaaga gggagacatt cgtccccaaa
 781 ccctctgggc agataaaaaca ggagccgaag ttccgcct catcgatg ctctgtcg
 841 catccccag

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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

source 1..848

/organism="Culex narnavirus 1"

/mol_type="genomic RNA"

/isolate="CMS001_034_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 21.827

/codon_start=1

/product="putative Robin"

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ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLALAVGEPRSAAGV
CLVFDKGQLALSALGMEPSSSGTAGKSAAPARAEPSTARAPVRSTGGGGCAPG
DSPLAQLAVGVGEMDRNRTSAGNYRRRKSISSLQPQRTEQNAAPNTRGSECSPKLGHGT
AAVRPPGRGQGAAGRGGTVGASPVLPIKGETFVPIPPGQVKQEPKVPPST"

CDS complement(36..842)

/codon_start=1

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/translation="MPNRASGRWRNLRLFNLPGYGDKCLPLDGQDRTGADGSATPG
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SDPNCELGEGGISRRASPTPASRPADWGPRGGDWSLGTGGGRFRPCPARARLHPESA
KGELAAFVEDKADASRRRARFSYHRQGVDSLTA CRSLY GRRCHRSRLSSTLSGLVRLN
HASPVSNRGQSRVISGRCRANACGYRIPTVSCTVRGWWFMTAASSFPT"

ORIGIN

1 ctagccgtta ctggacaacg atgggtgacg caccgtcacg tcggaaacga cgaggcggcg
61 gtcataaaacc accatccgcg aacagtgcag gaaacagtgg gaatgcggta cccgcaggcg
121 ttggcccgcc ggcacctccc actgataacc ctgctctgc cccccccgggtt actaaccggg
181 gatgcgtgat tgagcctgac aaggcccgaa agagttgaac tcaaccggga cctgtggcag
241 cggccggccgt aaaggctgcg gcatgcgc tc aggctgtca cctggccctg gcggtggtag
301 gagaaccgcg ctccggcgct ggctctgca caaaggctgc cagctcgccc
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481 gtggggatgc cgcgcggga gattcccccc tcgccaact cgca gttgg gtcggagaga
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601 cccagcggac agagcaaaaac gcccgtccga acacccgcgg ttccggatgt agcccaaat
661 tggggcatgg cacggctgca gtgcgacccc ccggaaagggg tcagggtgca gccggcggt
721 gcggaaccgt cggcgcctg cctgtctgc ccatcaagg ggagacattt gtcggatc
781 cccctggca ggttaaacag gagccgaagg ttccgcacatc gacctgatgc tctgtggc
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
 VCAAACRQAVDLALAVVGEPRSAAGV
 RLVFDKACQLALSALEPSTGRTADQKVNAAPARA
 EVPASTAKALVRRSTGGVGGCA
 PGDSPLAQLAVGVGEMDRTRTPVGNHRRRKTVPLIPRRTEQQAAPPTWREVCSPKLGH
 GTAAVRPPREDRGAAGRGGGVGAHPGRPIKG
 ETLGPKPPGSAKQEPEKSPPST"

CDS complement(64..846)
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 /product="ORF2"
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 GLLLCP SGDQRNGLPAPVVAHWRTGPIHL
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 GAGRRGV
 DLLVRRP
 TRARLQLE
 SAKGQLAR
 FVKDE
 AYAGRR
 ARFSNHC
 QGKIDSL
 PACRSLY
 GRR
 CQV
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 RRALAC
 GYR
 I
 STV
 RGWW"

ORIGIN

1 atccgtact ggacaacgat gggtgacgca ccgtcacgtc gaaaacgacg cggcggcagt
 61 catttaccac catccgcgaa cagtgacgga aacagtggag atgcggtagc cgccaggccaa
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 181 tgcgttagttt ggccgtcaag gacccgtatg agtggaaactt aaccggccca cctggcagcg
 241 gcggccgtaa aggctgcggc atgcccggcag gctgtcgatc ttggccctggc agtgggttgg
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 421 cccggccgcgc cccggccgttcc tgcatccact gcgaaaggcac tcgtccgcgc atcgacaggc
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 541 gagatggatc ggaccgtac gccagtgccc aaccaccggc gcagggaaagac cgttccgttgc
 601 atccccccgac ggacagagca acaaggccgca cctccaaactt ggcggggaggt gtgttagcccc

661 aaattggggc atggcacggc tgccgtgcgt cctccgagag aggcacagggg tgcagccggg
721 cgtggcgag gcgtccggc ccatccgtgc cggcccatca agggggagac acttggtccc
781 aaacccctcg ggtcgcaaa 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="MGDAPSRRRRGGGHKPPSANSAGNSGNNAVPGVSPPAPPTDNP
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDIALAVVGEPRSAAGV
CLVFDKGQLALSLGMEPSSSGTAGKSAAAPARAEAPVSTARAPVRRSTGGGGCAPG
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AAVRPPGRQQGAAGRGGTVGASPVLPIKGETFVPIPPGQIKQEPKVPPST"

CDS complement(32..838)
/codon_start=1
/product="ORF2"
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CTLTPSGGSHCSRAMPQFGATLRTAGVRSGVLLCPLGERDRLPASVVTCCRRTVAIHL
SDPNCELGEGLISRRASPTPASRPADWGPRGGDWLSGTGGRGRLSCRPARARLHPESA
KGELAAFVEDKADASRRARFSYHRQGQVDLTAACRSILYGRRCHRSRLSSTLGLVRLN

HASPVSNRGGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

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121 cccggccgca cctcccactg ataaccctgc tctgtcccccc ccggttacta accggggatg
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661 gcatggcacg gctgcagtgc gaccccccgg aaggggtcag ggtgcagccg ggcgtggcgg
721 aaccgtcggc gccagtcctg ttctgcccata caagggggag acatttgtcc ctatcccc
781 tgggcagatt aaacaggagc cgaaggttcc gccatcgacc tgcgtctg 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

/product="putative Robin"
/translation="MGDAPSRRNRRGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP
ALSSLVSNEGCVVRPARPGMSGTQPGPLAAAALKAAACRQAVDLALAVVGEPRSAAGV
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PGDSPAQLAAGVGETDRTRTPVSNYRRKSDPWIPQRTEQQAAPSTGGKVCSPNLGH
GTAAVCPLKDRGAAGRGGVGAAHPGRPIKGTLGPKPPGSAKQEPKSPPST"

ORIGIN

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61 tataccacca tccgcgaaca gtgcaggaaa cagtggagat gcggtacccg caggccaagg
121 cccgcggca ccctccactg gtaacctcgc tctgtcctcc ctcgttagta acgaagggtg
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781 acccccggg tcggcaaaac aggagccaa gtccgcgc tcgacactgat gtcctgcggg
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; Lenarviricota; 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"

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/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="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTDNP
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAAVKAAACRQAVDLALAVGEPRSAAGV
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DSPLAQLAVGVGEMDRHRTSAGNYRRRKSISLQPQRTEQNAAPNTQGSECSPKLGHGT
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CDS complement(32..838)
/codon_start=1
/product="ORF2"
/translation="MPNRASGRWRNLLFLYLPGRGYGDKCLPLDGQNRTGADGSATPG
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HASPVSNRGQSRVISGRCRRAHACGYRIPTSVCTRGWWFMTAACSSPT"
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721 aaccgtcggc gccagtctgt ttctgccc cat caagagggag acatttgcc ccataccctc
781 tgggcagata aaacaggagc cgaaggttcc gccatcgacc tgatctcg ttggcattcc
841 c
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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
 ALSSSVNNRGCVYEPDRARKSGTQPGPATATAASKAAVCRQAVDLALT
 VGEPRSVAGVRLVFDKACQLTCSALGMEPSTSGAASKLAAPARA
 EAPISTVRAPVRRSTGGGGCALG
 DSPLAQLAvgVGEMDRVRTTAGNYRRRHTVSSFPQRTEHKAVPDTH
 GPECPKLGHTAAVRPPGRGQGAAGRGGAI
 GTHPALPIKEETLGPKPPGQIKREPKVPPST"

CDS complement(39..845)
 /codon_start=1
 /product="ORF2"
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 HCSRAMPQFGATFR
 TVNGFMLCPLGERRDRMPATV
 TCRRTD
 PVHL
 SDPNCELGE
 GGVSQR
 ASPTP
 ASRPA
 DWSPHGGDWGLGAGGRGKLACRSAR
 ARLHPERA
 TGELARLV
 KDEAYACHGARFSYHRQGQV
 DSLTTDCSLRGRR
 RGSRLS
 STLSGP
 VR
 LI
 HAS
 SVINRGGQ
 SRVTSRGHRR
 ACACGYRF
 PTVSCTVR
 GWWFLTA
 ASSSPT"

ORIGIN

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601 tccccccagcg gacagagcat aaagccgtc cggcacccccca cggccggaa ttagccccca
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721 gtggcggagc tatccgcacc catccgcgtc tgcccatcaa ggaggagaca ctggcccca
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841 ggcaccccccc 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="MGDAPSRRRRGGHKPPSANSAGNSGNAVPAGVSPPAPPTGNP
ALSPPVSNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLAGLAVGEPRSAAGV
CLVFDKGQLALSALGMEPSPSGTAGKTAAPARAEAPVSTARAPVRRSTGGGGCALG
DSPLAQLAVGVGEMDRHRTSAGNYRRRKSISSLPQRTEQNAAPNTQGSECSPKLGP
AAVRPPGRGQGAAGRGGTVGANPVLPIKRETFVPIPQIKQEPKVPPST"

CDS complement(32..838)

/codon_start=1
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HASPVRNRGGQSRVTSGRCRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

1 cctgtactgg acaacgtatgg gtgacgcacc gtcacgtcg agacacgag gcggcggta
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121 cccgccccca cctcccactg gtaacctgc tctgtcccccc ccggttcta accggggatg
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301 acccgctcg gcggctggcg tctgcctgt ctgcacaaa ggctgccagc tcgcccctag
361 cgctctcggt atggagccca gcccggcg gacggcggt aaaaccgctg cggccggcc
421 cgccgaggct ccagtctcca ccgcggggc cccagtcgc cggtcactg ggggggtgg
481 gggatgcgc ctggagatt cccccctcg ccaactcgca gtggggtcg gagagatgga
541 tcgacaccgt acgtcgccg gcaactaccg ggcgcaggaa tcgatctcg ctctcccca
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661 gcctggcacg gctgcagtcg gaccccccgg aagggtcag ggtgcagccg ggcgtggccg
721 aaccgtcgcc gccaatctcg ttctgcccatt caagaggag acattcgacc ccataccctc
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841 cccctcgccc aactcgc

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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; 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 :: 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="MGDAPSRRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTDNP
ALSSPVNRGCVIEPDKARKSGTQPGPVAAA VKAACRQAVDLALAVVGEPRSAAGV
CLVFDKGQLALSALGMEPSSSGTAGKSAA PARAEAPVSTARAPVRRSTGGGGCAPG
DSPLAQLAVGVGEMDRNRTSAGNYRRRKSISSLQPQRTEQNAAPNTRGSECSPKLHGHT
AAVRPPGRGQGAAGRGGTVGASPVLPIKGETLVPPIPPQIKQEPEVPPST"
CDS complement(32..838)
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 /product="ORF2"
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SDPNCELGEGGISRRASPTPASRPADWGPRGGDWSLGTGGRGRFSCRPARARLHPESA
KGELAAFVEDKADASRRRARFSYHRQQVDSLTA CRSLYGRRCHRSRLSSTLSGLVRLN
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"
ORIGIN
1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg agacgacgag gcggcggtca
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121 cccgccccca cctccactg ataacctgc tctgtccctc ccgggtacta accggggatg
181 cgtgattgag cctgacaagg cccgaaagag tggaactcaa ccgggacctg tggcagcggc
241 ggccgtaaag gctgcggcat gccgtcaggc tgcgacccg gcccggccg tggtaggaga
301 accgcgcctcg gccgcgtggc tctgcctgt ctgcacaaa ggctgcacgc tcgcccctag

361 cgctctcggg atggagccct a gtcgagcgg gacggcagga aaatctgccg cgcggcccg
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481 gggatgcgcg cccggagatt ccccccgc ccaactcgca gtggggatcg gagagatgga
541 tcgcaaccgt acgtcggcag gtaactaccg acgcaggaag tcgatctcg ctctccccca
601 gcggacagag caaaaacgcgg cttccgaacac ccgcggatcg gagtgtagcc ccaaattggg
661 gcacggcagc gctgcagtgc gaccccccgg aagggttcg ggtcagccg ggcgtggcgg
721 aaccgtcggc gccagtcccg ttctgccc cat caagggggag acattggtcc ctatacccccc
781 tgggcagatt aaacaggagc cggaggatcc gccatcgacc tgatgctcg ttggcatcc
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"
 /isolate="CMS001_044_ALCO"
 /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="MGDAPSRRRRGGGHKPPSANSAGNSGNNAVPGVSPPAPPTDNP
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLALAVGEPRSAAGV
CLVFDKGQLALSALGMEPSSNGTAGKPAAPARAEAPVSTARAPVRRSTGGGRGCAGP
DSPLAQLAVGVGEMDRNRTSAGNYRRRKSISSLQRTEQNAAPNTRGSECSPKLGP
AAVRPPGRGQGAAGRGGTVGANPVLPIKGETFVPIPPGQVKQEPRFPPST"

CDS complement(37..843)
 /codon_start=1

/product="ORF2"
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CTLTPSGGSHCSRARPQFGATLRTAGVRSGILLCPLGERDRRLPASVVTCCRRTVAIHL
SDPNCELGEGGISRRASPTPASRPADWGPRGGDWSLGTGGRGRFPCRVRARLHPESA
KGELAAFVEDKADASRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

1 gtatccgt actggacaac gatgggtgac gcaccgtcac gtcggagacg acgaggcggc
61 ggtcataaac caccatccgc gaacagtca ggaacacagt ggaatgcggt acccgccaggc
121 gttagcccgc cggcacctcc cactgataac cctgctctgt cccccccggtaactaaccgg
181 ggatgcgtga ttgagcgtga caaggccga aagagtggaa ctaaccggg acctgtggca
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661 ttggggcctg gcacggctgc agtgcgaccc cccgaaagggtcagggtgc agccggcgt
721 ggcggaaaccgc tcggcgcacaa tcctgtctcg cccatcaagg gggagacatt tgtccccata
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841 catccc

//

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; Lenarviricota; 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
/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP
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PGDSPLAQLAAGVGETDRTRTPVSNYRRKSDPWIPQRTEQQAAPSTGGKVCSPNLGH
GTAAVRPLEKDRGAAGRGGVGAHPGRPIKGETLGPKPPGSAKQEPKSPPST"
CDS complement(116..928)
/codon_start=1
/product="ORF2"
/translation="MPRRASGRWRRRLRLFCRPRGFGTKCLPLDGPARMGADASATPG
CTPVLLQRTCSRAMPQIGATHLPAGGRCGLLCPLDPRIALPAPIAYRRTGTIRL
SDPSCKLGEGGISWRASPNPACRSADECLSGCRGLGAGRRGVDLLVRRPTRARLQLE
SAKGQLARFVKDEAYAGRRARFSNHCQGKIDSLPACRSLYGRRCQWTRLSSTHSGPCR
PNYAPFVTNEGGQSRVTSGGCRRALACGYRISTVSRGWWYMTAASSSPT"

ORIGIN

1 cagctcagaa gcggtttcca actgccatt cattcctgaa ggtttcctag cttccaaatc
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601 ccaacttgcg gctgggggttgg gagagacgga tcgttccgtt acggccgtaa gcaattatcg
661 ggcgcaggaaag agcgtatccgtt ggatccccc ggcgcaggaaag caacaaggccg cacccttccac
721 cggcggaaag gtgtgttagcc ccaattttggg gcatggcagc gtcgtcgtgc gtcctttgg
781 gaaggacagg ggtgcaggccg ggcgtggccg aggctgcgcg gccatccgtt gccggcccat
841 caaggggggag acacttggtc ccaaaccccc tgggtcggca aaacaggagc cgaagtctcc
901 gccatcgacc ttagtgcgtt cggggcatcc ccc
//

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"
 /isolate="CMS001_047_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 22..834
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 /product="putative Robin"
 /translation="MGDAPSSRRRRGGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP
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 RLVFDKACQLALSALELPSTGR
 TADQKVNAAPARA
 EA
 PASTAKALVRRSTGGVGGCA
 PGDSPLAQLAAGVGETDRTRTPVRNYRR
 RKS
 DPWIPQRTEQQAAPSTGGKVCSPNLGH
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 PKFPPST"
 CDS complement(37..849)
 /codon_start=1
 /product="ORF2"
 /translation="MPRRASGRWRKLRLFCRPRGF
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 MGADASATPG
 CTPVLLQRT
 HCSRAMPQIGATHLPAGGRC
 GLLLCPLGD
 PRIALPAPI
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 GTIRL
 SDPSCKLGE
 GEGGISWRAS
 PN
 PACRS
 ADECL
 RSGCRGLGAGRRGV
 DLLV
 RR
 P
 TRARLQLE
 SAKGQLAR
 FVK
 DEAYAGR
 RARFSNHC
 QGK
 IDSLP
 AC
 RSLY
 GRR
 QCW
 TRLS
 STHSGPCR
 PNYAP
 FVT
 NEGG
 QSR
 VT
 SGG
 C
 R
 R
 ALAC
 GYR
 IST
 V
 S
 CT
 VR
 G
 WWY
 MTA
 ASSSPT"
ORIGIN
 1 gttatcgt actggacaac gatgggtgac gcaccgtaa gtcggagacg acgaggccgc
 61 ggtcatatac caccatccgc gaacagtca gaaaaacagtg gagatgcggt accccgcag
 121 caaggccccgc cggcacccctc cactggtaac cctgcgtcgt cctccctcg tagtaacgaa
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 241 gcccggccg taaaggctgc ggcacccgg caggctgtcg atcttgcctt ggcagtgg
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 361 cttagcgctc tcgagctgga gccttagcagc ggtcgacgg cggacaaaaa ggtcaacgc
 421 gcccggccc gcccggacgc ccctgcattc actgcgaagg cactcgccg ccgatcgaca
 481 gcccgggtt gggatgcgc gccaggagat tccccctcg cccaacttgc agctgggtc
 541 ggagagacgg atcgatcccg tacggccgtt agaaatttac ggcgcaggaa gagcgatccg
 601 tggatcccccc agccggacaga gcaacaagcc gcacccatcca cccggccggaa ggttgttagc
 661 cccaaattgg ggcacccatcc ggcacccatcc ggtcgatcgt cgtcccttgg agaaggacag gggatgc
 721 gggatgcgc gggatgcgc cggccatcc tcaaggggaa gacacttgc
 781 cccaaacccc ctggatgcgc aaaacaggag ccgaaggatcc cggccatgcac ctgatgc
 841 gccccatccccc 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##
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/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"
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ALSSLVSNEGCVRPARPGMSGTQPGSLAAAVKAAACRQAVDLALAVVGEPRSAAGV
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GTAAVCPPREDRGAAGRGGVGAHPGRPIKGTLGPKPPGSAKQEPKSPPSTRCAG"
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61 tataccacca tccgcgaaca gtgcaggaaa cagtggagat gcgggtcccg caggccaagg
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181 cgttgtttagg cctgcacggc ccggaatgag tggaactcaa ccgggtctc tggcagcggc
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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##

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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 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
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CDS complement(42..848)
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KGELAAFVEDKADASRRARFSYHRQQVDSLTAACRSILYGRRCHRSRLSSTLGLVRLN
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841 ttggcatcc 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##
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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
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 /lat_lon="37.55697 N 122.07938 W"
 /collection_date="21-Sep-2017"
 /note="metagenomic; derived from metagenome: mosquito
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CDS 17..829
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EAPASTAKALVRRSTGGVGGCA
PGDSPLAQLAAGVGETDRTRTPVRNYRR
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CDS complement(32..844)
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LGDPRIALP
APIISYRRTGTIRL
SDPSCKLGE
GGGISWRASP
NPACRS
ADECLRS
GCRLGAGRRGV
DLLVRRP
TRARLQLE
SAKGQLAR
FVKDEAYAGRR
RARFSNH
CQGKIDSLP
ACRS
SLYGR
RCQW
TRLSS
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PNYAPF
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QSRV
TSGGC
RRA
LACGY
RISTV
RGWWY
MTAASSF
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721 tggcgaggc gtccgcgc atcctggcc gcccatcaag ggggagacac ttggcccaa
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841 gcatcccc

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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

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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"

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CDS complement(32..838)
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KGELAALVKDKADASRRARFSYHRQQVDSLTCRSLYGRRCHRSRLSSTLSGLVRLN
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841 cccg
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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
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 /mol_type="genomic RNA"
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 /isolation_source="female, blood fed, collected in
 marsh/swamp habitat"

/host="Culex erythrothorax"
/db_xref="taxon:2562539"
/environmental_sample
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/lat_lon="37.557 N 122.0794 W"
/collection_date="21-Sep-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

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ORIGIN

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841 tgccgggg

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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., 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 844)

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 :: 271.877445x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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/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
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/lat_lon="37.6683 N 122.15915 W"
/collection_date="24-Oct-2017"
/note="metagenomic; derived from metagenome: mosquito
metagenome"

CDS 17.823
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CDS complement(32..838)
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KGELAAFVEDKADASRRARFSYHRQGVDSLTCRSLYGRRCHRSRLSSTLGLVRLN
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ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg agacgacgag gcggcggtca
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121 cccgccccca cctcccactg ataacctgc tctgtctcc ccggtaacta accggggatg
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301 accgcgcctg gcggctggcg tctgcctgt ctgcacaaa ggctgccagc tcgcccctag
361 cgctctcggg atggagccca gccaagcgg gacagcggtt aaaaaccgcgt cgcccgcccg
421 tgccgaggct ccagtctcca ccgcgaggggc cccagtcgcg ccgtcactg gcgggggtgg
481 gggatgcgcg ctggagatt ccccccctgc ccaactcgcg gtgggggtcg gagatgg
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661 gcctggcacg gctcgactgc gaccccccgg aagggtcag ggtcagcc ggcgtggcg
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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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/translation="MGDAPSRRKRRGGGHIPPSANSAGNSGNNAVPGVSPVPPTGNP
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CDS complement(34..840)

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ORIGIN

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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; 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 :: 389.385309x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..853

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/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
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/translation="MGDAPSRRRRGGGHKPPSANSAGDSGNAPAGVSPPAPPTGNP
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DSPLAQLAVGVGEMDRDRTSAGNYRRRKSISSLQPQRTEQKAAPNSRGSECSPKLGP
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CDS complement(42..848)

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/product="ORF2"
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KGELAAFVEDKADASRRRARFSYHRQQVDSLTAACSLYGRRCHRSRLSSTLGLVRLN
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ORIGIN

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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

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/isolation_source="female, unfed, collected in
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/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
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CDS complement(117..923)
/codon_start=1
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KGELAAFVEDKANASRRARFSYHRQGVDSLACRSLYGRRCHRSRLSSTLSGLVRLN
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ORIGIN

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661 ggaagtcgat ctgcgtctc cccagccgg aagagaaaaa tgccgctccg aacacccgcg
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901 cgacctgatg ctctgtggg catcccccc

//

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., 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 844)

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 :: 580.211213x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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/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

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 CDS complement(32..838)
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 841 cccg
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 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"
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 /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
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CDS complement(41..847)
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ORIGIN

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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="MGDAPSRRRRRGGGHKPPSANSAGNSGDAVSAGVSPVPPTGDP
ALSSSVNNRCVIEPGRPGKSETRPGHLAAAALKAAACRQAVDLALAVVGEPRSAAGV
RLVFDKACSLALSALDMGPSTGGTADLRINAAPARAEPSTAKALVRSTGGGGCA
PGDSPLAQLAVVGELDRSGRTPVSNYRRRRTDPTLPQRT"

ORIGIN

1 cctgtactgg acagcgatgg gtgacgcacc gtcacgtcgg agacgacgag gcggcggtca
61 taaaccacca tccgcgaaca gtgcaggaaa cagtggat gccgttatcc caggcgtag
121 cccgcggta cccccactg gtgaccctgc tctgtctcc tctgttaata acagaggatg
181 cgtgattgag cctggcaggc cggcaagag tgaaactcga cccggccatt tggcagcggc
241 ggccgtaaag gctgcggcat gcccgcaggc tgcgcacccgc gcccgtcg tagtaggaga
301 accgcgcctcg gcccgcggcg tgcgcctgt ctgcacaaa gcgtgcgc tcgccttag
361 cgctctcgat atggggccta gcacgggagg gacgcggat cttaggatca acgcgcgc
421 cgccgcgc gaggccccac tcttaccgc gaaggccctc gtccgcggcgt cgacaggcgg
481 gggtggggta tgcgcgcgg gagattcccc ctcgcacaa ctgcagttt gggcggaga
541 gctcgatcgg tcggccgtc cgccagaatg caattaccgg cgccaggagga ccgcacccac
601 tctcccccac cgacaga

//

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

/codon_start=1
/product="putative Robin"
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGDAVSAGVCPPVPTGDP
ALSSSVNNRGCVEPGRPGKSETRPDHLAAA VKAACRQAVDLALA VGEPRSAAGV
RLVFDKACSLALSALDMGPSTGGTADLRINAAPARAGAPLSTA KALVR RSTGGGGCA
PGDSPAQLAVVGELDRSGRTPVSSYRRRKTDPTLPQRTEHQ AALDTRGPVCSPNLG
HGTAAVRPPGRGQGAAGRGGVVAHPARPIKGTLGP KPPGPIKQEPKTPPST"

CDS complement(104..919)

/codon_start=1
/product="ORF2"
/translation="MPYRASGRRRSLLNRPRGF GTKCLPLDGPSRMGADDSATPG
CTLSSSRRT HCSRAMPQIGATHWTPGVQCGLMLCPLGESIGLPAPVTAYRRTARPIE
LSDPNCELGEGGISRRASPTPACRPADEGLRGREW GPGAGGRGVDPKIRRPSRAGPHI
ESAKGERARFVEDKAHARRRARFSYYRKQVDSLACRSLYGRR CQMVRSSFTLAGPA
RLNYASSVINRGGQSRVTSGGYR RANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

1 ccccaactgg taccctgctc tgtccctc ttttaataac agaggatgcg tagttgagcc
61 tggcggggtt atccctgtact ggacaacgtt gggtgacgca ccgtcacgtc ggcgacgacg
121 aggccggcgtt cattaaaccac catcccgaa cagtgcagga aacagtgggg atgcggatc
181 cgcaggcgtt tgcccgccgg tacccccac ttgtgaccct gctctgcct cctctgtta
241 taacagagga tgcgtatgtt agcctggcag gcccggcaag atgtaaaactc gaccggacca
301 ttggcagcg cgccgcgtaa aggctggcgc atgcccggc gctgtcgacc tggccctgc
361 ggttagtagga gaaccgcgt cggccgggg cgtgcgcctt gtctcgaca aacgcgtgc
421 gctcgccctt agcgtctcg atatggggcc cagcacggga gggacggcgg atcttcggat
481 caacgcgcgc cccgcccgc cccggggcc actctctacc gcaaggccc tcgtccgc
541 gtcgacaggc ggggtgggg gatgcgcgc gggagattcc cccctcgccc aactcgca
601 tggggtcgga gagctcgatc ggtcgccgg tacccggta agcagttaacc ggcgcaggaa
661 gaccgatccc actctccccc agcggacaga gcatcaagcc gcaactggaca cccggggtcc
721 aagtgttagc cccaaattgg ggcatggc ac ggctgcagtg cgtccctcg gaagaggaca
781 ggggtcagcc gggcgtggcg gagtcgtcgg cggccatcc tgcggccca tcaaggggg
841 gacacttggt cccaaacccc ctggccgat taagcaggag cccaagactc cggcgtcgac
901 ctgatgctc ttagggcattt ccccaacgtc ggcgacgacg aggcggcggt cattaaac

//

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="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTDNP
ALSPPVTNRGCVIEPDKARKSGTQPGVAAAALKAAACRQAVDLALAVGEPRSAAGV
CLVFDKGQLALSALGMEPSSGTAGKSAAPARAEPVSTARAPVRRSTGGGGCAPG
DSPLAQLAVGVGEMDRNRTSAGNYRRRKSISSLPQRTEQNAAPNTRGSECSPKLGHGT
AAVRPPGRQQGAAGRGGTVGASPVLPIKGETFVPIPPGQIKQEPKVPPST"
CDS complement(33..839)
/codon_start=1
/product="ORF2"
/translation="MPNRASGRWRNLRLFNLPGYRDKCLPLDGQNRTGADGSATPG
CTLTPSGGSHCSRAMPQFGATLRTAGVRSGVLLCPLGERRDRLPASVTCRRTVAIHL
SDPNCELGEGGISRRASPTPASRPADWGPRGGDWSLGTGGRGRFSCRPARARLHPESA
KGELAAFVEDKADASRRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSTLGLVRLN
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"
ORIGIN
1 tcctgtactg gacaacgatg ggtgacgcac cgtcacgtcg gagacgacga ggcggccgtc
61 ataaaccacc atccgcgaac agtgcaggaa acagtggaa tgccgtaccc gcaggcgta
121 gccccccgc acctcccaact gataaccctg ctctgtcccc cccggttact aaccggggat
181 gcggtattga gcctgacaag gcccggaaaga gtggaaactca accgggacct gtggcagcgg
241 cggccgtaaa ggctgcggca tgccgtcagg ctgtcgaccc ggcctggcg gtggtaggag
301 aaccgcgcgc ggcggctggc gtctgcctg tcttcgacaa aggctgccag ctgcggcc
361 gcgctctcggtatggagct agtcgagcgg gacggcagg aaaatctgcc ggcggccccc

421 gtgccgaggc tccagtcacc accgcgaggg ccccagtccg ccgtcgact ggccggggtg
481 gggatgcgc gccggagat tccccctcg cccaactcgc agtggggtc ggagagatgg
541 atcgaaccg tacgtcgca ggttaactacc gacgaggaa gtcgatctcg tctctcccc
601 agccgacaga gaaaaacgcc gctccaaaca cccgcggtc ggagtgtac cccaaattgg
661 ggcatggcac ggctcagtg cgaccccccgaaggggtca gggcagcc gggctggcg
721 gaaccgtcg cgccagtctt gttctccca tcaagggga gacattgtc cctatacc
781 ctgggcagat taaacaggag ccgaagggtc cgccatcgac ctgatgctt gttggcatt
841 ccccccctgc ccaactcgca

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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="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPGVSPPAPPTDNP
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLALAVGEPRSAAGV
CLVFDKGQLALSALGMEPSSSGTAGKSAAPARAEAPISTARAPVRRSTGGGGCAPG
DSPLAQLAVGVGEMDRNRTSAGNYRRKSISLPRTEQNAAPNTRGSECSPKLGHGT
AAVRPPGRGQGAAGRGGTVGASPVLPIKGETFVPIPPGQIKQEPKVPPST"

CDS complement(41..847)
/codon_start=1
/product="ORF2"

/translation="MPNRASGRWRNLRLLFNLPRGYRDKCLPLDGQNRTGADGSATPG
CTLTPSGGSHCSRAMPQFGATLRTAGVRSGVLLCPPGERRDRLPASVVTCRRTVAIHL
SDPNCELGEGGISRRASPTPASRPADWGPRGGDWSLGTGGRGRFSCRPARARLHPESA
KGELAAFVEDKADASRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSP"

ORIGIN

1 cgggttatac ctgtactgga caacgatggg tgacgcaccg tcacgtcggaa gacgacgagg
61 cggcggtcat aaaccaccaat ccgcgaacacag tgcagggaaac agtgggaatg cggtacccgc
121 aggccgttagc ccgcggcac ctccccactga taaccctgt ctgtcccccc cggttactaa
181 cggggatgc gtgattgagc ctgacaaggc ccgaaagagt ggaactcaac cgggacctgt
241 ggcagcggcg gccgtaaagg ctgcggcatg ccgtcaggct gtgcacctgg ccctggcggt
301 gtaggagaa ccgcgtctgg cggctggcg tgcgttcgtc ttgcacaaag gtcgcacgt
361 cggcccttagc gctctcgaaa tggagccat ctcgagcggg acggcaggaa aatcgccgc
421 gcccggccgt gccgaggctc caatctccac cgcgaggcc ccagtccgccc ggtcgactgg
481 cgggggtggg ggatgcgcgc cgggagattc cccctcgcc caactcgac ttggggtcgg
541 agagatggat cgcaaccgta cgtcggcagg taactaccga cgcaggaagt cgatctcgac
601 tctcccccgg cggacagagc aaaacgcgc tccgaacacc cgcgggttcgg agtgtagccc
661 caaatgggg catggcacgg ctgcagtgcg acccccccga aggggtcagg gtgcagccgg
721 gcgtggcgga accgtcggcg ccagtcgtc tctgcccata aagggggaga cattgtccc
781 tatacccccggc gggcagatta aacaggagcc gaaggttcgg ccatcgacct gatgctctgt
841 tggcatcccccc cccctcgccca actcgacgtt 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="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTDNP
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLAGLAVGEPRSAAGV
CLVFDKGQLALSLGMEPSSSGTAGKTAAPARAEAPVSTARAPVRRSTGGGGCALG
DSPLAQLAVGVGEMDRHRTPAGNYRRKSISLSPQRTEQNAAPNTQGSECSPKLGHGT
AAVRPPGRGQGAAGRGGTVGASPVLIKRETFVPIPSQIKQEPKVPPST"
CDS complement(32..838)
/codon_start=1
/product="ORF2"
/translation="MPNRASGRWRNLRLFYLPREGYGDCLPLDGQNRTGADGSTTPG
CTLTPSGSHCSRAMPQFGATLRTLGVRSVLLCPLGERRDRLPAPVVTCCRRTVSIHL
SDPNCELGEGGISQRASPTPASRPADWGPRGGDWSLGTGGRSGFTRCPARARLHPESA
KGELAAFVEDKADASRRARFSYHRQQVDSLTAACRSILYGRRCHRSRLSSTLSGLVRLN
HASPVSNRGGSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAAASSP"

ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg agacgacgag gcggcggtca
61 taaaccacca tccgcgaaca gtgcaggaaa cagtggaat gcggtacccg caggcgtag
121 cccgccccca cctcccactg ataaccctgc tctgtcccccc ccgggtacta accggggatg
181 cgtgattgag cctgacaagg cccgaaagag tggactcaa ccgggacctg tggcagcggc
241 gcccgtaaag gctgcggcat gccgtcaggc tgcgacccctg gcccggcgg tggtaggaga
301 accgcgcctcg gcggctggcg tctgcctgt ctgcacaaa ggctgcagg tcgccttag
361 cgctctcggt atggagccca gctcgagcg gacagcggt aaaaccgcgt cgcccgcccg
421 tgccgaggct ccagtctcca ccgcgaggcc cccagtcgc cggcgtactg gcgggggtgg
481 gggatgcgcg ctggagatt ccccccctcg ccaactcgca gtggggtcg gagagatgga
541 tcgacaccgt acgcggcag gtaactaccg gcgcaggaaag tcgatctcg ctctcccca
601 gcggacagag caaaacgcgg ctccgaacac ccagggttcg gagtgtagcc ccaaattggg
661 gcatggcacg gctgcagtgc gaccccccgg aagggttcg ggtgcagccg ggcgtggtgg
721 aaccgtcgcc gccagtccctg ttctgccc cataggggg acattcgcc ccataccctc
781 tggcagata aaacaggagc cgaaggttcc gccatcgacc tgatgcctg tggcatcc
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., 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 858)

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 :: 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
 ALSPPVTNRGCVIEPDKARKSGTQPGPVAAA
 VAAACRQAVDLALAVGEPRSAAGV
 CLVFDKGQLALSALGMEPSSSGTAGKPAAPARA
 EAPVSTARAPVRRSTGGGRGCAGP
 DSPLAQLAVGVGEMDRNRTSAGNYRRKSISL
 PQRTEQNAAPNTRGSECSPKLGPGT
 AAVRPPGRGQGAAGRGGTVGANPVLIKGETF
 VPIPPGQVKQEPRFPPST"

CDS complement(39..845)
 /codon_start=1
 /product="ORF2"
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 SLTGTGGGRGRFSCRPTRARLHPESA
 KGELAAFVEDKADASRRARFSYHRQQVDSL
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 PTSVCRGWWFMTAASSSPT"

ORIGIN

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181 ggggatgcgttattgagccgt gacaaggccc gaaagagtgg aactcaaccg ggacctgtgg
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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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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; Lenaviricota; 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
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 /mol_type="genomic RNA"
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 /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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CDS complement(32..847)
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ORIGIN
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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; Lenarviricota; Amabiliviricetes;
 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

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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
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 /product="putative Robin"
 /translation="MGDAPSRRRRGGGHKPPSANSAGNSGDAVSAGVSPPVPTGDP
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PKTPPST"

CDS complement(42..857)
 /codon_start=1
 /product="ORF2"

/translation="MPYRASGRWRSLLNRPRGFGTKCLPLDGPSRMGADDSATPG
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ESAKGERARFVEDKAHARRRARFSYYRKQVDSLACRSLYGRRCQMVRSSFTLAGPA
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ORIGIN

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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

source 1..899

/organism="Culex narnavirus 1"
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/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
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CDS complement(66..881)
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ESAKGERARFVEDKAHARRRARFSYYRK
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ORIGIN

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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

source 1..860
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 /isolation_source="unknown sex, unfed, collected in agriculture & residential habitat"
 /host="Culex erythrothorax"
 /db_xref="taxon:2562539"
 /environmental_sample
 /country="USA: Placer Valley, California"
 /lat_lon="38.836781 N 121.39119 W"
 /collection_date="21-Nov-2017"
 /note="metagenomic; derived from metagenome: mosquito metagenome"

CDS 27..839
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 ALSSLVSNEGCVRPARPGMSGTQPGPLAAA
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 PGDSPLAQLAVGVGETDRTRTPVGNYRRKSDPWIPR
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CDS complement(42..854)
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 SDPNCKLGE
 GEGGISWRASP
 NPACRS
 ADECLRG
 CRDLGAGRRGV
 DLLVRRP
 TRARLQLE
 SAKGQLARF
 VKDEAYAGRR
 ARFSNHC
 QGKIDSLP
 ACRS
 LNGRRC
 QWTRL
 SSHTG
 PCR
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 RRALAC
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 ISTV
 RGWWY
 MTA
 ASSS
 ST"

ORIGIN

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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
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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;
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##
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LOCUS MW434180 3151 bp RNA linear ENV 18-FEB-2021
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##
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 Sequencing Technology :: Illumina
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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., 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 3132)

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 :: 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##
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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

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 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; Lenarviricota; 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
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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
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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

##Assembly-Data-END##

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; 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 :: 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; Lenarviricetes; 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 :: 92.627234x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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DEFINITION Culex narnavirus 1 isolate CMS001_036_ALCO genomic sequence.
ACCESSION MW434190
VERSION MW434190
DBLINK BioProject: PRJNA605178
BioSample: SAMN14051476
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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 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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Coverage :: 66.032712x
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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
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FEATURES Location/Qualifiers

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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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LOCUS MW434193 3145 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS001_040_ALCO genomic sequence.

ACCESSION MW434193

VERSION MW434193

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051480

Sequence Read Archive: SRR11035283

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 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.

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 :: 135.722295x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434194 3137 bp RNA linear ENV 18-FEB-2021
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; 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

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##

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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
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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; Lenarviricota; 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##
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 Sequencing Technology :: Illumina
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DEFINITION Culex narnavirus 1 isolate CMS001_045_ALCO genomic sequence.
ACCESSION MW434197
VERSION MW434197
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 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##
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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##
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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., 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 3112)
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##
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 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
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Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 114.15482x
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DEFINITION Culex narnavirus 1 isolate CMS001_052_ALCO genomic sequence.
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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##

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ORIGIN

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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##
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LOCUS MW434203 3140 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001_058_ALCO genomic sequence.

ACCESSION MW434203

VERSION MW434203

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 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 :: 71.370878x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434204 3154 bp RNA linear ENV 18-FEB-2021

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

##Assembly-Data-END##

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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
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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; 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 :: 582.525105x
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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; 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 :: 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;
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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
COMMENT ##Assembly-Data-START##
 Assembly Method :: IDSeq pipeline v. 3.2
 Coverage :: 703.74927x
 Sequencing Technology :: Illumina
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LOCUS MW434211 3158 bp RNA linear ENV 18-FEB-2021
DEFINITION Culex narnavirus 1 isolate CMS002_028e_WVAL genomic sequence.
ACCESSION MW434211
VERSION MW434211
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 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 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.

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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##

FEATURES Location/Qualifiers

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DEFINITION Culex narnavirus 1 isolate CMS002_029c_WVAL genomic sequence.
ACCESSION MW434212
VERSION MW434212
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 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.
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JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,
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COMMENT ##Assembly-Data-START##
Assembly Method :: IDSeq pipeline v. 3.2
Coverage :: 190.115272x
Sequencing Technology :: Illumina
##Assembly-Data-END##

FEATURES Location/Qualifiers

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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
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DEFINITION Culex narnavirus 1 isolate CMS002_046a_WVAL genomic sequence.
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ORGANISM Culex narnavirus 1
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;
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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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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

##Assembly-Data-END##

FEATURES Location/Qualifiers

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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

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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DEFINITION Culex narnavirus 1 isolate CMS002_047f_WVAL genomic sequence.
ACCESSION MW434217
VERSION MW434217
DBLINK BioProject: PRJNA605178
BioSample: SAMN14051577
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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 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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LOCUS MW434218 3164 bp RNA linear ENV 18-FEB-2021
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; 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 :: 625.481697x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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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

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 :: 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

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 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 :: 354.941577x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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