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**[Ext] GenBank MW434135-MW434220**

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

Fri, Mar 5, 2021 at 4:40 AM

Dear GenBank Submitter:

Thank you for your submission.

Based on the data submitted to us, the scheduled release date for your submission is:

Mar 10, 2021

If this date is not correct, please let us know as soon as possible, otherwise this submission will be released on the date indicated above. The data will become available from our different servers within a few days of release. The data are simultaneously made available to ENA in Europe and the DNA Data Bank of Japan.

Changes may have been made to your original submission in order to conform to database annotation conventions including:

- Strings of N's, low quality sequence, vector or linker trimmed from ends
- Feature spans corrected and descriptions modified for all feature types including coding regions
- Nomenclature edited to 'official' gene names, product labels, etc.
- Exon spans adjusted to conform to the splice donor/acceptor consensus sequences, GT and AG, respectively
- Any mRNA or ribosomal RNA sequences submitted on the minus-strand have been reverse-complemented
- Taxonomic and source data edited, including unpublished organism names changed to temporary names. Please notify us when the organism names are published and we will update them accordingly.

If your submission needs revision, do not submit a new sequence. Instead,

please follow the directions to update a sequence record at:

<https://www.ncbi.nlm.nih.gov/Genbank/update.html> Since the flatfile record is a display format only and is not an editable format of the data, do not make changes directly to a flatfile. Send properly formatted updates to: [gb-admin@ncbi.nlm.nih.gov](mailto:gb-admin@ncbi.nlm.nih.gov)

An accession number has been assigned to each nucleotide sequence and was previously provided to you. Note that during the processing, we have assigned protein identifiers to any proteins within the submission. This is fielded as /protein\_id.

We strongly recommend that these numbers appear in any publication which reports or discusses these data, so that readers may easily retrieve your data from our databases.

Please reply using the current Subject line.

Sincerely,

Linda Frisse, PhD  
GenBank Direct Submission Staff  
[gb-admin@ncbi.nlm.nih.gov](mailto:gb-admin@ncbi.nlm.nih.gov)

GenBank flat file:

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##  
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        wildlife refuge / park habitat"  
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    /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"  
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CDS complement(37..843)  
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/protein\_id="QSM01508"  
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KGELAAFVEDKADASRRARFSYHRQQVDSLTAACSLYGRRCHRSRLSSTLSGLVRLN  
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAAASSP"

ORIGIN

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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

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/mol\_type="genomic RNA"

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/isolation\_source="female, blood fed, collected in  
industrial (waste water treatment plant) habitat"

/host="Culex pipiens"

/db\_xref="taxon:2562539"

/environmental\_sample

/country="USA: Alameda County, California"

/lat\_lon="37.7152 N 122.19431 W"  
/collection\_date="12-Sep-2017"  
/note="metagenomic; derived from metagenome: mosquito  
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KGELAAFVEDKADASRRRARFSYHRQQVDSLARRSLYGRRCHRSRLSSTLSGLVRLN  
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## ORIGIN

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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##  
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     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"  
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     PGDSPAQLAAGVGETDRTRTPVRNYRRRKSDPWIPQRTEQQAAPSTGGKVCSPNLGH  
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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##

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wildlife refuge / park habitat"  
/host="Culex erythrothorax"  
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KALVRRSTGGGGCA  
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CDS complement(37..852)  
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ENAKGERAR  
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GQVDSLAA  
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SQMVRSSFT  
LAGPA  
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INRGGQS  
RVTS  
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NACGYRI  
PTVS  
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FMTA  
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ORIGIN

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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)  
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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  
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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="04-Oct-2017"  
/note="metagenomic; derived from metagenome: mosquito  
metagenome"  
CDS 24..836  
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RLVFDKACQLALSALELEPSTGRTADQKVNAAPARAEPASTAKALVRRSTGGVGCA  
PGDSPLAQLAVGVGEMDRIRTPVGNHRRRKTVPLIPRTEQQAAPPTWREVCSPKLGH  
GTAAVRPPREDRGAAGRGGGVGAHPGRPIKGTFGPPIP GSAKQEPKSLPST"  
CDS complement(69..851)  
/note="ORF2"  
/codon\_start=1  
/product="hypothetical protein"

/protein\_id="QSM01516"  
/translation="MPRRASGRWQRLRLLFCRPRGYGTKCLPLDGPARMGADASATPG  
CTPVLSRRTHCSRAMPQFGATHLPPSWRCGLLCPSGDQRNGLPAPVVAHRRADPIHL  
SDPNCKLGEGGISWRASPNCRSADECLRSGCRCLGAGRRGVDLLVRPTRARLQE  
SAKGQLARFVKDEAYAGRARRFSNHQCQGKIDSLPACRSLNRRQCQVGRLSSTHTGPCR  
PNYAPFVTNEGGQSRVISGGYRRALACGYRISTVSCTVRGWW"

ORIGIN

1 gggttatcct gtactggaca acgatgggt acgcaccgtc acgtccggaga cgacgaggcg  
61 gccgtcattt accaccatcc gcgaacagtgc cagggaaacag tggagatgcg gtatccgcag  
121 gccaaggccc gccggatccc tccactgata accctgctct gtcctccctc gtagtaacg  
181 aagggtgcgt agttaggcct gcaaggaccg gtatgagtgg aactcaaccg gcccacctgg  
241 cagcggcggc cgttaaggct gcggcatgcc ggcaggctgt cgatcttgcc ctggcagtgg  
301 ttggagaacc gcgcgtggc gccggcgatcc gcctcgatcc tgacaaagcg tgccagctgg  
361 cccttagcgc tctcgagctg gagcctagca cgggtcgac ggcggaccaa aaggtaacg  
421 cccgcggc cccgcggcag gcacccatgc ccactgcgaa ggcactcgcc cgccgatcga  
481 caggcggggt tggggatgc gcgcaggag attccccct cgcacaactt gcagttgggg  
541 tcggagagat ggatcgatc cgcacccgg tggcaacca caggcgcagg aagaccgtt  
601 cgttgatccc cgcacggaca gagcaacaag cgcacccatcc aacttggcg gagggtgtta  
661 gccccaaatt ggggcatggc acggctcgag tgccctcc gagagaggac aggggtgcag  
721 cccggcgtgg cggaggcgtc ggcgcatac ctggccggcc catcaagggg gagacattt  
781 gtcccatacc ccctggatcg gcaaaacagg agccgaagtc tctgccatcg acctgatgct  
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  
 /codon\_start=1  
 /product="putative Robin"  
 /protein\_id="QSM01517"  
 /translation="MGDAPSRRRRGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP  
 ALSSLVSNEGVVRPARPGMSGTQPGPLAAAALKAAACRQAVDLALAVVGEPRSAAGV  
 RLVFDKACQLALSALLEPSTGRTADQKVNAAPARAEPASTAKALVRRSTGGVGGCA  
 PGDSPLAQLAAGVGETDRTRTPVRNYRRRKSDPWIPQRTEQQAAPSTGGKVCSPNLGH  
 GTAAVRPLEKDGRGAAGRGGVGAAHPGRPIKGETLGPKPPGSAKQEPKSPPST"

CDS        complement(32..844)  
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 /codon\_start=1  
 /product="hypothetical protein"  
 /protein\_id="QSM01518"  
 /translation="MPRRASGRWRRRLFLCRPRGFGTCKLPLDGPARMGADASATPG  
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 SDPSCKLGEGGGISWRASPNCACRSADECLRSRGCRGLGAGRRGVDLLVRRPTRARLQE  
 SAKGQLARFKVDEAYAGRRARFSNHCQGKIDSPLACRSLYGRRCQWTRLSSTHSGPCR  
 PNYAPFVTNEGGQSRVTSGGCRRALACGYRISTVSRGWWYMTAASSST"

ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcga agacgacgag gcggcggtca  
 61 tataccacca tccgcgaaca gtgcaggaaa cagtggagat gcggtacccg caggccaagg  
 121 cccgcggca ccctccactg gtaaccctgc tctgtcctcc ctgcgttagta acgaagggtg  
 181 cgtagttagg cctgcacggc ccggaatgag tggaactcaa ccgggtccac tggcagcggc  
 241 ggccgtaaag gctgcggcat gcccgcggc tgcgtatctt gccctggcag tggttggaga  
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 361 cgctctcgag ctggagccata gcacgggtcg gacggcgac caaaagggtca acgcccggcc  
 421 gccccgcgc gaggccctg catccactgc gaaggcactc gtccgcgcgt cgacaggcgg  
 481 gttttggggta tgccgcgcag gagattcccc ctcgcggcaa ctgcgcgtg gggtcggaga  
 541 gacggatcgat acccgtaacgc cggtaagaaa ttatcgccgc aggaagagcg atccgttat  
 601 cccccagcg acagagaac aagccgcacc ttccaccggc gggaaagggtgt gtatccccaa  
 661 ttggggcat ggcacggctg cagtgcgtc ttggagaag gacagggtgt cagccggccg  
 721 tggcggagggc gtcggcgccc atccgtccg gcccatcaag ggggagacac ttgtcccaa  
 781 accccctggg tcggcaaaac aggagccaa gtccgcgcata tcgacccatgt gctctcgcc  
 841 qcatccccccq

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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"  
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/isolation\_source="female, blood fed, collected in marsh habitat"  
/host="Culex erythrothorax"  
/db\_xref="taxon:2562539"  
/environmental\_sample  
/country="USA: Alameda County, California"  
/lat\_lon="37.58191 N 122.04838 W"  
/collection\_date="06-Oct-2017"  
/note="metagenomic; derived from metagenome: mosquito metagenome"

CDS 17..829  
/codon\_start=1  
/product="putative Robin"  
/protein\_id="QSM01519"  
/translation="MGDAPSRRKRRGGGHIPPSANSAGNSGDAVPAGQQGPPAPSTGNP  
ALSSLVSNEGCVVRPARPGMSGTQPGPLAAA  
VKAACRQAVDLALA  
VVGEPRSAAGV  
RLVFDKACQLA  
LSALELEPSTGR  
TADQKVNAAPARA  
EAPASTAKALV  
RRSTGGVGGCA  
PGDSPA  
LAQAGVGETDRTRTP  
VRNYRRRKSDP  
WIPQRTEQQAAP  
STGGKVC  
SPNLGH  
GTA  
AVRPLEKD  
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GGVG  
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KPPG  
SAKQE  
PKS  
PPT"

CDS complement(32..844)  
/note="ORF2"  
/codon\_start=1  
/product="hypothetical protein"  
/protein\_id="QSM01520"  
/translation="MPRRASGRWRRLLFCRPRGF  
TKCLPLDGPAR  
MGADASATPG  
CTPVLLQRT  
HCSRA  
MPQIGATHLP  
PAGGRC  
GLLCPLGD  
PRIALP  
APII  
SYRRTGT  
IRL  
SDPSCKL  
GEGGISW  
RASP  
NPAC  
RSADECL  
RS  
GCRGL  
GAGRRGV  
D  
LLV  
R  
P  
TRAR  
LQ  
LE  
SAKGQL  
LARF  
VKDE  
AYAG  
RRAR  
FSNH  
CQGK  
IDSL  
PAC  
RS  
LYG  
RRC  
QW  
TRL  
SS  
THSG  
PCR  
PNYAP  
FVT  
NEGG  
QSR  
VTSG  
GC  
RRA  
LAC  
GYR  
ISTV  
RGWW  
YMTA  
ASSF  
ST"

ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcga aaacgacgag gcggcggtca  
61 tataccacca tccgcgaaca gtgcaggaaa cagtggagat gcggtacccg caggccaagg  
121 cccgcggca ccctccactg gtaacctgc tctgtcctcc ctgcgttagta acgaagggtg  
181 cgttgttagg cctgcacggc ccggaatgag ttgaaactcaa ccgggtccac tggcagcggc  
241 ggccgtaaag gctgcggcat gcccgcggc tgcgcgttat cttgcataaa gcgtgccagc tggcccttag  
301 accgcgctcg gcccgcggcg tacgcctcg tttgacaaaa gcgtgccagc tggcccttag  
361 cgctctcgag ctggagccta gcacggctg gacggcggac caaaagggtca acgcccgcgg  
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481 ggtggggga tgccgcgcag gagattcccc ctcgcggccaa ctgcgcgtg gggcggaga  
541 gacggatcgatccgc cggtaagaaaa ttatccgcgc aggaagagcg atccgtggat  
601 ccccccagcg acagagcaac aagccgcacc ttccacccggc gggaaagggtgt gtagccccaa  
661 ttggggcat ggcacggctg cagtgcgtcc ttggagaag gacagggtg cagccggcg  
721 tggcggaggg gtcggcgccc atcctggccg gcccataag ggggagacac ttggcccaa  
781 acccccctggg tcggcaaaac aggagccgaa gtctccgcca tcgacactgat gctctgcggg  
841 gcatcccccg

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

DEFINITION Culex narnavirus 1 isolate CMS001\_028\_ALCO genomic sequence.

ACCESSION MW434142

VERSION MW434142

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051468

Sequence Read Archive: SRR11035296

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

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

REFERENCE 1 (bases 1 to 844)

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

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

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 844)

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

TITLE Direct Submission

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

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 110.650587x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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"  
/protein\_id="QSM01521"  
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTDNP  
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLALAVGEPRSAAGV  
CLVFDKGQLALSALGMEPSSSGTAGKTAAPARAEAPVSTARAPVRRSTGGGGCALG  
DSPLAQLAVVGEMDRHRTSAGNYRRKSISLQPQRTEQNAAPNTQGSECSPKLGHGT  
AAVRPPGRGQGAAGRGGTVGASPVLPIKRETFVPIPSEGQIKQEPKVPPST"

CDS complement(32..838)

/note="ORF2"  
/codon\_start=1  
/product="hypothetical protein"  
/protein\_id="QSM01522"  
/translation="MPNRASGRWRNLRLFYLPRGYGDKCLPLDGQNRTGADGSATPG  
CTLTPSGGSHCSRAMPQFGATLRTLGVRSVLLCPLGERDRLPAPVTCRRTVSIHL  
SDPNCELGEGGISQRASPTPASRPADWGPRGGDWSLGTGGRSGFTRCPARARLHPESA  
KGELAAFVEDKADASRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSLGVLRLN  
HASPVSNRGQSRVISGRCCRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg agacgacgag gcggcggtca  
61 taaaccacca tccgcgaaca gtgcaggaaa cagtggaat gcggtacccg caggcgtag  
121 cccgccccca cctcccactg ataacctgc tctgtcccccc cgggtacta accggggatg  
181 cgtgattgag cctgacaagg cccgaaagag tggaactcaa cccggacctg tggcagcggc  
241 ggccgtaaag gctgcggcat gccgtcaggc tgcgtacccg gccctggcgg tggtaggaga  
301 accgcgctcg gccgtggcg tctgcctgt ctgcacaaa ggctgccagc tcgccccatg  
361 cgctctcggt atggaggcta gctcgagcgg gacagcggtt aaaaccgcgtg cggccggcc  
421 tgccgaggct ccagtctcca cccgaggccc cccagtcgcg cggcgtactg gcgggggtgg  
481 gggatgcgcg ctggagatt ccccccctcgc ccaactcgca gtggggtcg gagagatgga  
541 tcgacaccgt acgtcggcag gtaactaccg ggcgcaggaa tcgatctcgctctccccca

601 gcggacagag caaaacgccc ctccgaacac ccagggttcg gagtgtagcc ccaaattggg  
661 gcatggcacg gctgcagtgc gaccccccgg aagggtcag ggtgcagccg ggcgtggccg  
721 aaccgtccgc gccagtccgt ttctgccccat caagagggag acatttgc tccataccctc  
781 tgggcagata aaacaggagc cgaaggttcc gccatcgacc tgatgctctg ttgggcattcc  
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

source 1..929  
/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  
/codon\_start=1  
/product="putative Robin"  
/protein\_id="QSM01523"  
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTDNP  
ALSPPVTNRGCVIEPDKARKSGTQPGVAAA  
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CLVFDKGCGQLALSALGMEPSSSGTAGKSAA  
PARAEAPVSTARAPVRRSTGGGRGCAPG  
DSPLAQLAVGVGEMDRNRTSAGNYRRKSIS  
SLPQRTEQNAAPNTRGSECSPKLGP  
AAVRPPGRGQGAAGRGGTVGANPVLPIKGETFV  
PIPPGQIKQEPKFPST"

CDS complement(117..923)  
/note="ORF2"  
/codon\_start=1  
/product="hypothetical protein"

/protein\_id="QSM01524"  
/translation="MPNRASGRWRKLRLFNLPRLPRGYRDKCLPLDGQNRIGADGSATPG  
CTLTPSGGSHCSRARPQFGATLRTAGVRSGVLLCPLGERRDRLPASVVTCCRRTVAIHL  
SDPNCELGEGGISRRASPTPASRPADWSPRGDWSLGTGGRRFRFSCRTRARLHPESA  
KGELAAFVEDKADASRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSTLPGLVRLN  
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

1 gccttgttctt cgacaaaaggc tgccagtcgc cccttagcgc ttcgggatg gaggctatgt  
61 cgagtgggac ggcaggagggttataactgt actggacaac gatgggtac gcaccgtcac  
121 gtcggagacg acgaggccgc ggtcataaac caccatccgc gaacagtca ggaaacagt  
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241 cccccccgt tactaacccggatgtcgta ttgagccgtca caaggccgg aagagtggaa  
301 ctaacccggg acctgtggca gcccggccg taaaggctgc ggcacccgt caggctgtcg  
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481 cagaaaaatc tgccgcgcccccgtccgc aggtccatgttccaccgcg agggtccag  
541 tccggccgtc gactggccggg ggttagggat ggcgcggccggg agattccccctcgccccaac  
601 tcgcagtgg ggtcgagat atggatcgca accgtacgtc ggcaggttac taccgacgca  
661 ggaagtcgat ctcgtctc ccccgccgaa cagagaaaaa cccgcctcg aacaccgcg  
721 gttcggagtg tagcccaaaa ttggggctgtgc acggctgtc agtgcgaccc cccggaagg  
781 gtcagggtgc agccggcgttggccaa tccgttctgc cccatcaagg  
841 gggagacatt tgtccctata 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  
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/protein\_id="QSM01525"  
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CDS        complement(37..843)  
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SDPNCELGECCISQRASPTPASRPADWSPRGDWLSGTDGRSGFTRCPARARLHPESA  
KGELAAFVEDKADASRRRARFSYHRQQVDSLTCRSLYGRRCHRSRLSSTLSGLVRLN  
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## ORIGIN

1 gttatcctgt actggacaac gatgggtgac gcaccgtac gcgggaacg acgaggccgc  
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301 ggagaaccgcg gtcggccgc tggcgtctgc ctgttgcg acaaaggctgc  
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601 ccccaaccggcagagaaaaa cggccgtccg aacaccagg gttcggagtg tagccccgg  
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841 catccccccag

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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##  
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 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  
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 CDS 21..827  
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 /product="putative Robin"  
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 CLVFDKGQLALSALGMEPSSSGTAGKSAAPARAEPSTARAPVRRSTGGGGCAPG  
 DSPLAQLAVVGEMDRNRTSAGNYRRRKSISSLQPQTEQNAAPNTRGSECSPKLGHGT  
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 CDS complement(36..842)  
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 /codon\_start=1  
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 121 ttggcccgcc ggcacactcc actgataacc ctgtctgtc cccccgggtt actaaccggg  
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 841 atcccccg  
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 LOCUS MW434146 852 bp RNA linear ENV 18-FEB-2021  
 DEFINITION Culex narnavirus 1 isolate CMS001\_035\_ALCO genomic sequence.  
 ACCESSION MW434146  
 VERSION MW434146  
 DBLINK BioProject: PRJNA605178  
 BioSample: SAMN14051475  
 Sequence Read Archive: SRR11035288  
 KEYWORDS ENV.  
 SOURCE Culex narnavirus 1 (mosquito metagenome)

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

REFERENCE 1 (bases 1 to 852)  
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
Logan,P., Ratnasiri,K. and Retallack,H.  
TITLE Single mosquito metatranscriptomics identifies vectors, emerging  
pathogens and reservoirs in one assay  
JOURNAL bioRxiv (2020) In press  
REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 852)  
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
Logan,P., Ratnasiri,K. and Retallack,H.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,  
499 Illinois St, San Francisco, CA 94158, USA  
COMMENT ##Assembly-Data-START##  
Assembly Method :: IDSeq pipeline v. 3.2  
Coverage :: 414.313548x  
Sequencing Technology :: Illumina  
##Assembly-Data-END##

FEATURES Location/Qualifiers

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/mol\_type="genomic RNA"  
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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  
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ALSSLVSNEGCVVRPARTGMSGTQPAHLAAAALKAAACRQAVDLALAVVGEPRSAAGV  
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CDS complement(64..846)  
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SAKGQLARFKVDEAYAGRRARFSNHCGKIDSPLACRSLYGRRCQVGRLLSHTGPCR  
PNYAPFVTNEGGQSRVISGGYRRALACGYRISTVSTVRGWW"

ORIGIN

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241 gccccgtaa aggctgcggc atgccggcag gctgtcgatc ttgccctggc agtggttgga  
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421 ccggcccgccg ccgagggttcc tgcatccact gcgaaaggcac tcgtccggcc atcgacaggc  
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541 gagatggatc ggacccgtac gccagtggc aaccaccggc gcaggaagac cgttccgttg  
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661 aaattggggc atggcacggc tgccgtcgct cctccgagag aggacaggggg tgcagccggg  
721 cgtggcggag gcgtccggc ccacatccggc cggcccata agggggagac acttggtccc  
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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

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/mol\_type="genomic RNA"  
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/isolation\_source="female, blood fed, collected in marsh /  
wildlife refuge / park habitat"  
/host="Culex tarsalis"  
/db\_xref="taxon:2562539"  
/environmental\_sample  
/country="USA: Alameda County, California"  
/lat\_lon="37.55697 N 122.07938 W"  
/collection\_date="11-Sep-2017"  
/note="metagenomic; derived from metagenome: mosquito  
metagenome"

CDS 17..823  
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/protein\_id="QSM01531"  
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ALSPPVTNRGCVIEPDKARKSGTQPGVAAA  
VKAACRQAVDLALAVVGEPRSAAGV  
CLVFDKGCGQLALSALGMEPSSGTAGKSAA  
PARAEAPVSTARAPVRRSTGGGGCAPG  
DSPLAQLAVGVGEMDRNRTSAGNYRRKSISL  
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CDS complement(32..838)  
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/product="hypothetical protein"

/protein\_id="QSM01532"  
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SDPNCELGEGGISRRASPTPASRPADWGPRGGDWSLGTGGRGLSCRPARALHPESA  
KGELAAFVEDKADASRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN  
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

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61 taaaccacca tccgcgaaca gtgcaggaaa cagtggaat gcggtacccg caggcgtag  
121 cccgcggca cctcccactg ataacctgc tctgtcccccc ccgggtacta accggggatg  
181 cgtgattgag cctgacaagg cccgaaagag tggactcaa ccgggacctg tggcagcgg  
241 gcccgtaaag gctcgccat gccgtcaggc tgcgacactg gcccggcgg tggtaggaga  
301 accgcgcctcg gcggctggcg tctgcctgt ctgcacaaa ggctgcacgc tcggcccttag  
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421 tgccgaggct ccagtctcca ccgcgaggcc cccagtcgcg ccgtcgactg gcgggggtgg  
481 gggatgcgcg ccgggagatt ccccccctgc ccaactcgca gttgggtcg gagagatgga  
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661 gcatggcgcg gctgcagtgc gaccccccgg aagggtcag ggtcagccg ggcgtggccg  
721 aaccgtcgcc gccagtccgt ttctgccc cat caagggggag acatttgcc ctatcccc  
781 tgggcagatt aaacaggagc cgaaggttcc gccatcgacc tgatgctcg ttgggcattcc  
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  
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PGDSPAQLAAGVGETDRTRTPVSNYRRRKSDPWIPQRTEQQAAPSTGGKVCSPNLGH  
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ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg aatcgacgag gcggcggtca  
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121 cccgcggca ccctccactg gtaaccctgc tctgtcctcc ctgcgttagt acgaagggtg  
181 cgtagtttagg cctgcacggc cggaaatgg tagaaactcaa ccgggtccac tggcagcggc  
241 ggccgtaaag gctgcggcat gcccgcaggc tgcgcattt gcccggcag tggttgaga  
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361 cgctctcgag ctggagccta gcacgggtcg gacggcagac caaaagggtca acgcccgc  
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601 ccccccagcgj acagagcaac aagccgcacc ttccaccggc gggaaagggtgt gtatccccaa  
661 ttggggcat ggcacggctg cagtgttcc ttggagaag gacaggggtg cagccggc  
721 tggcggaggc gtcggcgccc atccgcgc gcccataag ggggagacac ttggcccaa  
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841 gcg

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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

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/organism="Culex narnavirus 1"

/mol\_type="genomic RNA"

/isolate="CMS001\_038\_ALCO"

/isolation\_source="female, blood fed, collected in marsh"

habitat"  
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 /db\_xref="taxon:2562539"  
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 /collection\_date="24-Aug-2017"  
 /note="metagenomic; derived from metagenome: mosquito  
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CDS        17.823  
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CDS        complement(32..838)  
 /note="ORF2"  
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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##  
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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##  
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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; Lenarviricetes; 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  
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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

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## ORIGIN

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541 atggatcgca accgtacgtc ggcaggtaa taccgacgc ggaagtgcgt ctgcgtctc  
601 ccccaacggc acaaaaaa tgccgcctcg aacaccgcg gttcggagtg tagccccaaa  
661 tggggccctg gcacggctgc agtgcgaccc cccggaaagg gtcagggtgc agccggcg  
721 ggcggaaaccg tcggcccaa tcctgtctg cccatcaagg gggagacatt tgccccata  
781 cccctggc aggttaagca ggagccgagg ttccgcct cgacctgtatg ctctgtggg  
841 catccc

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LOCUS MW434154 933 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001\_045\_ALCO genomic sequence.

ACCESSION MW434154

VERSION MW434154

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051485

Sequence Read Archive: SRR11035277

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; 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"

/protein\_id="QSM01544"

/translation="MGDAPSRRRRGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP  
ALSSLVSNEGCVVRPARPGMSGTQPGPLAAAAVKAAACRQAVDLALAVVGEPRSAAGV  
RLVFDKACQLALSALELEPSTGRADQKVNAAPARAEAPASTAKALVRRSTGGVGGCA  
PGDSPLAQLAAGVGGETDRTRTPVSNYRRRKSDPWIPQRTEQQAAPSTGGKVCSPNLGH  
GTAAVRPLEKDRGAAGRGGGVGAHPGRPIKGETLGPKPPGSAKQEPKSPPST"

CDS complement(116..928)

/note="ORF2"

/codon\_start=1

/product="hypothetical protein"

/protein\_id="QSM01545"

/translation="MPRRASGRWRRLLFCRPRGFGTKLPLDPARMGADASATPG  
CTPVLLQRTHCSRAMPQIGATHLPAGGRGCGLLCPLDPRIALPAPIIAYRRTGTIRL  
SDPSCKLGEGGISWRASPNCRSADECLRSGCRGLGAGRRGVDLLVRRPTRARLQLE  
SAKGQLARFKVDEAYAGRARRFSNHCGKIDSPLACRSLYGRRCQWTRLSTSHTSGPCR  
PNYAPFVTNEGGQSRVTSGGCRRALACGYRISTVSCTVRGWWYMTAASSSPT"

ORIGIN

1 cagctcagaa gcggttcca acttgcatt cattcctgaa ggttccatg cttccaaatc

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121 tcggagacga cgaggcgccgtcataacc accatcccgcaacagtgcag gaaacagtg

181 agatcggtatcccgaggcc aaggcccgcgcgcaccctccactggtaaccctgtctgtc

241 ctcctcgtt agtaacgaag ggtgcgtatgtgcgcgaa tgagtggaa

301 tcaaccgggtt ccactggcag cggccggcgtaaaggctgcgcgcgcaggctgcga

361 tcttgcctg gcaatgggtt gagaaccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc

421 caaacgcgtc cagctggccc ttgcgcgtctcgatgcgtggagcctgcgcgcgcgc

481 ggacaaaaag gtcaacgc

541 actcgccgc cgtatcgacag gccccgggttggatgcgcgcgcgcgcgcgcgcgcgc

601 ccaacttgcgcgtgggttggatcccgatggccatggatcccgatggccatggatcccg

661 ggcgcaggaaag agcgtatccgttggatcccgatggccatggatcccgatggccat

721 cggcggaaatggatccgttggatccgttggatccgttggatccgttggatccgttggat

781 gaaggacagg ggtgcaggccggccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc

841 caaggggggat acacttggtc ccaaaccccc tggatccgttggatccgttggatcc

901 gccatcgacc tcatcgatcgatcgatcgatcgatcgatcgatcgatcgatcgatcgat

//

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  
    /codon\_start=1  
    /product="putative Robin"  
    /protein\_id="QSM01546"  
    /translation="MGDAPSSRRRRGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP  
ALSSLVSNEGCVVRPARPGMSGTQPGPLAAA VKAAACRQAVDLALAVVGEPRSAAGV  
RLVFDKACQLALSALELEPSTGR TADQKVNAAPARAEAPASTAKALVRRSTGGVGGCA  
PGDSPA LAAGVG ETDRTTRTPVRNYRRRKS DPWIPQRTEQQAAPSTGGKVCSPNLGH  
GTA AVRPLEKDRGAAGRGGGVGAHPGRPIKG ET LGPKPPGSAKQE PKFPPST"  
CDS complement(37..849)  
    /note="ORF2"  
    /codon\_start=1  
    /product="hypothetical protein"  
    /protein\_id="QSM01547"  
    /translation="MPRRASGRWRKLRLFCRPRGFGTKCLPLDPARMGADASATPG  
CTPVLLQRT HCSRAMPQIGATHLPAGGRCGLLCP LDGP RIALPAPIISYRRTGTIRL  
SDPSCKLGE GGISWRASP NPACRSADE CLRSGC RGLGAGRRGV DLLVRRP TRAR LQE  
SAKGQLARFVKDEAYAGRRARFSNHCQGKIDS LPACRSLYGRRCQWTRL SSTHSGPCR  
PNYAPFVTNEGGQSRVTSGGC RRALACGYRISTV RGWWYMTAASSSPT"  
ORIGIN  
1 gttatctgt actggacaac gatgggtgac gcaccgtca a gtcggagacg acgaggccgc  
61 ggcatatac caccatccgc gaacagtca ggaaacagtg gagatgcggt acccgccaggc  
121 caaggccccgc cggcacccctc cactgtaac cctgc tctgt cctccctcg tagtaacgaa  
181 gggtgcgtag ttaggcctgc acggcccgga atgagtggaa ctcaaccggg tccactggca

241 gcggcggccg taaaggctgc ggcatgccgg caggctgtcg atcttgcctt ggcagtgggt  
301 ggagaaccgc gctcggccgc cggcgtacgc ctgcgtttt acaaagcgtg ccagctggcc  
361 cttagcgctc tcgagctgga gcctagcagc ggtcgacgg cggacaaaa ggtcaacgccc  
421 gcgccggccc gcgccgaggc ccctgcattc actgcgaagg cactcgtccg ccgatcgaca  
481 ggcggggttg gggatgcgc gccaggagat tccccctcg cccaacttgc agctgggttc  
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601 tggatcccccc agcggacaga gcaacaagcc gcaccccca cccggggaa ggtgtgttagc  
661 cccaaattgg ggcatggcac ggctgcgtg cgtccttgg agaaggacag gggtcagcc  
721 gggctggcg gaggcgtcg cgcccatctt ggcggccca tcaagggggaa gacacttgtt  
781 cccaaacccc ctgggtcgcc aaaacaggag ccgaagttc cggccatcgac ctgatgctct  
841 gcggggcatc 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; Lenarviricetes; Amabiliviricetes;  
Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 840)

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

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

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 840)

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

TITLE Direct Submission

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

COMMENT ##Assembly-Data-START##  
Assembly Method :: IDSeq pipeline v. 3.2  
Coverage :: 152.897772x  
Sequencing Technology :: Illumina  
##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..840  
/organism="Culex narnavirus 1"  
/mol\_type="genomic RNA"  
/isolate="CMS001\_048\_ALCO"  
/isolation\_source="female, blood fed, collected in marsh /  
wildlife refuge / park habitat"  
/host="Culex erythrothorax"  
/db\_xref="taxon:2562539"  
/environmental\_sample  
/country="USA: Alameda County, California"  
/lat\_lon="37.55697 N 122.07938 W"  
/collection\_date="03-Aug-2017"  
/note="metagenomic; derived from metagenome: mosquito  
metagenome"

CDS 17..>840  
/codon\_start=1  
/product="putative Robin"  
/protein\_id="QSM01548"  
/translation="MGDAPSRRKRRGGGHIPPSANSAGNSGDAVPAGQGPPAPSTGNP  
ALSSLVSNEGCVVRPARPGMSGTQPGLSAAAVKAAACRQAVDLALAVVGEPRSAAGV  
RLVFDKACQLALSALELPSTGRADQKVNAAPARAEV PASTAKALVRRSTGGGGCA  
PGDSPAQLAVGVGETDRIRTPVSYRRRKSDPWIPRRTEQQAAPPTWREVCSPLKLGH

GTAAVCPPREDRGAAGRGGVGAHPGRPIKGETLGPKPPGSAKQEPKSPPSTRCSAG"

ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcga aaacgacgag gcggcggtca  
61 tataccacca tccgcgaaca gtgcaggaaa cagtggat gcgggcccg caggccaagg  
121 cccggccgca ccctccactg gtaaccctgc tctgtccctc ctgcgttagta acgaagggtg  
181 cgtagtttagg cctgcacggc ccggaatgag tgaaactcaa ccgggctctc tggcagcggc  
241 ggccgtaaag gctgcagcat gccggcaggc tgcgcattt gcccggcag tggttggaga  
301 accgcgctcg gcggccggcg tacgcctcg tttgacaaa gcgtgccagc tggcccttag  
361 cgctctcgag ctggagccta gcacgggtcg gacggcggac caaaagggtca acgcccgcacc  
421 ggcccgcgc gagggtccctg catccactgc gaaggcactc gtccggcgat cgacaggcgg  
481 ggggtggggga tgccgcggcag gagattcccc cctcgcccaa ctgcgttg gggtcggaga  
541 gacggatcgatccgtacgc cggtagtttag ctatcgccgc aggaagagcg atccgtggat  
601 ccccccacgg acagagcaac aagccgcacc tccaaacttgg cgggagggtgt gtggcccaa  
661 attggggcat ggcacggctg cagtgttcc tccgagagag gacaggggtg cagccggcgg  
721 tggcggaggg gtcggccccc atccctggccg gcccatcaag ggggagacac ttggtcccaa  
781 acccccctggg tcggcaaaac aggagccgaa gtctccgcca tgaccccgat gctctgcggg

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LOCUS MW434157 854 bp RNA linear ENV 18-FEB-2021  
DEFINITION Culex narnavirus 1 isolate CMS001\_051\_ALCO genomic sequence.

ACCESSION MW434157

VERSION MW434157

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051491

Sequence Read Archive: SRR11035270

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

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

REFERENCE 1 (bases 1 to 854)

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

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

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 854)

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

TITLE Direct Submission

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

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 462.212355x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..854

/organism="Culex narnavirus 1"

/mol\_type="genomic RNA"

/isolate="CMS001\_051\_ALCO"

/isolation\_source="female, blood fed, collected in marsh

habitat"

/host="Culex tarsalis"

/db\_xref="taxon:2562539"

/environmental\_sample

/country="USA: Alameda County, California"

/lat\_lon="37.50608 N 121.99857 W"

/collection\_date="17-Oct-2017"

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

CDS 27.833

/codon\_start=1

/product="putative Robin"

/protein\_id="QSM01549"  
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTDNP  
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAALKAAACRQAVDLALAVGEPRSAAGV  
CLVFDKGQLALSALGMEPSSSGTAGRSAAPARAEAPVSTARAPVRRSTGGGGCAPG  
DSPLAQLAVGVGEMDRNRTSTGNCRRKSISLPLQRTEQHAAPNTRGSECSPKLGHGT  
AAVRPPGRGQGAAGRGGTVGASPVLPIKGETFVPIPPGQVKQEPKVPPST"  
CDS complement(42..848)  
/note="ORF2"  
/codon\_start=1  
/product="hypothetical protein"  
/protein\_id="QSM01550"  
/translation="MPNRASGRWRNLRLFNLPGYGDKCLPLDGQDRTGADGSATPG  
CTLTPSGGSHCSRAMPQFGATLRTAGVRSGVLLCPLGERRDRLPASAVTCRRTVAIHL  
SDPNCELGEGGISRRASPTPASRPADWGPRGGDWSLGTGGRGRSSCRPARARLHTESA  
KGELAAFVEDKADASRRRARFSYHRQQVDSLTA CRSLY GRRCHRSRLSSTLSGLVRLN  
HASPVSNRGGSQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"

## ORIGIN

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121 caggcgtagt cccgcggca cctcccactg ataaccctgc tctgtcccccc ccggttacta  
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301 tggtaggaga accgcgctcg gcccgtggcg tctgcctgt ctgcacaaa gggtgccagc  
361 tcgccttag cgctctcggt atggagccca gctcgagcgg gacggcagga agatctgccc  
421 cgcccgcccg tgccgaggct ccagtctcca ccgcgaggc cccagtcgc cggtcgactg  
481 gcgggggtgg gggatgcgcg ccgggagatt ccccccgc ccaactcgca gttggggtcg  
541 gagagatgga tcgcaaccgt acgtcgacag gtaactgccc acgcaggaag tcgatctcg  
601 ctctcccca gcccggacagag caacacgcgg ctccgaacac ccgcgggtcg gagtgtagcc  
661 ccaaattggg gcatggcacg gctgcagtgc gaccccccgg aagggggtcag ggtgcagccg  
721 ggcgtggcgg aaccgtcgcc gccagtcctg tccgcctcat caagggggag acatttgtcc  
781 ccataccccc tggcaggtt aaacaggagc cgaaggttcc gccatcgacc tgatgctctg  
841 tgggcatcc 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., Ratnasury,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., Ratnasury,K. and Retallack,H.

TITLE Direct Submission

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

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 315.13342x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..849

/organism="Culex narnavirus 1"  
 /mol\_type="genomic RNA"  
 /isolate="CMS001\_052\_ALCO"  
 /isolation\_source="female, blood fed, collected in marsh /  
 wildlife refuge / park habitat"  
 /host="Culex erythrothorax"  
 /db\_xref="taxon:2562539"  
 /environmental\_sample  
 /country="USA: Alameda County, California"  
 /lat\_lon="37.55697 N 122.07938 W"  
 /collection\_date="21-Sep-2017"  
 /note="metagenomic; derived from metagenome: mosquito  
 metagenome"

**CDS**  
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 /product="putative Robin"  
 /protein\_id="QSM01551"  
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 ALSSLVSNEGCVVRPARPGMSGTQPGPLAAAALKAAACRQAVDLALAVVGEPRSAAGV  
 RLVFDKACQLALSALEPSTGRADQKVNAAPARAEPASTAKALVRRSTGGVGGCA  
 PGDSPLAQLAAGVGETDRTRTPVRNYRRRKSDFWIPQRTEQQAAPSTGGKVCSPNLGH  
 GTAAVRPLEKDGRGAAGRGGVGAAHPGRPIKGETLGPKPPGSAKQEPKSPPST"

**CDS**  
 complement(32..844)  
 /note="ORF2"  
 /codon\_start=1  
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 /translation="MPRRASGRWRRRLFCRPRGFGTKCLPLDGPARMGADASATPG  
 CTPVLLQRTHCSRAMPQIGATHLPAGGRGCGLLCPLGDPRIALPAPIISYRRTGTIRL  
 SDPSCKLGEGGISWRASPNPACRSADECLRGCRGLGAGRRGVDLLVRRPTRARLQLE  
 SAKGQLARFKVDEAYAGRRRARFSNHCQGKIDSPLACRSLYGRRCQWTRLSSTHSGPCR  
 PNYAPFVTNEGGQSRVTSGGCRALACGYRISTVSRGWWYMTAASSFST"

**ORIGIN**  
 1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcga gaacgacgag gcggcggtca  
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 121 cccgcggca ccctccactg gtaaccctgc tctgtcctcc ctgcgttagta acgaagggtg  
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 361 cgctctcgag ctggagccta gcacgggtcg gacggcgac caaaagggtca acgcccgc  
 421 ggccccgcgc gaggccctcg catccactgc gaaggcactc gtccgcgcgat cgacaggcg  
 481 ggttggggga tgccgcgcag gagatcccc ctcgcgcgc cttgcgcgtg gggcggaga  
 541 gacggatcgatcgatcgacccgatcgacccgatcgatcgatcgatcgatcgatcgatcgatcg  
 601 ccccccacggc acagacaaac aagccgcacc ttccaccggc gggaaagggtgt gtagccccaa  
 661 ttggggcat ggcacggctg cagtgcgtcc ttggagaag gacaggggtg cagccggcg  
 721 tggccggagggc gtcggcgcccc atcctggccg gcccataag gggagacac ttggcccaaa  
 781 acccccggg tcggcaaaac aggagccgaa gtctccgcca tcgacccgtat gctctcgccg  
 841 gcatcccc

//

**LOCUS** MW434159        844 bp    **RNA**    linear    ENV 18-FEB-2021  
**DEFINITION** Culex narnavirus 1 isolate CMS001\_054\_ALCO genomic sequence.  
**ACCESSION** MW434159  
**VERSION** MW434159  
**DBLINK** BioProject: PRJNA605178  
 BioSample: SAMN14051494  
 Sequence Read Archive: SRR11035267  
**KEYWORDS** ENV.  
**SOURCE** Culex narnavirus 1 (mosquito metagenome)  
**ORGANISM** Culex narnavirus 1  
 Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;  
 Wolframvirales; Narnaviridae; unclassified Narnaviridae.  
**REFERENCE** 1 (bases 1 to 844)  
**AUTHORS** Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
 Logan,P., Ratnasiri,K. and Retallack,H.  
**TITLE** Single mosquito metatranscriptomics identifies vectors, emerging

pathogens and reservoirs in one assay

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 844)

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

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

TITLE Direct Submission

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

499 Illinois St, San Francisco, CA 94158, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 88.254237x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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/mol\_type="genomic RNA"

/isolate="CMS001\_054\_ALCO"

/isolation\_source="female, blood fed, collected in marsh /  
wildlife refuge / park habitat"

/host="Culex pipiens"

/db\_xref="taxon:2562539"

/environmental\_sample

/country="USA: Alameda County, California"

/lat\_lon="37.63083 N 122.14267 W"

/collection\_date="10-Feb-2016"

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

CDS 17..823

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/protein\_id="QSM01553"

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DSPLAQLAVGVGEMDRHRTSAGNYRRRKSISSLPQRTEQNAAPNTQGSECSPELPGPT  
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CDS complement(32..838)

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/codon\_start=1

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KGELAALVKDKADASRRRARFSYHRQGVDSLTAACRSILYGRRCHRSRLSSLGVLVRLN  
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ORIGIN

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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  
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        marsh/swamp habitat"  
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121 ccaaggccccg ccggtacctt ccactggtaa ccctgctctg tcctccctcg tttagtaacga  
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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., Ratnasiri,K. and Retallack,H.  
TITLE Single mosquito metatranscriptomics identifies vectors, emerging  
    pathogens and reservoirs in one assay  
JOURNAL bioRxiv (2020) In press  
REMARK DOI: 10.1101/2020.02.10.942854  
REFERENCE 2 (bases 1 to 844)  
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
    Logan,P., Ratnasiri,K. and Retallack,H.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,  
    499 Illinois St, San Francisco, CA 94158, USA  
COMMENT ##Assembly-Data-START##  
    Assembly Method :: IDSeq pipeline v. 3.2  
    Coverage :: 271.877445x  
    Sequencing Technology :: Illumina  
    ##Assembly-Data-END##  
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    /isolation\_source="female, blood fed, collected in  
        industrial (waste water treatment plant) habitat"  
    /host="Culex pipiens"  
    /db\_xref="taxon:2562539"  
    /environmental\_sample  
    /country="USA: Alameda County, California"  
    /lat\_lon="37.6683 N 122.15915 W"  
    /collection\_date="24-Oct-2017"  
    /note="metagenomic; derived from metagenome: mosquito  
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CDS 17..823  
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    /product="putative Robin"  
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        DSPLAQLAVGVGEMDRHRTSAGNYRRKSISLQPQTEQNAAPNTQGSECSPKLGP  
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CDS complement(32..838)  
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    /protein\_id="QSM01557"

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KGELAAVEDKADASRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN  
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ORIGIN

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241 ggccgtaaag gctgcggcat gccgtcaggc tgtgcacgtg gcccggcgg tggtaggaga  
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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

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/organism="Culex narnavirus 1"

/mol\_type="genomic RNA"

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/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"

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CDS complement(34..840)  
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KGELAAFKDKADASRRARLSYHRQGVDSLTSRSLYGRRCHRSRLSSTLGLARLN  
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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**

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/mol\_type="genomic RNA"  
/isolate="CMS002\_022a\_SAND"  
/isolation\_source="female, unfed, collected in undeveloped habitat"  
/host="Culex quinquefasciatus"  
/db\_xref="taxon:2562539"  
/environmental\_sample  
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/lat\_lon="32.552783 N 117.0559469 W"  
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/note="metagenomic; derived from metagenome: mosquito metagenome"

CDS 27..833  
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DSPLAQLAVGVGEMDRRTSAGNYRRRKSISLPQRTEQKAAPNSRGSECSPKLGPGT  
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CDS complement(42..848)  
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**ORIGIN**

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721 ggcgtggcg aaccgtcgcc gccaatctg tccgtcccat caagggggag acatggtcc  
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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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commerical/industrial/transportation habitat"  
/host="Culex quinquefasciatus"  
/db\_xref="taxon:2562539"  
/environmental\_sample  
/country="USA: San Diego County, California"  
/lat\_lon="32.5928337 N 117.0575668 W"  
/collection\_date="27-Dec-2017"  
/note="metagenomic; derived from metagenome: mosquito  
metagenome"

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DSPLAQLAVGVGEMDRNRTSAGNYRRKSISLPLQRTEQNAAPNTRGSECSPKLGP GT  
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CDS complement(117..923)  
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KGELAAFVEDKANASRRARFSYHRQGQVDSLTA CRSLY GRRCHRSRLSSTLSGLVRLN  
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ORIGIN

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121 gtcggagacg acgaggccgc ggtcataaac caccatccgc gaacagtca ggaaacagt  
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301 ctaaaccggg acctgtggca gcggcggccg taaaaggctgc ggcattccgt caggctgtcg  
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601 tcgcagttgg ggtcgagag atggatcgca accgtacgtc ggcaggtaac taccgacca

661 ggaagtcat ctgcgtctc ccccaagcgaa cagagcaaaa tgccgctccg aacaccgcg  
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781 gtcagggtgc agccggcgt ggccgaaccg tcggcgccaa tccgtcctg cccatcaagg  
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LOCUS MW434165 844 bp RNA linear ENV 18-FEB-2021  
DEFINITION Culex narnavirus 1 isolate CMS002\_027a\_WVAL genomic sequence.  
ACCESSION MW434165  
VERSION MW434165  
DBLINK BioProject: PRJNA605178  
BioSample: SAMN14051534  
Sequence Read Archive: SRR11035223  
KEYWORDS ENV.  
SOURCE Culex narnavirus 1 (mosquito metagenome)  
ORGANISM Culex narnavirus 1  
Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;  
Wolframvirales; Narnaviridae; unclassified Narnaviridae.  
REFERENCE 1 (bases 1 to 844)  
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
Logan,P., Ratnasiri,K. and Retallack,H.  
TITLE Single mosquito metatranscriptomics identifies vectors, emerging  
pathogens and reservoirs in one assay  
JOURNAL bioRxiv (2020) In press  
REMARK DOI: 10.1101/2020.02.10.942854  
REFERENCE 2 (bases 1 to 844)  
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
Logan,P., Ratnasiri,K. and Retallack,H.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,  
499 Illinois St, San Francisco, CA 94158, USA  
COMMENT ##Assembly-Data-START##  
Assembly Method :: IDSeq pipeline v. 3.2  
Coverage :: 580.211213x  
Sequencing Technology :: Illumina  
##Assembly-Data-END##  
FEATURES Location/Qualifiers  
source 1..844  
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residential habitat"  
/host="Culex quinquefasciatus"  
/db\_xref="taxon:2562539"  
/environmental\_sample  
/country="USA: West Valley, California"  
/lat\_lon="34.150853 N 117.642917 W"  
/collection\_date="15-Nov-2017"  
/note="metagenomic; derived from metagenome: mosquito  
metagenome"  
CDS 17..823  
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CLVFDKGCLALSLGMEPSSGTAGKPAAPARA  
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DSPLAQLAVGVGEMDRNRTSAGNYRRKSISL  
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CDS complement(32..838)  
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SDPNCELGEGGISWRASPTPASRPADWGPREGDWSLGTGGRGRFSCRPTRARLHPESA  
KGELAAVEDKADASRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN  
HASPVSNRGGQSRVTSGRCRRANACGYRIPTVSCTVRGWWFMFTAASSSPT"

ORIGIN

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121 cccggcggca cctcccactg gtaacctgc tctgtcccccc ccggttacta accggggatg  
181 cgtgattgag cctgacaagg cccgaaagag tggactcaa ccgggacctg tggcagcgg  
241 ggccgtaaag gctgcggcat gccgtcaggc tgtgcacctg gcccggcgg tggtaggaga  
301 accgcgcctg gcggctggcg tctgcctgt ctgcacaaa ggctgcagc tcgcccctag  
361 cgctctcggg atggagcata gctcgagttgg gacggcaggaa aacactgcgg cgcccgcccg  
421 tgccgaggct ccagtctcca ccgcgagggc cccagtcgcg cggcgcactg gcgggggttag  
481 gggatgcgcg ccaggagatt ccccccctgc ccaactgcgca ttgggggtcg gagatggaa  
541 tcgcaaccgt acgtcggcag gtaactaccg acgcaggaaatcgatctcgatctcc  
601 gcggacagag caaaacgcgg ctccgaacac ctgcgggtcg gagtgtagcc ccaaattggg  
661 gcctggcacg gctgcagtgc gaccccccgg aagggttcag ggtgcagccg ggcgtggcgg  
721 aaccgtcgcc gccaatctg tcccccattt caagggggag acatttgtcc cccatcccc  
781 tgggcagggtt aaacaggagc cgagggttcc gccatcgacc tgatgcctgt ttggcattcc  
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"  
/isolate="CMS002\_027b\_WVAL"  
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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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KGELAAFVEDKADASRRARFSYHRQGVDSLTA  
CRSLYGRRCHRSRLSSTLGLVRLN  
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFVTAASSSPT"

## ORIGIN

1 cgggttata ctgtactgga caacgatggg tgacgtaccg tcacgtcgg aacgacgagg  
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cccgc  
121 aggcttagc ccgcggcac ctccccactga taacctctgc ctgtcccccc cggtactaa  
181 ccggggatgc gtgattgagc ctgacaaggc ccgaaagagt ggaactcaac cgggac  
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241 ggcagcggcg gccgtaaagg ctgcggcatg ccgtcaggct gtcgac  
ctgg  
301 ggttaggagaa ccgcgtc  
ctgg  
361 cgccttagc gctctcg  
gg  
421 gcccggcgt gccgaggc  
tc  
481 cggggtagg gatgcgc  
cg  
541 agagatggat cgcaacc  
ta  
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cg  
661 caaatgggg cctgg  
ac  
721 gcgtggcg  
aa  
781 catacc  
cc  
841 tgg  
ca  
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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##

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CDS	17..>618 /codon_start=1 /product="putative Robin" /protein_id="QSM01568" /translation="MGDAPSRRRRGGHKPPSANSAGNSGDAVSAGVSPVPPTGDP ALSSSVNNRGCVIEPGRPGKSETRPGHLAAAALKAAACRQAVDLALAVGEPRSAAGV RLVFDKACSLALSALDMGPSTGGTADLRINAAPARAEPALSTAKALVRRSTGGGGCA PGDSPLAQLAVGVGELDRSGRTPVSNYRRRTDPTLPQRT"

#### ORIGIN

1 cctgtactgg acagcgtatgg gtgacgcacc gtcacgtcgg agacgcacgag gcggcggtca  
61 taaaccacca tccgcgaaca gtgcaggaaa cagtggggat gccgttatccg caggcgtag  
121 cccgcggta cccccactg gtgaccctgc tctgtctcc tctgttaata acagaggatg  
181 cgtgatttag cctggcaggc cggcaagag tgaaactcga cccggccatt tggcagcggc  
241 ggccgtaaag gctgcggcat gccgcaggc tgcgcacgtg gcccgtgcgg tagtaggaga  
301 accgcgcctcg gcggcgggc tgccgcctgt ctgcacaaa gcgtgcgc tcgcgccttag  
361 cgctctcgat atggggccta gcacgggagg gacggcggat cttaggatca acgcgcgc  
421 cgccgcgc gaggccccac tcttaccgc gaaggccctc gtccgcggcgt cgacaggcgg  
481 ggggtggggta tgccgcggc gagattcccc cctgcaccaa ctgcgcgtt gggcggaga  
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601 tctcccccac cgacaga

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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**  
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   /host="Culex erythrothorax"  
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   /country="USA: West Valley, California"  
   /lat\_lon="33.935 N 117.655833 W"  
   /collection\_date="15-Nov-2017"  
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     KALVRRSTGGGGCA  
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     AALDTRGPVCSPNLG  
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 121 aggccggcgtt cataaaccac catccgcgaa cagtgcagga aacagtgggg atgcggatc  
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 541 gtcgacaggc ggggggtgggg gatgcgcgc gggagattcc cccctcgccc aactcgc  
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 781 ggggtcagcc gggcgtggcg gagtcgtcg gccccatcc tcaagggggaa  
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 LOCUS MW434169 860 bp RNA linear ENV 18-FEB-2021  
 DEFINITION Culex narnavirus 1 isolate CMS002\_029c\_WVAL genomic sequence.  
 ACCESSION MW434169  
 VERSION MW434169  
 DBLINK BioProject: PRJNA605178  
   BioSample: SAMN14051543  
   Sequence Read Archive: SRR11035372  
 KEYWORDS ENV.  
 SOURCE Culex narnavirus 1 (mosquito metagenome)

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

REFERENCE 1 (bases 1 to 860)  
 AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
 Logan,P., Ratnasiri,K. and Retallack,H.  
 TITLE Single mosquito metatranscriptomics identifies vectors, emerging  
 pathogens and reservoirs in one assay  
 JOURNAL bioRxiv (2020) In press  
 REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 860)  
 AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
 Logan,P., Ratnasiri,K. and Retallack,H.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,  
 499 Illinois St, San Francisco, CA 94158, USA  
 COMMENT ##Assembly-Data-START##  
 Assembly Method :: IDSeq pipeline v. 3.2  
 Coverage :: 501.581098x  
 Sequencing Technology :: Illumina  
 ##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..860  
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 /host="Culex tarsalis"  
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 /environmental\_sample  
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 /lat\_lon="33.925833 N 117.659722 W"  
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 /note="metagenomic; derived from metagenome: mosquito  
 metagenome"

CDS 18..824  
 /codon\_start=1  
 /product="putative Robin"  
 /protein\_id="QSM01571"  
 /translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAPAVGVSPPAPPTDNP  
 ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAAVKAAACRQAVDLALAVGEPRSAAGV  
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 DSPLAQLAVGVGEMDRNRTSAGNYRRKSISLQPQTEQNAAPNTRGSECSPKLGHGT  
 AAVRPPGRGQGAAGRGGTVGASPVLPIKGETFVPIPQKQEPKVPPST"

CDS complement(33..839)  
 /note="ORF2"  
 /codon\_start=1  
 /product="hypothetical protein"  
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 CTLTPSGGSHCSRAMPQFGATLRTAGVRSGVLLCPLGERRDRLPASVVTCCRRTVAIHL  
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 KGELAAFVEDKADASRRRARFSYHRQGQVDSLTA CRSLY GRRCHRSRLSSTLSGLVRLN  
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ORIGIN

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1 tcctgtactg gacaacgatg ggtgacgcac cgtaacgtcg gagacgacga ggccggcgtc
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181 gcgtgattga gcctgacaag gcccggaaaga gtggaactca accgggacct gtggcagcgg
241 cggccgtaaa ggctgcccga tgccgtcagg ctgtcgaccc gcccggccgt gtggtaggag
301 aaccgcgcgc ggcggctggc gtctgccttg tcttcgacaa aggctgcag ctgcggcc
361 ggcgcgtcgg gatggagct agctcgacgc ggacggcagg aaaatctgcc ggcggccccc
421 gtgcggagcc tccagtcgg accgcggaggg ccccgatccg ccggcgtact ggcgggggtg
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661 ggcatggcac ggctcagtg cgaccccccga gaaggggtca ggggtcagcc gggcgtggcg  
721 gaaccgtcg cgccagtctt gttctgccta tcaaggggga gacattgtc cctatacccc  
781 ctgggcagat taaacaggag ccgaagggtc cgccatcgac ctgatgctt gtggggcatt  
841 ccccccctcgc 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  
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/product="putative Robin"  
/protein\_id="QSM01573"  
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPGVSPPAPPTDNP  
ALSPPVTNRGCVIEPDKARKSGTQPGVAAA  
VKAACRQAVDLALAVVGEPRSAAGV  
CLVFDKGCGQLALSALGMEPSSGTAGKSAA  
PARAEAPISTARAPVRRSTGGGGCAPG  
DSPLAQLAVGVGEMDRNRTSAGNYRRKS  
SISSLPRRTEQNAAPNTRGSECSPKLGHGT  
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CDS complement(41..847)  
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/protein\_id="QSM01574"  
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KGELAAFVEDKADASRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSTLSGLVRLN  
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

1 cgggttatac ctgtactgga caacgatggg tgacgcaccg tcacgtcgga gacgacgagg  
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121 aggcttagc ccgcggcac ctcccactga taacccctgc ctgtcccccc cggtactaa  
181 ccggggatgc gtgattgagc ctgacaaggc ccgaaagagt ggaactcaac cgggacctgt  
241 ggcagcggcg gccgtaaagg ctgcggcatg ccgtcaggct gtcgacccgt cccgtggcggt  
301 ggttaggagaa ccgcgtcgcc cggctggcgct ctgcctgtc ttgcacaaag gtcgcccag  
361 cgccttagc gctctcgga tggagccatg ctgcagccgg acggcaggaa aatcgccgc  
421 gcccggccgt gccgaggctc caatctccac cgcgaggccgc ccagtccgccc ggtcgactgg  
481 cgggggtggg ggatgcgcgc cggagggattc cccctcgcc caactcgccatg ttggggtcgg  
541 agagatggat cgcaaccgta cgtcgccagg taactaccga cgcaggaagt cgatctcgic  
601 tctccccccgg cgacagagc aaaacgcgc tccgaacacc cgcgggtcgg agtgtagccc  
661 caaatgggg catggcacgg ctgcagtgcg acccccccgg aagggtcagg gtgcagccgg  
721 gcgtggcgga accgtcgccg ccagtctgt ctgcctcata aaggggaga cattgtccc  
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841 tgggcatccccccca actcgccatg ggg

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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  
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/product="putative Robin"  
/protein\_id="QSM01575"  
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTDNP  
ALSPPVTNRGCVIEPDKARKSGTQPGPVAAAACRQAVDLALAVGEPRSAAGV  
CLVFDKGQLALSALGMEPSSSGTAGKTAAPARAEAPVSTARAPVRRSTGGGGCALG  
DSPLAQLAVGVGEMDRH RTPAGNYRRRKSISSLQPQRTEQNAAPNTQGSECSPKLGHGT  
AAVRPPGRQQGAAGRGGTVGASPVLPIKRETFVPIPQIKQEPKVPPST"  
CDS        complement(32..838)  
/note="ORF2"  
/codon\_start=1  
/product="hypothetical protein"  
/protein\_id="QSM01576"  
/translation="MPNRASGRWRNLRLFYLPRLRGYGDCLPLDGQNRTGADGSTTPG  
CTLTPSGGSHCSRAMPQFGATLRTLGVRSVLLCPLGERDRLPAPVTCRRTVSIHL  
SDPNCELGEGGISQRASPTPASRPADWGPREGDWLSLTGGRSGFTRCPARARLHPESA  
KGELAAFVEDKADASRRRARFSYHRQQVDSLTA CRSLYGRRCHRSRLS TLSGLVRLN  
HASPVSNRGQSRVISGRCRRANACGYRIPTVSCTVRGWWFMTAAASSP"

## ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg agacgacgag gcggcggtca  
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121 cccgccggca cctcccactg ataacctgc tctgtcccccc ccggftacta accggggatg  
181 cgtgattgag cctgacaagg cccgaaagag tggactcaa ccgggacctg tggcagcggc  
241 ggccgtaaag gctgcggcat gccgtcaggc tgcgacccctg gcccggcgg tggtaggaga  
301 accgcgctcg gccgcggcg tctgcctgt ctgcacaaa ggctgccagc tcgccttag  
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421 tgccgaggct ccagtctcca ccgcgaggggc cccagtcgcg cggtcgactg gcgggggtgg  
481 gggatgcgcg ctgggagatt ccccccctcg ccaactcgca gtggggtcg gagatggaa  
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661 gcatggcacg gctgcagtgc gaccccccgg aagggtcag ggtgcagccg ggcgtggtgg  
721 aaccgtcgcc gccagtccgt ttctgcccata caagagggag acattcgcc ccataccctc  
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841 ccc

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LOCUS MW434172            858 bp RNA linear ENV 18-FEB-2021  
DEFINITION Culex narnavirus 1 isolate CMS002\_046a\_WVAL genomic sequence.

ACCESSION MW434172

VERSION MW434172

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051570

Sequence Read Archive: SRR11035343

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

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

REFERENCE 1 (bases 1 to 858)

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

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

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 858)

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

TITLE Direct Submission

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

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2  
Coverage :: 1681.380282x  
Sequencing Technology :: Illumina  
##Assembly-Data-END##

FEATURES Location/Qualifiers

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/organism="Culex narnavirus 1"  
/mol\_type="genomic RNA"  
/isolate="CMS002\_046a\_WVAL"  
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/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  
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/product="putative Robin"  
/protein\_id="QSM01577"  
/translation="MGDAPSRRRRGGGHKPPSANSAGNSGNAVPAGVSPPAPPTGNP  
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CLVFDKGQLALSLALGMEPSSSGTAGKPAAPARAEAPVSTARAPVRRSTGGGRGCAPG  
DSPLAQLAVGVGEMDRNRTSAGNYRRKSISLPLQRTEQNAAPNTRGSECSPKLGP GT  
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CDS complement(39..845)  
/note="ORF2"  
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/product="hypothetical protein"  
/protein\_id="QSM01578"  
/translation="MPNRASGRWRKPRLLLNLPRGYGDKCLPLDGQDRIGADGSATPG  
CTLTPSGGSHCSRARPQFGATLRTAGVRSGVLLCPLGERRDRLPASVVTCCR VAIHL  
SDPNCELGE GGISRRASPTPASRPADWGPRGGDWLSGTGGGRGFSCRPTRARLHPESA  
KGELAAFVEDKADASRRARFSYHRQGQVDSL TARRSLY GRRCHRSRLS TLSGLVRLN  
HASPVSNRGQSRVTSGRCRRANACGYRIPTVSCTVRGWWFMTAASSSPT"

ORIGIN

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121 gcgttagccc gccggcacct cccactggta accctgtct gtcccccccg ttactaacc  
181 ggggatgcgt gattgagct gacaaggccc gaaagagtgg aactcaaccg ggacctgtgg  
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601 tcccccagcg gacagagcaa aacgcccctc cgaacaccgg cggttcggag tgtagcccc  
661 aattggggcc tggcacggct gcagtgcgac ccccccggaaag gggtcagggt gcagccggc  
721 gtggcggAAC cgtcggcgcc aatcctgtcc tgcccatcaa gggggagaca ttgtcccc  
781 tacccccctgg gcaggtaag caggagccga ggttccgccc atcgacctga tgctctgttg  
841 ggcattcccc ctcggccca

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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

/codon\_start=1  
/product="putative Robin"  
/protein\_id="QSM01579"  
/translation="MGDAPSRRKRRGGHKPPSANSAGNSGNAPAVPAGVSPPVPTGNP  
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CLVFDKGQLALSALGMEPSSSGTAGKSAAAPARAEPVSTARAPVRRSTGGGGCAPG  
DSPLAQLAVGVGEMDRDRTSAGNYRRRKSIISPLPRTEQNAAPNTRGSECSPKLGP  
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CDS complement(33..839)

/note="ORF2"  
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KGELAAFVEDKADASRRARFSYHRQQVDSLTAACRSLYGRRCHRSRLSSLPGLVRLN  
HASPVSNRGQSRVTSGRYRRANACGYRIPTVSCTVRGWWFMTAASSFPT"

ORIGIN

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121 gccccgggtt acctccccact ggttaaccccg ctctgtcccc cccggttact aaccggggat  
181 gcgtgattga gcctgacaag gcccggaga gtggaaactca accgggacct gtggcagcgg  
241 cggccgtaaa ggctgcccga tgccgtcagg ctgtcgacct gcccctggcg gtggtaggag  
301 aaccgcgcgc ggcggctggc gtctgccttg tcttcgaccaa aggctgccg ctccccccta  
361 gcgctctcgatggagact agtcgacgcg ggacggcagg aaaatctgcc gcgccggccc  
421 gtccggaggg tccagtcacc accgcggaggccc ccccaactcgcc cccgtcgact ggcgggggtg  
481 ggggatgcgc gcccggagat tccccctcg ccccaactcgcc agtcgggggtc ggagagatgg  
541 atcgcgaccg tacgtcgccga ggttaactacc gacgcaggaa gtcgatctcg cctctcccccc

601 ggccggacaga gcaaaacgcc gctccgaaca cccgcgggtc ggagtgtac cccaagttgg  
661 ggcctggcac ggctgcagtg cgaccggcc gaagggggtca gggtgccagcc gggcggtggcg  
721 gaaccgtcg cgccaatcct gtccgtccca tcaaggggga gacattgtc cccatcccc  
781 ctgggcaggc taagcaggag ccgagggttc cgccatcgac ctgatgctct gttgggcata  
841 cccctcgcc caactcgac tcgggg

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LOCUS MW434174 864 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002\_047a\_WVAL genomic sequence.

ACCESSION MW434174

VERSION MW434174

DBLINK BioProject: PRJNA605178  
BioSample: SAMN14051572  
Sequence Read Archive: SRR11035340

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

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

REFERENCE 1 (bases 1 to 864)

AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
Logan,P., 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 864)

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 :: 437.84244x  
Sequencing Technology :: Illumina  
##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..864  
/organism="Culex narnavirus 1"  
/mol\_type="genomic RNA"  
/isolate="CMS002\_047a\_WVAL"  
/isolation\_source="unknown sex, unfed, collected in  
marsh/swamp habitat"  
/host="Culex erythrothorax"  
/db\_xref="taxon:2562539"  
/environmental\_sample  
/country="USA: West Valley, California"  
/lat\_lon="33.93778 N 117.633056 W"  
/collection\_date="29-Nov-2017"  
/note="metagenomic; derived from metagenome: mosquito  
metagenome"

CDS 17..832  
/codon\_start=1  
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ESAKGERARFVEDKAHARRRARFSYYREGQVDSLAAACRSLYGRRCQMVRSAGFTLAGPA  
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ORIGIN

1 cctgtactgg acaacgatgg gtgacgcacc gtcacgtcgg agacgacgag gcggcggtca  
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841 agggcatccc actctccccc agcg

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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

source 1..874

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/isolation\_source="unknown sex, unfed, collected in  
marsh/swamp habitat"  
/host="Culex erythrothorax"  
/db\_xref="taxon:2562539"  
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/country="USA: West Valley, California"  
/lat\_lon="33.93778 N 117.633056 W"  
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/note="metagenomic; derived from metagenome: mosquito metagenome"  
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CDS complement(42..857)  
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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
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CDS	51..866 /codon_start=1 /product="putative Robin" /protein_id="QSM01585" /translation="MGDAPSRRRRGGHKPPSANSAGNSGDAVSAGVSPVPPTGDP ALSSSVNNRGCVVEPGRPGKSGTRPDHLAAAALKAAACRQAVDLALAVVGEPRSAAGV RLVFDKACSLALSALDMGPSTGGTADLRINAAPARAGAPLSTA KALVRRSTGGGGCA PGDSPLAQLAVVGELDRSGRTPVSNYRRRKTDPTLPQRTEHQ AALDTRGPVCSPNSHGTA AVRPPARGQGAAGRGGVVAHPARPIKGETLGP KPPGPIKQEPKTPPST"
CDS	complement(66..881) /note="ORF2" /codon_start=1 /product="hypothetical protein" /protein_id="QSM01586" /translation="MPYRASGRWRSLLNRPRGF GTKCLPLDGPSRMGADDSATPG CTLSPRRRTHCSRAMPRIGATHWTAGVQCGLMLCPL GESIGILPAPVIAYWRTARPIE LSDPNCELGEGGISRRASPTPACRPADEGLRGREWG PGPAGGRRGVDPKIRRPSRAGPHI ESAKGERARFVEDKAHARRRARFSYYRK QVDSLACRSLYGRRCQMVRSSSTLAGPA RLNYASSVINRGGQSRVTSGGYRRANACGYRI PTVSCTVRGWWFMTAASSSPT"

## 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

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agriculture & residential habitat"  
/host="Culex erythrothorax"  
/db\_xref="taxon:2562539"  
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/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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SAKGQLARF V KDEAYAGRRARFSNHCQGKIDS LPA CRSLN GRCQWTRL SSHTGPCR  
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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  
Sequencing Technology :: Illumina  
##Assembly-Data-END##

FEATURES Location/Qualifiers

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/mol\_type="genomic RNA"  
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/isolation\_source="female, blood fed, collected in marsh /  
wildlife refuge / park habitat"  
/host="Culex tarsalis"  
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/environmental\_sample  
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/collection\_date="21-Sep-2017"  
/note="metagenomic; derived from metagenome: mosquito  
metagenome"

CDS complement(42..3068)  
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CDS 54..3140

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YNLA VAD MAC SPV GVVQ VGVA PIA RG DDL VAI PP GEAD RYEE LIA LTG GEAN RLKS  
FRSATA FV LAERT FRV ET QEIPD RV RGL PRG WR RVS RFG DP ALP PLLT REH QP GLR  
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AFLSPTVDDGGRSKTKYPSL GDIA RRLKRI REVTSKCKFD PRF VPKDRV QRDS FFEK  
LRMLRGSETVLPVDSRPV RVTWDPARHADPE LDN DCGY PGRRH LLRALDREEGG  
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ORIGIN

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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., 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 3148)

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 :: 123.031911x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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## ORIGIN

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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##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 188.837671x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES	Location/Qualifiers
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## ORIGIN

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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  
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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  
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    BioSample: SAMN14051459  
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KEYWORDS ENV.  
SOURCE Culex narnavirus 1 (mosquito metagenome)  
ORGANISM Culex narnavirus 1  
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    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  
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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; Lenarviricetes; Amabiliviricetes;  
Wolframvirales; Narnaviridae; unclassified Narnaviridae.  
REFERENCE 1 (bases 1 to 3123)  
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
Logan,P., Ratnasiri,K. and Retallack,H.  
TITLE Single mosquito metatranscriptomics identifies vectors, emerging  
pathogens and reservoirs in one assay  
JOURNAL bioRxiv (2020) In press  
REMARK DOI: 10.1101/2020.02.10.942854  
REFERENCE 2 (bases 1 to 3123)  
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
Logan,P., Ratnasiri,K. and Retallack,H.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,  
499 Illinois St, San Francisco, CA 94158, USA  
COMMENT ##Assembly-Data-START##  
Assembly Method :: IDSeq pipeline v. 3.2  
Coverage :: 37.561392x  
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## ORIGIN

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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

COMMENT ##Assembly-Data-START##  
 Assembly Method :: IDSeq pipeline v. 3.2  
 Coverage :: 28.188012x  
 Sequencing Technology :: Illumina  
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## ORIGIN

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

DEFINITION Culex narnavirus 1 isolate CMS001\_029\_ALCO genomic sequence.

ACCESSION MW434186

VERSION MW434186

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051469

Sequence Read Archive: SRR11035295

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

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

REFERENCE 1 (bases 1 to 3151)

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

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

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3151)

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

TITLE Direct Submission

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

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 424.830514x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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CDS complement(42..3068)

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## ORIGIN

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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., 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 3150)

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 :: 270.617963x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS MW434189 3154 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001\_035\_ALCO genomic sequence.

ACCESSION MW434189

VERSION MW434189

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051475

Sequence Read Archive: SRR11035288

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

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

REFERENCE 1 (bases 1 to 3154)

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

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LOCUS MW434190 3134 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001\_036\_ALCO genomic sequence.

ACCESSION MW434190

VERSION MW434190

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051476

Sequence Read Archive: SRR11035287

KEYWORDS ENV

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3134)

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

TITLE Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay  
JOURNAL bioRxiv (2020) In press  
REMARK DOI: 10.1101/2020.02.10.942854  
REFERENCE 2 (bases 1 to 3134)  
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
Logan,P., Ratnasiri,K. and Retallack,H.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,  
499 Illinois St, San Francisco, CA 94158, USA  
COMMENT ##Assembly-Data-START##  
Assembly Method :: IDSeq pipeline v. 3.2  
Coverage :: 66.032712x  
Sequencing Technology :: Illumina  
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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  
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BioSample: SAMN14051477  
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KEYWORDS ENV.  
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Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;  
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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  
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#### ORIGIN

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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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/lat\_lon="37.58391 N 122.09238 W"

/collection\_date="24-Aug-2017"

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CDS complement(41..3067)

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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; Lenarviricota; 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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VERSION MW434194  
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SOURCE Culex narnavirus 1 (mosquito metagenome)  
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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##  
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VERSION MW434195  
DBLINK BioProject: PRJNA605178  
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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 3148)

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

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

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3148)

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

TITLE Direct Submission

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

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 206.454575x

Sequencing Technology :: Illumina

##Assembly-Data-END##

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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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DEFINITION Culex narnavirus 1 isolate CMS001\_045\_ALCO genomic sequence.

ACCESSION MW434197

VERSION MW434197

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 3144)

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

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

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3144)

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

TITLE Direct Submission

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

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 29.941311x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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## ORIGIN

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LOCUS MW434198 3151 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS001\_047\_ALCO genomic sequence.

ACCESSION MW434198

VERSION MW434198

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 3151)

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

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

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3151)

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

TITLE Direct Submission

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

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 50.828887x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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ORIGIN

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

DEFINITION Culex narnavirus 1 isolate CMS001\_048\_ALCO genomic sequence.

ACCESSION MW434199

VERSION MW434199

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051488

Sequence Read Archive: SRR11035274

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; Lenarviricota; Amabiliviricetes;

Wolframvirales; Narnaviridae; unclassified Narnaviridae.

REFERENCE 1 (bases 1 to 3112)  
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
Logan,P., Ratnasiri,K. and Retallack,H.  
TITLE Single mosquito metatranscriptomics identifies vectors, emerging  
pathogens and reservoirs in one assay  
JOURNAL bioRxiv (2020) In press  
REMARK DOI: 10.1101/2020.02.10.942854  
REFERENCE 2 (bases 1 to 3112)  
AUTHORS Batson,J., Dudas,G., Haas-Stapleton,E., Kistler,A.L., Li,L.M.,  
Logan,P., Ratnasiri,K. and Retallack,H.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2020) Infectious Disease Initiative, CZ Biohub,  
499 Illinois St, San Francisco, CA 94158, USA  
COMMENT ##Assembly-Data-START##  
Assembly Method :: IDSeq pipeline v. 3.2  
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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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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  
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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,  
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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##

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DEFINITION Culex narnavirus 1 isolate CMS001\_059\_ALCO genomic sequence.  
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VERSION MW434204  
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BioSample: SAMN14051499

Sequence Read Archive: SRR11035262  
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SOURCE Culex narnavirus 1 (mosquito metagenome)  
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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##  
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DEFINITION Culex narnavirus 1 isolate CMS002\_001a\_SAND genomic sequence.

ACCESSION MW434205

VERSION MW434205

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    BioSample: SAMN14051501  
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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 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 MW434206 3164 bp RNA linear ENV 18-FEB-2021  
DEFINITION Culex narnavirus 1 isolate CMS002\_022a\_SAND genomic sequence.

ACCESSION MW434206

VERSION MW434206

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051521

Sequence Read Archive: SRR11035237

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

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

REFERENCE 1 (bases 1 to 3164)

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

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

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3164)

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

TITLE Direct Submission

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

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 273.961451x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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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  
Sequencing Technology :: Illumina  
##Assembly-Data-END##

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LOCUS MW434208 3148 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002\_027a\_WVAL genomic sequence.

ACCESSION MW434208

VERSION MW434208

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051534

Sequence Read Archive: SRR11035223

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

Viruses; Riboviria; Orthornavirae; 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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## ORIGIN

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LOCUS MW434210 3160 bp RNA linear ENV 18-FEB-2021  
DEFINITION Culex narnavirus 1 isolate CMS002\_028d\_WVAL genomic sequence.

ACCESSION MW434210

VERSION MW434210

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051539

Sequence Read Archive: SRR11035218

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

ORGANISM Culex narnavirus 1

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

REFERENCE 1 (bases 1 to 3160)

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

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

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3160)

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

TITLE Direct Submission

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

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 703.74927x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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## ORIGIN

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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

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 3158)

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

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

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3158)

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

TITLE Direct Submission

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

COMMENT ##Assembly-Data-START##

Assembly Method :: IDSeq pipeline v. 3.2

Coverage :: 1037.473872x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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## ORIGIN

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LOCUS MW434212 3148 bp RNA linear ENV 18-FEB-2021  
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.

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 :: 190.115272x

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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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  
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DEFINITION Culex narnavirus 1 isolate CMS002\_046a\_WVAL genomic sequence.  
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VERSION MW434214  
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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  
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    499 Illinois St, San Francisco, CA 94158, USA  
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## ORIGIN

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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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DEFINITION Culex narnavirus 1 isolate CMS002\_047a\_WVAL genomic sequence.  
ACCESSION MW434216  
VERSION MW434216  
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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 :: 138.320442x  
Sequencing Technology :: Illumina  
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LOCUS MW434217 3159 bp RNA linear ENV 18-FEB-2021

DEFINITION Culex narnavirus 1 isolate CMS002\_047f\_WVAL genomic sequence.

ACCESSION MW434217

VERSION MW434217

DBLINK BioProject: PRJNA605178

BioSample: SAMN14051577  
Sequence Read Archive: SRR11035335

KEYWORDS ENV.

SOURCE Culex narnavirus 1 (mosquito metagenome)

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

REFERENCE 1 (bases 1 to 3159)

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

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

JOURNAL bioRxiv (2020) In press

REMARK DOI: 10.1101/2020.02.10.942854

REFERENCE 2 (bases 1 to 3159)

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

TITLE Direct Submission

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

COMMENT ##Assembly-Data-START##  
Assembly Method :: IDSeq pipeline v. 3.2  
Coverage :: 111.901363x  
Sequencing Technology :: Illumina  
##Assembly-Data-END##

FEATURES Location/Qualifiers

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## ORIGIN

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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##

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## ORIGIN

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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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## ORIGIN

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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  
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ORIGIN

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