

Cyprinid herpesvirus 2 isolate H. Fukuda intercapsomeric triplex protein gene, complete cds

GenBank: EU349286.1

[FASTA Graphics](#)

[Go to:](#)

LOCUS EU349286 1113 bp DNA linear VRL 01-JUL-2009
DEFINITION Cyprinid herpesvirus 2 isolate H. Fukuda intercapsomeric triplex protein gene, complete cds.
ACCESSION EU349286
VERSION EU349286.1
KEYWORDS .
SOURCE Cyprinid herpesvirus 2 (CyHV-2)
ORGANISM [Cyprinid herpesvirus 2](#)
Viruses; Duplodnaviria; Heunggongvirae; Pelloviricota;
Herviviricetes; Herpesvirales; Alloherpesviridae; Cyprinivirus.
REFERENCE 1 (bases 1 to 1113)
AUTHORS Waltzek,T.B., Kelley,G.O., Alfaro,M.E., Kurobe,T., Davison,A.J.
and
Hedrick,R.P.
TITLE Phylogenetic relationships in the family Alloherpesviridae
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1113)
AUTHORS Waltzek,T.B., Kelley,G.O., Alfaro,M.E., Kurobe,T., Davison,A.J.
and
Hedrick,R.P.
TITLE Direct Submission
JOURNAL Submitted (18-DEC-2007) VMME, University of California, Davis,
One
Shields Avenue, Davis, CA 95616, USA
FEATURES Location/Qualifiers
source 1..1113
/organism="Cyprinid herpesvirus 2"
/mol_type="genomic DNA"
/isolate="H. Fukuda"
/db_xref="taxon:[317878](#)"
/country="Japan"
[CDS](#) 1..1113
/codon_start=1
/product="intercapsomeric triplex protein"
/protein_id="[ACD84550.1](#)"
/translation="MYGLNNAQGFI DT EWIDRQSIAMTAQETSRLNPNYLATKGQRVD
PSNLYIPDGIFVITYTPTGPDPGVAHGGGYYRPSLQGFSGMMDEADTLDLQANVLYS
NQGWTRLALCGLANAANYPIDLYDQKDTKYRIINTGAEPLHSGDAFVVEPPSVEASK
AQVDSMKNNITIRAEFSFRPGNMALGGYPATNRVPSELTHRMKHMVARDIGMCVDLVQS
GSSGMSQGISRLYNTQTELGQSVKNTVMATTLDALDSISVLLVMMKRVASLPTPVLRI

FGDYYNFKHNKGQLDPSVLIEIWKNPAVADLFMDSMDFGMKSIHRLKNGTYGSAIKST
EANPTSMRGEVMYNAYGGQYLTGDTFEGIIHSFNGL"

ORIGIN

```
1 atgtacggct taaacaacgc gcaaggattc atcgataccg aatggatcga caggcagagt
61 atcgccatga ccgcccagga gaccagcaga ctggtgaacc cgtaccttgc caccaaggga
121 cagcgggtcg atccgtctaa cttgtacatt cccgacggta tctttgtgac ttacacgcct
181 actggaccag accccggagt ggcgcacggt ggcggttact attacagacc ttcgctgcag
241 ggtttcggct ctatgatgga cgaggcggat acgttggacg atctgcaggc caacgttctg
301 tatagcaatc agggtcagtg gacgagactg gcgttgtgcg gtctggccaa cgcggccaac
361 taccatcatc atctgtacga ccagaaggac accaagtaca gaatcatcaa caccggggcc
421 gagcctctgc actctggcga cgcgtttgtg gttgaaccgc catcgggtga ggcttcaaag
481 gcgcaggtgg acagcatgaa aaacaacacc atcagagccg agggttcctt cagaccgggt
541 aacatggctc tgggaggcta cccggccacc aacagagtac cctctgaact gacgcaccgc
601 atgaaacacg ttatggcccg agacattggc atgtgcgtcg acctagtaca gtctggtagc
661 agcggcatgt ctcagggtat ctgcggctg tacaatacac agaccgagct cggacagagc
721 gtcaagaaca ctgtgatggc aaccaccctc gacgctttgg acagcatcag cgtcctcttg
781 gtcatgatga aaagggtagc ctctctaccc accccggtcc tccgtatctt tggggactat
841 tacaatttca aacacaacaa gggccaattg gacccatccg tcctgatcga gatctggaaa
901 aaccagccg tcgccgatct ctttatggac tctatggact ttggcatgaa atccatccac
961 cgactcaaaa acggtaccta cggctctgcc atcaaatacca cagaagccaa ccccatcgc
1021 atgagaggag aagtcatgta caacgcttat ggcggatcaat acctcacagg ggacaccttt
1081 gagggcatca tacattcatt caacggcctc taa
```

//