

Reference sequence (1): Pithovirus_massiliensis_LC8
Identities normalised by aligned length.
Colored by: identity + property

Table with 3 columns: Accession, Identity, and Sequence. Row 1: Pithovirus_massiliensis_LC8 (100.0%). Row 2: Armadillidium_vulgare_iridescent_virus_YP_009046748.1 (17.6%). Row 3: Cedratvirus_All_YP_009329068.1 (45.2%). Row 4: Cedratvirus_lausanensis_S0B74375.1 (45.5%). Row 5: Cherax_quadricarinatus_iridovirus_ASZ84981.1 (16.7%). Row 6: Invertebrate_iridescent_virus_30_YP_009010370.1 (14.8%). Row 7: Invertebrate_iridovirus_22_YP_008357369.1 (14.8%). Row 8: Invertebrate_iridovirus_25_YP_009010611.1 (15.6%). Row 9: Orpheovirus_IHUMI-LCC2_YP_009449240.1 (14.4%). Row 10: Melbournevirus_YP_009094806.1 (14.9%). Row 11: Marseillevirus_marseillevirus_YP_003407071.1 (14.9%). Row 12: Brazilian_marseillevirus_YP_009238902.1 (14.9%). Row 13: Golden_marseillevirus_YP_009310340.1 (12.3%). Row 14: mine_drainage_metagenome_EQD26795.1 (21.6%). Row 15: Pithovirus_sibericum_YP_009001361.1 (95.1%). Row 16: Shrimp_hemocyte_iridescent_virus_ATE87157.1 (16.7%). Row 17: Wiseana_iridescent_virus_YP_004732793.1 (15.0%). Row 18: PCJ29163.1_COA94_02315_Rickettsiales (22.3%). Consensus: 100%, 90%, 80%, 70%.

Table with 3 columns: Accession, Identity, and Sequence. Row 1: Pithovirus_massiliensis_LC8 (100.0%). Row 2: Armadillidium_vulgare_iridescent_virus_YP_009046748.1 (17.6%). Row 3: Cedratvirus_All_YP_009329068.1 (45.2%). Row 4: Cedratvirus_lausanensis_S0B74375.1 (45.5%). Row 5: Cherax_quadricarinatus_iridovirus_ASZ84981.1 (16.7%). Row 6: Invertebrate_iridescent_virus_30_YP_009010370.1 (14.8%). Row 7: Invertebrate_iridovirus_22_YP_008357369.1 (14.8%). Row 8: Invertebrate_iridovirus_25_YP_009010611.1 (15.6%). Row 9: Orpheovirus_IHUMI-LCC2_YP_009449240.1 (14.4%). Row 10: Melbournevirus_YP_009094806.1 (14.9%). Row 11: Marseillevirus_marseillevirus_YP_003407071.1 (14.9%). Row 12: Brazilian_marseillevirus_YP_009238902.1 (14.9%). Row 13: Golden_marseillevirus_YP_009310340.1 (12.3%). Row 14: mine_drainage_metagenome_EQD26795.1 (21.6%). Row 15: Pithovirus_sibericum_YP_009001361.1 (95.1%). Row 16: Shrimp_hemocyte_iridescent_virus_ATE87157.1 (16.7%). Row 17: Wiseana_iridescent_virus_YP_004732793.1 (15.0%). Row 18: PCJ29163.1_COA94_02315_Rickettsiales (22.3%). Consensus: 100%, 90%, 80%, 70%.

Table with 3 columns: Accession, Identity, and Sequence. Row 1: Pithovirus_massiliensis_LC8 (100.0%). Row 2: Armadillidium_vulgare_iridescent_virus_YP_009046748.1 (17.6%). Row 3: Cedratvirus_All_YP_009329068.1 (45.2%). Row 4: Cedratvirus_lausanensis_S0B74375.1 (45.5%). Row 5: Cherax_quadricarinatus_iridovirus_ASZ84981.1 (16.7%). Row 6: Invertebrate_iridescent_virus_30_YP_009010370.1 (14.8%). Row 7: Invertebrate_iridovirus_22_YP_008357369.1 (14.8%). Row 8: Invertebrate_iridovirus_25_YP_009010611.1 (15.6%). Row 9: Orpheovirus_IHUMI-LCC2_YP_009449240.1 (14.4%). Row 10: Melbournevirus_YP_009094806.1 (14.9%). Row 11: Marseillevirus_marseillevirus_YP_003407071.1 (14.9%). Row 12: Brazilian_marseillevirus_YP_009238902.1 (14.9%). Row 13: Golden_marseillevirus_YP_009310340.1 (12.3%). Row 14: mine_drainage_metagenome_EQD26795.1 (21.6%). Row 15: Pithovirus_sibericum_YP_009001361.1 (95.1%). Row 16: Shrimp_hemocyte_iridescent_virus_ATE87157.1 (16.7%). Row 17: Wiseana_iridescent_virus_YP_004732793.1 (15.0%). Row 18: PCJ29163.1_COA94_02315_Rickettsiales (22.3%). Consensus: 100%, 90%, 80%, 70%.

Table with 3 columns: Accession, Identity, and Sequence. Row 1: Pithovirus_massiliensis_LC8 (100.0%). Row 2: Armadillidium_vulgare_iridescent_virus_YP_009046748.1 (17.6%). Row 3: Cedratvirus_All_YP_009329068.1 (45.2%). Row 4: Cedratvirus_lausanensis_S0B74375.1 (45.5%). Row 5: Cherax_quadricarinatus_iridovirus_ASZ84981.1 (16.7%). Row 6: Invertebrate_iridescent_virus_30_YP_009010370.1 (14.8%). Row 7: Invertebrate_iridovirus_22_YP_008357369.1 (14.8%). Row 8: Invertebrate_iridovirus_25_YP_009010611.1 (15.6%). Row 9: Orpheovirus_IHUMI-LCC2_YP_009449240.1 (14.4%). Row 10: Melbournevirus_YP_009094806.1 (14.9%). Row 11: Marseillevirus_marseillevirus_YP_003407071.1 (14.9%). Row 12: Brazilian_marseillevirus_YP_009238902.1 (14.9%). Row 13: Golden_marseillevirus_YP_009310340.1 (12.3%). Row 14: mine_drainage_metagenome_EQD26795.1 (21.6%). Consensus: 100%, 90%, 80%, 70%.

15 Pithovirus_sibericum_YP_009001361.1 95.1%
 16 Shrimp_hemocyte_iridescent_virus_ATE87157.1 16.7%
 17 Wiseana_iridescent_virus_YP_004732793.1 15.0%
 18 PCJ29163_1_COA94_02315_Rickettsiales 22.3%
 consensus/100%
 consensus/90%
 consensus/80%
 consensus/70%

KE---SVQFEYTFKKSIFDLRFKIRAE-GEDW-EEVPFHKNFIEFVSA--DGGILSPPTIMEGYSKITIEEEQ-AIKN
 KWNKLRIDFEFRNWTELLILENVGAHN-GEKNPKVPOVGSDDIA-----VAPLSNVQVWVNGGLIPEAERA-RMGC
 PYNEHQINFNFRDWTETLLVLQNSALVAP-ASPY-VPIV-VPHTLT-----VAPVLGVPQVWANYAIVSNEERR-RMGC
 KD---SVKFEFKFNLNFSLLIRMRKIGE-NGNWECEIKYDSKYLKGIN----DKQRIPSPQMFAYLIMLESERKWLSE
ph.h.hp...ph..L.p.t.h.....t..l.s.hhshp.h...t....htt
pl.php.ppl..L.p.thh...s.....t..l.s.hhshphshl..tEc..thtt
plpaphp.hpllh.L.p.thht...h...hs.h...t.....stsslsst.hhspYuhl.ppEc..phtp
 ..pp.pIppa+phpphlsL.phtlhss ss.a.s.l.s.sthphs.....susslssspshpYuhlpp-E+h +hup

321

1 Pithovirus_massiliensis_LC8 100.0%
 2 Armadillidium_vulgare_iridescent_virus_YP_009046748.1 17.6%
 3 Cedratvirus_All_YP_009329068.1 45.2%
 4 Cedratvirus_lausannensis_S0B74375.1 45.5%
 5 Cherax_quadricarinatus_iridovirus_ASZ84981.1 16.7%
 6 Invertebrate_iridescent_virus_30_YP_009010370.1 14.8%
 7 Invertebrate_iridovirus_22_YP_008357369.1 14.8%
 8 Invertebrate_iridovirus_25_YP_009010611.1 15.6%
 9 Orpheovirus_IHUMI-LCC2_YP_009449240.1 14.4%
 10 Melbournevirus_YP_009094806.1 14.9%
 11 Marseillevirus_marseillevirus_YP_003407071.1 14.9%
 12 Brazilian_marseillevirus_YP_009238902.1 12.3%
 13 Golden_marseillevirus_YP_009310340.1 21.6%
 14 mine_drainage_metagenome_EQD26795.1 95.1%
 15 Pithovirus_sibericum_YP_009001361.1 16.7%
 16 Shrimp_hemocyte_iridescent_virus_ATE87157.1 15.0%
 17 Wiseana_iridescent_virus_YP_004732793.1 22.3%
 18 PCJ29163_1_COA94_02315_Rickettsiales
 consensus/100%
 consensus/90%
 consensus/80%
 consensus/70%

NDKH-----CAVEDILTfKTELVD--KVTPLAQVQIKTKYPLKGLFYVAENVDAATRLN-----NFSNFSTCS
 SVRD-----ILIEQVQTAPRHVYN-PNTNDEPSYDIRFSAHAIKALFFAVRN--TTFKN-----VMSNYTTAS
 DMDH-----YVVEDIKRFSSEIVN--KTNPKVTIEVDIEDSIKGLFYVAENLDATLTN-----NLSNFSTNA
 DMDH-----YVVEDIKRFSSEIVN--KTNPKVTIEVDIEDSIKGLFYVAENLDATLTN-----NLSNFSTNA
 VHRD-----MLIESIQTSKLNFN-PVLNPNPSYDIRFQRTVKALFFGVNRN--TTNPN-----VMSNYTTAS
 AIRD-----ILIEQVQTAPRQNYT-PLTNASPTFDIRFSAHAIKALFFAVRN--KTGAS-----EWSNYATSS
 AIRD-----ILIEQVQTAPRQNYT-PLTNASPTFDIRFSAHAIKALFFAVRN--KTGAS-----EWSNYATSS
 AIRD-----ILIEQVQTAPRQNYT-PLTNASPTFDIRFSAHAIKALFFAVRN--KTSAS-----EWSNYATSS
 GVLV-----QYIREVINLDRDETA--RLGTVKIPINKPGLSQAIFVSAENNLKPTSKDTSLVPLNYSNYTTNI
 NPRD-----MVIZKQVQVNETTINLSQLNALVPIIDIRVSHAVVGYFYAIRN--SSTTG-----EWSNYTT--
 NPRD-----MVIZKQVQVNETTINLSQLNALVPIIDIRVSHAVVGYFYAIRN--SSTTG-----EWSNYTT--
 NPRD-----MVIZKQVQVNETTINLSQLNALVPIIDIRVSHAVVGYFYAIRN--SSTPG-----EWSNYTT--
 NPRD-----MVIZKQVQVNETTINLSQLNALVPIIDIRVSHAVVGYFYAIRN--SSTPG-----EWSNYTT--
 FKIDKEGKYKDEVLFRIRVIAICDDINPS--KFGSYSSIDLTTSNPCLAI FWSAENNTAKSYN-----YHNSNYTTAE
 NDKH-----CAVEDILTfKTELVD--KVTPLAQVQIKTKYPLKGLFYVAENVDAATRLN-----NFSNFSTCA
 VHRD-----MLIESIQTSKLNFN-PVLNPNPSYDIRFQRTVKALFFGVNRN--KTGAS-----EWSNYATSS
 AIRD-----ILIEQVQTAPRQNYT-PLTNASPTFDIRFSAHAIKALFFAVRN--KTSAS-----EWSNYATSS
 SSHK-----IYARDMVRVSSMVVR--EGGDRVDININCSPNITHIYVTAENMEQNKLN-----NLSNYTTSG
hhcph.t.p...t...hss...h.lph...thahs.ps...p.....hp.atp..
 s.c.c hhlCpl.p..p..hs...hss...hplphp.shhuhFashpN..tp..s .hSNasT..
 s.c.c hhlCpl.phsp..hs...hss.sshpIchppslhuhFashcN..tot.s .hSNasTt..
 s.+c hlCplppsscpshs..hNs.ssh-I+hpcslpuLFasscN..tophs pasNYoTsu

401

1 Pithovirus_massiliensis_LC8 100.0%
 2 Armadillidium_vulgare_iridescent_virus_YP_009046748.1 17.6%
 3 Cedratvirus_All_YP_009329068.1 45.2%
 4 Cedratvirus_lausannensis_S0B74375.1 45.5%
 5 Cherax_quadricarinatus_iridovirus_ASZ84981.1 16.7%
 6 Invertebrate_iridescent_virus_30_YP_009010370.1 14.8%
 7 Invertebrate_iridovirus_22_YP_008357369.1 14.8%
 8 Invertebrate_iridovirus_25_YP_009010611.1 15.6%
 9 Orpheovirus_IHUMI-LCC2_YP_009449240.1 14.4%
 10 Melbournevirus_YP_009094806.1 14.9%
 11 Marseillevirus_marseillevirus_YP_003407071.1 14.9%
 12 Brazilian_marseillevirus_YP_009238902.1 12.3%
 13 Golden_marseillevirus_YP_009310340.1 21.6%
 14 mine_drainage_metagenome_EQD26795.1 95.1%
 15 Pithovirus_sibericum_YP_009001361.1 16.7%
 16 Shrimp_hemocyte_iridescent_virus_ATE87157.1 15.0%
 17 Wiseana_iridescent_virus_YP_004732793.1 22.3%
 18 PCJ29163_1_COA94_02315_Rickettsiales
 consensus/100%
 consensus/90%
 consensus/80%
 consensus/70%

-----EDMSEGVSPICSV
 QVVTPTTIVIFEPSTGAFDPIDHT
 -----TEILDGDKPIKGI
 -----TEILDGDKPIKGI
 PVPDADKIDFDPDQSAFDPIGTA
 PVVIGSTVNFPEA-GSFDPIANT
 PVVTGATVNFPEA-GSFDPIANT
 PVVTGATVNFPEA-GSFDPIANT
 -----YDVKSGSYPYI
 -----EPAYAGLDPLEAA
 -----EPAYAGLDPLEAA
 -----EPAYAGLDPLEAA
 PMPVLTSLRLSLCTSRPLVPSAT
 -----GDSKIGYDPKIST
 -----EDMSEGVSPICSV
 PVPDADKIDFDPDQSAFDPIGTA
 PVVTGATVNFPEA-GSFDPIANT
 DESGKNPI--HKRSMYGLERD
u..Plt..
u.tPltth
ps..tuhsPltss
csh.suhcPItss