**A. MSA between the full ORF1ab CDS from Wuhan, China, and partial ORF1ab CDS from Iran**

CLUSTAL O(1.2.4) multiple sequence alignment

NC\_045512.2:266-21555 ATGGAGAGCCTTGTCCCTGGTTTCAACGAGAAAACACACGTCCAACTCAGTTTGCCTGTT 60

MT152900.1 ------------------------------------------------------------ 0

NC\_045512.2:266-21555 TTACAGGTTCGCGACGTGCTCGTACGTGGCTTTGGAGACTCCGTGGAGGAGGTCTTATCA 120

MT152900.1 ------------------------------------------------------------ 0

NC\_045512.2:266-21555 GAGGCACGTCAACATCTTAAAGATGGCACTTGTGGCTTAGTAGAAGTTGAAAAAGGCGTT 180

MT152900.1 ------------------------------------------------------------ 0

NC\_045512.2:266-21555 TTGCCTCAACTTGAACAGCCCTATGTGTTCATCAAACGTTCGGATGCTCGAACTGCACCT 240

MT152900.1 --------------------------------------------------------ACCT 4

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NC\_045512.2:266-21555 CATGGTCATGTTATGGTTGAGCTGGTAGCAGAACTCGAAGGCATTCAGTACGGTCGTAGT 300

MT152900.1 CATGGTCATGTTATGGTTGAGCTGGTAGCAGAACTCGAAGGCATTCAGTACGGTCGTAGT 64

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

NC\_045512.2:266-21555 GGTGAGACACTTGGTGTCCTTGTCCCTCATGTGGGCGAAATACCAGTGGCTTACCGCAAG 360

MT152900.1 GGTGAGACACTTGGTGTCCTTGTCCCTCATGTGGGCGAAATACCAGTGGCTTACCGCAAG 124

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

NC\_045512.2:266-21555 GTTCTTCTTCGTAAGAACGGTAATAAAGGAGCTGGTGGCCATAGTTACGGCGCCGATCTA 420

MT152900.1 GTTCTTCTTCGTAAGAACGGTAATAAAGGAGCTGGTGGCCATAGTTACGGCGCCGATCTA 184

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

NC\_045512.2:266-21555 AAGTCATTTGACTTAGGCGACGAGCTTGGCACTGATCCTTATGAAGATTTTCAAGAAAAC 480

MT152900.1 AAGTCATTTGACTTAGGCGACGAGCTTGGCACTGATCCTTATGAAGATTTTCAAGAAAAC 244

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

NC\_045512.2:266-21555 TGGAACACTAAACATAGCAGTGGTGTTACCCGTGAACTCATGCGTGAGCTTAACGGAGGG 540

MT152900.1 TGGAACACTAAACATAGCAGTGGTGTTACCCGTGAACTCATGCGTGAGCTTAACGGAGGG 304

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

NC\_045512.2:266-21555 GCATACACTCGCTATGTCGATAACAACTTCTGTGGCCCTGATGGCTACCCTCTTGAGTGC 600

MT152900.1 GCATACACTCGCTATGTC------------------------------------------ 322

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NC\_045512.2:266-21555 ATTAAAGACCTTCTAGCACGTGCTGGTAAAGCTTCATGCACTTTGTCCGAACAACTGGAC 660

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TTTATTGACACTAAGAGGGGTGTATACTGCTGCCGTGAACATGAGCATGAAATTGCTTGG 720

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TACACGGAACGTTCTGAAAAGAGCTATGAATTGCAGACACCTTTTGAAATTAAATTGGCA 780

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 AAGAAATTTGACACCTTCAATGGGGAATGTCCAAATTTTGTATTTCCCTTAAATTCCATA 840

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 ATCAAGACTATTCAACCAAGGGTTGAAAAGAAAAAGCTTGATGGCTTTATGGGTAGAATT 900

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 CGATCTGTCTATCCAGTTGCGTCACCAAATGAATGCAACCAAATGTGCCTTTCAACTCTC 960

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 ATGAAGTGTGATCATTGTGGTGAAACTTCATGGCAGACGGGCGATTTTGTTAAAGCCACT 1020

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TGCGAATTTTGTGGCACTGAGAATTTGACTAAAGAAGGTGCCACTACTTGTGGTTACTTA 1080

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 CCCCAAAATGCTGTTGTTAAAATTTATTGTCCAGCATGTCACAATTCAGAAGTAGGACCT 1140

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GAGCATAGTCTTGCCGAATACCATAATGAATCTGGCTTGAAAACCATTCTTCGTAAGGGT 1200

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GGTCGCACTATTGCCTTTGGAGGCTGTGTGTTCTCTTATGTTGGTTGCCATAACAAGTGT 1260

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GCCTATTGGGTTCCACGTGCTAGCGCTAACATAGGTTGTAACCATACAGGTGTTGTTGGA 1320

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GAAGGTTCCGAAGGTCTTAATGACAACCTTCTTGAAATACTCCAAAAAGAGAAAGTCAAC 1380

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NC\_045512.2:266-21555 ATCAATATTGTTGGTGACTTTAAACTTAATGAAGAGATCGCCATTATTTTGGCATCTTTT 1440

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NC\_045512.2:266-21555 TCTGCTTCCACAAGTGCTTTTGTGGAAACTGTGAAAGGTTTGGATTATAAAGCATTCAAA 1500

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 CAAATTGTTGAATCCTGTGGTAATTTTAAAGTTACAAAAGGAAAAGCTAAAAAAGGTGCC 1560

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TGGAATATTGGTGAACAGAAATCAATACTGAGTCCTCTTTATGCATTTGCATCAGAGGCT 1620

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GCTCGTGTTGTACGATCAATTTTCTCCCGCACTCTTGAAACTGCTCAAAATTCTGTGCGT 1680

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GTTTTACAGAAGGCCGCTATAACAATACTAGATGGAATTTCACAGTATTCACTGAGACTC 1740

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 ATTGATGCTATGATGTTCACATCTGATTTGGCTACTAACAATCTAGTTGTAATGGCCTAC 1800

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NC\_045512.2:266-21555 ATTACAGGTGGTGTTGTTCAGTTGACTTCGCAGTGGCTAACTAACATCTTTGGCACTGTT 1860

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NC\_045512.2:266-21555 TATGAAAAACTCAAACCCGTCCTTGATTGGCTTGAAGAGAAGTTTAAGGAAGGTGTAGAG 1920

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TTTCTTAGAGACGGTTGGGAAATTGTTAAATTTATCTCAACCTGTGCTTGTGAAATTGTC 1980

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GGTGGACAAATTGTCACCTGTGCAAAGGAAATTAAGGAGAGTGTTCAGACATTCTTTAAG 2040

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NC\_045512.2:266-21555 CTTGTAAATAAATTTTTGGCTTTGTGTGCTGACTCTATCATTATTGGTGGAGCTAAACTT 2100

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 AAAGCCTTGAATTTAGGTGAAACATTTGTCACGCACTCAAAGGGATTGTACAGAAAGTGT 2160

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GTTAAATCCAGAGAAGAAACTGGCCTACTCATGCCTCTAAAAGCCCCAAAAGAAATTATC 2220

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TTCTTAGAGGGAGAAACACTTCCCACAGAAGTGTTAACAGAGGAAGTTGTCTTGAAAACT 2280

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GGTGATTTACAACCATTAGAACAACCTACTAGTGAAGCTGTTGAAGCTCCATTGGTTGGT 2340

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 ACACCAGTTTGTATTAACGGGCTTATGTTGCTCGAAATCAAAGACACAGAAAAGTACTGT 2400

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GCCCTTGCACCTAATATGATGGTAACAAACAATACCTTCACACTCAAAGGCGGTGCACCA 2460

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 ACAAAGGTTACTTTTGGTGATGACACTGTGATAGAAGTGCAAGGTTACAAGAGTGTGAAT 2520

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 ATCACTTTTGAACTTGATGAAAGGATTGATAAAGTACTTAATGAGAAGTGCTCTGCCTAT 2580

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 ACAGTTGAACTCGGTACAGAAGTAAATGAGTTCGCCTGTGTTGTGGCAGATGCTGTCATA 2640

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NC\_045512.2:266-21555 AAAACTTTGCAACCAGTATCTGAATTACTTACACCACTGGGCATTGATTTAGATGAGTGG 2700

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 AGTATGGCTACATACTACTTATTTGATGAGTCTGGTGAGTTTAAATTGGCTTCACATATG 2760

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TATTGTTCTTTCTACCCTCCAGATGAGGATGAAGAAGAAGGTGATTGTGAAGAAGAAGAG 2820

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TTTGAGCCATCAACTCAATATGAGTATGGTACTGAAGATGATTACCAAGGTAAACCTTTG 2880

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NC\_045512.2:266-21555 GAATTTGGTGCCACTTCTGCTGCTCTTCAACCTGAAGAAGAGCAAGAAGAAGATTGGTTA 2940

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NC\_045512.2:266-21555 GATGATGATAGTCAACAAACTGTTGGTCAACAAGACGGCAGTGAGGACAATCAGACAACT 3000

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NC\_045512.2:266-21555 ACTATTCAAACAATTGTTGAGGTTCAACCTCAATTAGAGATGGAACTTACACCAGTTGTT 3060

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MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 AAAAATGCAGACATTGTGGAAGAAGCTAAAAAGGTAAAACCAACAGTGGTTGTTAATGCA 3180

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GCCAATGTTTACCTTAAACATGGAGGAGGTGTTGCAGGAGCCTTAAATAAGGCTACTAAC 3240

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NC\_045512.2:266-21555 AATGCCATGCAAGTTGAATCTGATGATTACATAGCTACTAATGGACCACTTAAAGTGGGT 3300

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NC\_045512.2:266-21555 GGTAGTTGTGTTTTAAGCGGACACAATCTTGCTAAACACTGTCTTCATGTTGTCGGCCCA 3360

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 AATGTTAACAAAGGTGAAGACATTCAACTTCTTAAGAGTGCTTATGAAAATTTTAATCAG 3420

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NC\_045512.2:266-21555 CACGAAGTTCTACTTGCACCATTATTATCAGCTGGTATTTTTGGTGCTGACCCTATACAT 3480

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NC\_045512.2:266-21555 TCTTTAAGAGTTTGTGTAGATACTGTTCGCACAAATGTCTACTTAGCTGTCTTTGATAAA 3540

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NC\_045512.2:266-21555 AATCTCTATGACAAACTTGTTTCAAGCTTTTTGGAAATGAAGAGTGAAAAGCAAGTTGAA 3600

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NC\_045512.2:266-21555 CAAAAGATCGCTGAGATTCCTAAAGAGGAAGTTAAGCCATTTATAACTGAAAGTAAACCT 3660

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NC\_045512.2:266-21555 TCAGTTGAACAGAGAAAACAAGATGATAAGAAAATCAAAGCTTGTGTTGAAGAAGTTACA 3720

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NC\_045512.2:266-21555 ACAACTCTGGAAGAAACTAAGTTCCTCACAGAAAACTTGTTACTTTATATTGACATTAAT 3780

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NC\_045512.2:266-21555 GGCAATCTTCATCCAGATTCTGCCACTCTTGTTAGTGACATTGACATCACTTTCTTAAAG 3840

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NC\_045512.2:266-21555 AAAGATGCTCCATATATAGTGGGTGATGTTGTTCAAGAGGGTGTTTTAACTGCTGTGGTT 3900

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NC\_045512.2:266-21555 ATACCTACTAAAAAGGCTGGTGGCACTACTGAAATGCTAGCGAAAGCTTTGAGAAAAGTG 3960

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 CCAACAGACAATTATATAACCACTTACCCGGGTCAGGGTTTAAATGGTTACACTGTAGAG 4020

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NC\_045512.2:266-21555 GAGGCAAAGACAGTGCTTAAAAAGTGTAAAAGTGCCTTTTACATTCTACCATCTATTATC 4080

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NC\_045512.2:266-21555 TCTAATGAGAAGCAAGAAATTCTTGGAACTGTTTCTTGGAATTTGCGAGAAATGCTTGCA 4140

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NC\_045512.2:266-21555 ACTATACAGCGTAAATATAAGGGTATTAAAATACAAGAGGGTGTGGTTGATTATGGTGCT 4260

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NC\_045512.2:266-21555 AGATTTTACTTTTACACCAGTAAAACAACTGTAGCGTCACTTATCAACACACTTAACGAT 4320

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 CTAAATGAAACTCTTGTTACAATGCCACTTGGCTATGTAACACATGGCTTAAATTTGGAA 4380

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GAAGCTGCTCGGTATATGAGATCTCTCAAAGTGCCAGCTACAGTTTCTGTTTCTTCACCT 4440

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NC\_045512.2:266-21555 GATGCTGTTACAGCGTATAATGGTTATCTTACTTCTTCTTCTAAAACACCTGAAGAACAT 4500

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TTTATTGAAACCATCTCACTTGCTGGTTCCTATAAAGATTGGTCCTATTCTGGACAATCT 4560

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 ACACAACTAGGTATAGAATTTCTTAAGAGAGGTGATAAAAGTGTATATTACACTAGTAAT 4620

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NC\_045512.2:266-21555 CCTACCACATTCCACCTAGATGGTGAAGTTATCACCTTTGACAATCTTAAGACACTTCTT 4680

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NC\_045512.2:266-21555 TCTTTGAGAGAAGTGAGGACTATTAAGGTGTTTACAACAGTAGACAACATTAACCTCCAC 4740

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NC\_045512.2:266-21555 ACGCAAGTTGTGGACATGTCAATGACATATGGACAACAGTTTGGTCCAACTTATTTGGAT 4800

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NC\_045512.2:266-21555 GGAGCTGATGTTACTAAAATAAAACCTCATAATTCACATGAAGGTAAAACATTTTATGTT 4860

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NC\_045512.2:266-21555 TTACCTAATGATGACACTCTACGTGTTGAGGCTTTTGAGTACTACCACACAACTGATCCT 4920

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 AGTTTTCTGGGTAGGTACATGTCAGCATTAAATCACACTAAAAAGTGGAAATACCCACAA 4980

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NC\_045512.2:266-21555 GTTAATGGTTTAACTTCTATTAAATGGGCAGATAACAACTGTTATCTTGCCACTGCATTG 5040

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NC\_045512.2:266-21555 TTAACACTCCAACAAATAGAGTTGAAGTTTAATCCACCTGCTCTACAAGATGCTTATTAC 5100

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NC\_045512.2:266-21555 AGAGCAAGGGCTGGTGAAGCTGCTAACTTTTGTGCACTTATCTTAGCCTACTGTAATAAG 5160

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NC\_045512.2:266-21555 ACAGTAGGTGAGTTAGGTGATGTTAGAGAAACAATGAGTTACTTGTTTCAACATGCCAAT 5220

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TTAGATTCTTGCAAAAGAGTCTTGAACGTGGTGTGTAAAACTTGTGGACAACAGCAGACA 5280

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 ACCCTTAAGGGTGTAGAAGCTGTTATGTACATGGGCACACTTTCTTATGAACAATTTAAG 5340

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 AAAGGTGTTCAGATACCTTGTACGTGTGGTAAACAAGCTACAAAATATCTAGTACAACAG 5400

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GAGTCACCTTTTGTTATGATGTCAGCACCACCTGCTCAGTATGAACTTAAGCATGGTACA 5460

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TTTACTTGTGCTAGTGAGTACACTGGTAATTACCAGTGTGGTCACTATAAACATATAACT 5520

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TCTAAAGAAACTTTGTATTGCATAGACGGTGCTTTACTTACAAAGTCCTCAGAATACAAA 5580

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NC\_045512.2:266-21555 GGTCCTATTACGGATGTTTTCTACAAAGAAAACAGTTACACAACAACCATAAAACCAGTT 5640

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NC\_045512.2:266-21555 ACTTATAAATTGGATGGTGTTGTTTGTACAGAAATTGACCCTAAGTTGGACAATTATTAT 5700

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NC\_045512.2:266-21555 AAGAAAGACAATTCTTATTTCACAGAGCAACCAATTGATCTTGTACCAAACCAACCATAT 5760

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NC\_045512.2:266-21555 CCAAACGCAAGCTTCGATAATTTTAAGTTTGTATGTGATAATATCAAATTTGCTGATGAT 5820

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NC\_045512.2:266-21555 TTAAACCAGTTAACTGGTTATAAGAAACCTGCTTCAAGAGAGCTTAAAGTTACATTTTTC 5880

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NC\_045512.2:266-21555 CCTGACTTAAATGGTGATGTGGTGGCTATTGATTATAAACACTACACACCCTCTTTTAAG 5940

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NC\_045512.2:266-21555 AAAGGAGCTAAATTGTTACATAAACCTATTGTTTGGCATGTTAACAATGCAACTAATAAA 6000

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GCCACGTATAAACCAAATACCTGGTGTATACGTTGTCTTTGGAGCACAAAACCAGTTGAA 6060

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 ACATCAAATTCGTTTGATGTACTGAAGTCAGAGGACGCGCAGGGAATGGATAATCTTGCC 6120

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TGCGAAGATCTAAAACCAGTCTCTGAAGAAGTAGTGGAAAATCCTACCATACAGAAAGAC 6180

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GTTCTTGAGTGTAATGTGAAAACTACCGAAGTTGTAGGAGACATTATACTTAAACCAGCA 6240

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NC\_045512.2:266-21555 AATAATAGTTTAAAAATTACAGAAGAGGTTGGCCACACAGATCTAATGGCTGCTTATGTA 6300

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GACAATTCTAGTCTTACTATTAAGAAACCTAATGAATTATCTAGAGTATTAGGTTTGAAA 6360

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 ACCCTTGCTACTCATGGTTTAGCTGCTGTTAATAGTGTCCCTTGGGATACTATAGCTAAT 6420

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TATGCTAAGCCTTTTCTTAACAAAGTTGTTAGTACAACTACTAACATAGTTACACGGTGT 6480

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TTAAACCGTGTTTGTACTAATTATATGCCTTATTTCTTTACTTTATTGCTACAATTGTGT 6540

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NC\_045512.2:266-21555 ACTTTTACTAGAAGTACAAATTCTAGAATTAAAGCATCTATGCCGACTACTATAGCAAAG 6600

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NC\_045512.2:266-21555 AATACTGTTAAGAGTGTCGGTAAATTTTGTCTAGAGGCTTCATTTAATTATTTGAAGTCA 6660

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NC\_045512.2:266-21555 CCTAATTTTTCTAAACTGATAAATATTATAATTTGGTTTTTACTATTAAGTGTTTGCCTA 6720

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NC\_045512.2:266-21555 GGTTCTTTAATCTACTCAACCGCTGCTTTAGGTGTTTTAATGTCTAATTTAGGCATGCCT 6780

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NC\_045512.2:266-21555 TCTTACTGTACTGGTTACAGAGAAGGCTATTTGAACTCTACTAATGTCACTATTGCAACC 6840

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NC\_045512.2:266-21555 TACTGTACTGGTTCTATACCTTGTAGTGTTTGTCTTAGTGGTTTAGATTCTTTAGACACC 6900

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NC\_045512.2:266-21555 TATCCTTCTTTAGAAACTATACAAATTACCATTTCATCTTTTAAATGGGATTTAACTGCT 6960

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NC\_045512.2:266-21555 TTTGGCTTAGTTGCAGAGTGGTTTTTGGCATATATTCTTTTCACTAGGTTTTTCTATGTA 7020

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NC\_045512.2:266-21555 CTTGGATTGGCTGCAATCATGCAATTGTTTTTCAGCTATTTTGCAGTACATTTTATTAGT 7080

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NC\_045512.2:266-21555 AATTCTTGGCTTATGTGGTTAATAATTAATCTTGTACAAATGGCCCCGATTTCAGCTATG 7140

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NC\_045512.2:266-21555 GTTAGAATGTACATCTTCTTTGCATCATTTTATTATGTATGGAAAAGTTATGTGCATGTT 7200

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NC\_045512.2:266-21555 GTAGACGGTTGTAATTCATCAACTTGTATGATGTGTTACAAACGTAATAGAGCAACAAGA 7260

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NC\_045512.2:266-21555 GTCGAATGTACAACTATTGTTAATGGTGTTAGAAGGTCCTTTTATGTCTATGCTAATGGA 7320

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NC\_045512.2:266-21555 GGTAAAGGCTTTTGCAAACTACACAATTGGAATTGTGTTAATTGTGATACATTCTGTGCT 7380

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NC\_045512.2:266-21555 GGTAGTACATTTATTAGTGATGAAGTTGCGAGAGACTTGTCACTACAGTTTAAAAGACCA 7440

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NC\_045512.2:266-21555 ATAAATCCTACTGACCAGTCTTCTTACATCGTTGATAGTGTTACAGTGAAGAATGGTTCC 7500

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NC\_045512.2:266-21555 ATCCATCTTTACTTTGATAAAGCTGGTCAAAAGACTTATGAAAGACATTCTCTCTCTCAT 7560

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NC\_045512.2:266-21555 TTTGTTAACTTAGACAACCTGAGAGCTAATAACACTAAAGGTTCATTGCCTATTAATGTT 7620

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NC\_045512.2:266-21555 ATAGTTTTTGATGGTAAATCAAAATGTGAAGAATCATCTGCAAAATCAGCGTCTGTTTAC 7680

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NC\_045512.2:266-21555 TACAGTCAGCTTATGTGTCAACCTATACTGTTACTAGATCAGGCATTAGTGTCTGATGTT 7740

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NC\_045512.2:266-21555 GGTGATAGTGCGGAAGTTGCAGTTAAAATGTTTGATGCTTACGTTAATACGTTTTCATCA 7800

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NC\_045512.2:266-21555 ACTTTTAACGTACCAATGGAAAAACTCAAAACACTAGTTGCAACTGCAGAAGCTGAACTT 7860

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GCAAAGAATGTGTCCTTAGACAATGTCTTATCTACTTTTATTTCAGCAGCTCGGCAAGGG 7920

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TTTGTTGATTCAGATGTAGAAACTAAAGATGTTGTTGAATGTCTTAAATTGTCACATCAA 7980

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 TCTGACATAGAAGTTACTGGCGATAGTTGTAATAACTATATGCTCACCTATAACAAAGTT 8040

MT152900.1 ------------------------------------------------------------ 322

NC\_045512.2:266-21555 GAAAACATGACACCCCGTGACCTTGGTGCTTGTATTGACTGTAGTGCGCGTCATATTAAT 8100

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NC\_045512.2:266-21555 GCGCAGGTAGCAAAAAGTCACAACATTGCTTTGATATGGAACGTTAAAGATTTCATGTCA 8160

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NC\_045512.2:266-21555 TTGTCTGAACAACTACGAAAACAAATACGTAGTGCTGCTAAAAAGAATAACTTACCTTTT 8220

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NC\_045512.2:266-21555 AAGTTGACATGTGCAACTACTAGACAAGTTGTTAATGTTGTAACAACAAAGATAGCACTT 8280

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NC\_045512.2:266-21555 AAGGGTGGTAAAATTGTTAATAATTGGTTGAAGCAGTTAATTAAAGTTACACTTGTGTTC 8340

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NC\_045512.2:266-21555 CTTTTTGTTGCTGCTATTTTCTATTTAATAACACCTGTTCATGTCATGTCTAAACATACT 8400

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NC\_045512.2:266-21555 GACTTTTCAAGTGAAATCATAGGATACAAGGCTATTGATGGTGGTGTCACTCGTGACATA 8460

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NC\_045512.2:266-21555 GCATCTACAGATACTTGTTTTGCTAACAAACATGCTGATTTTGACACATGGTTTAGCCAG 8520

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NC\_045512.2:266-21555 CGTGGTGGTAGTTATACTAATGACAAAGCTTGCCCATTGATTGCTGCAGTCATAACAAGA 8580

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NC\_045512.2:266-21555 GAAGTGGGTTTTGTCGTGCCTGGTTTGCCTGGCACGATATTACGCACAACTAATGGTGAC 8640

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NC\_045512.2:266-21555 TTTTTGCATTTCTTACCTAGAGTTTTTAGTGCAGTTGGTAACATCTGTTACACACCATCA 8700

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NC\_045512.2:266-21555 CACAGAATGCTGTAGCCTCAAAGATTTTGGGACTACCAACTCAAACTGTTGATTCATCAC 17580

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NC\_045512.2:266-21555 AGTATTTTGTGAAAATAGGACCTGAGCGCACCTGTTGTCTATGTGATAGACGTGCCACAT 18420

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NC\_045512.2:266-21555 GCTTTTCCACTGCTTCAGACACTTATGCCTGTTGGCATCATTCTATTGGATTTGATTACG 18480

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NC\_045512.2:266-21555 TCTATAATCCGTTTATGATTGATGTTCAACAATGGGGTTTTACAGGTAACCTACAAAGCA 18540

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NC\_045512.2:266-21555 ACCATGATCTGTATTGTCAAGTCCATGGTAATGCACATGTAGCTAGTTGTGATGCAATCA 18600

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NC\_045512.2:266-21555 TGACTAGGTGTCTAGCTGTCCACGAGTGCTTTGTTAAGCGTGTTGACTGGACTATTGAAT 18660

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NC\_045512.2:266-21555 ATCCTATAATTGGTGATGAACTGAAGATTAATGCGGCTTGTAGAAAGGTTCAACACATGG 18720

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NC\_045512.2:266-21555 TTGTTAAAGCTGCATTATTAGCAGACAAATTCCCAGTTCTTCACGACATTGGTAACCCTA 18780

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NC\_045512.2:266-21555 AAGCTATTAAGTGTGTACCTCAAGCTGATGTAGAATGGAAGTTCTATGATGCACAGCCTT 18840

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NC\_045512.2:266-21555 GTAGTGACAAAGCTTATAAAATAGAAGAATTATTCTATTCTTATGCCACACATTCTGACA 18900

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NC\_045512.2:266-21555 AATTCACAGATGGTGTATGCCTATTTTGGAATTGCAATGTCGATAGATATCCTGCTAATT 18960

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NC\_045512.2:266-21555 CCATTGTTTGTAGATTTGACACTAGAGTGCTATCTAACCTTAACTTGCCTGGTTGTGATG 19020

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NC\_045512.2:266-21555 GTGGCAGTTTGTATGTAAATAAACATGCATTCCACACACCAGCTTTTGATAAAAGTGCTT 19080

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NC\_045512.2:266-21555 GTTGCAATTTAGGTGGTGCTGTCTGTAGACATCATGCTAATGAGTACAGATTGTATCTCG 19260

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NC\_045512.2:266-21555 CTTATAACCTCTGGAACACTTTTACAAGACTTCAGAGTTTAGAAAATGTGGCTTTTAATG 19380

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NC\_045512.2:266-21555 TACCTGTTAATGTAGCATTTGAGCTTTGGGCTAAGCGCAACATTAAACCAGTACCAGAGG 19560

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NC\_045512.2:266-21555 TGAAAATACTCAATAATTTGGGTGTGGACATTGCTGCTAATACTGTGATCTGGGACTACA 19620

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NC\_045512.2:266-21555 AAAGAGATGCTCCAGCACATATATCTACTATTGGTGTTTGTTCTATGACTGACATAGCCA 19680

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NC\_045512.2:266-21555 AGAAACCAACTGAAACGATTTGTGCACCACTCACTGTCTTTTTTGATGGTAGAGTTGATG 19740

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NC\_045512.2:266-21555 GTCAAGTAGACTTATTTAGAAATGCCCGTAATGGTGTTCTTATTACAGAAGGTAGTGTTA 19800

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NC\_045512.2:266-21555 AAGGTTTACAACCATCTGTAGGTCCCAAACAAGCTAGTCTTAATGGAGTCACATTAATTG 19860

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NC\_045512.2:266-21555 TACCTGAAACTTACTTTACTCAGAGTAGAAATTTACAAGAATTTAAACCCAGGAGTCAAA 19980

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NC\_045512.2:266-21555 TGGAAATTGATTTCTTAGAATTAGCTATGGATGAATTCATTGAACGGTATAAATTAGAAG 20040

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NC\_045512.2:266-21555 GCTATGCCTTCGAACATATCGTTTATGGAGATTTTAGTCATAGTCAGTTAGGTGGTTTAC 20100

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NC\_045512.2:266-21555 ATCTACTGATTGGACTAGCTAAACGTTTTAAGGAATCACCTTTTGAATTAGAAGATTTTA 20160

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NC\_045512.2:266-21555 TTCCTATGGACAGTACAGTTAAAAACTATTTCATAACAGATGCGCAAACAGGTTCATCTA 20220

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NC\_045512.2:266-21555 TTATGCTTTGGTGTAAAGATGGCCATGTAGAAACATTTTACCCAAAATTACAATCTAGTC 20400

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NC\_045512.2:266-21555 AAGCGTGGCAACCGGGTGTTGCTATGCCTAATCTTTACAAAATGCAAAGAATGCTATTAG 20460

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NC\_045512.2:266-21555 ATAATATGAGAGTTATACATTTTGGTGCTGGTTCTGATAAAGGAGTTGCACCAGGTACAG 20640

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**B. MSA between the full ORF1ab protein sequence from Wuhan, China, and partial ORF1ab protein sequence from Iran**

CLUSTAL O(1.2.4) multiple sequence alignment

QIH55230.1 ------------------------------------------------------------ 0

YP\_009724389.1 MESLVPGFNEKTHVQLSLPVLQVRDVLVRGFGDSVEEVLSEARQHLKDGTCGLVEVEKGV 60

QIH55230.1 -------------------PHGHVMVELVAELEGIQYGRSGETLGVLVPHVGEIPVAYRK 41

YP\_009724389.1 LPQLEQPYVFIKRSDARTAPHGHVMVELVAELEGIQYGRSGETLGVLVPHVGEIPVAYRK 120

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QIH55230.1 VLLRKNGNKGAGGHSYGADLKSFDLGDELGTDPYEDFQENWNTKHSSGVTRELMRELNGG 101

YP\_009724389.1 VLLRKNGNKGAGGHSYGADLKSFDLGDELGTDPYEDFQENWNTKHSSGVTRELMRELNGG 180

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

QIH55230.1 AYTRYV------------------------------------------------------ 107

YP\_009724389.1 AYTRYVDNNFCGPDGYPLECIKDLLARAGKASCTLSEQLDFIDTKRGVYCCREHEHEIAW 240

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YP\_009724389.1 YTERSEKSYELQTPFEIKLAKKFDTFNGECPNFVFPLNSIIKTIQPRVEKKKLDGFMGRI 300

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YP\_009724389.1 RSVYPVASPNECNQMCLSTLMKCDHCGETSWQTGDFVKATCEFCGTENLTKEGATTCGYL 360

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YP\_009724389.1 PQNAVVKIYCPACHNSEVGPEHSLAEYHNESGLKTILRKGGRTIAFGGCVFSYVGCHNKC 420

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YP\_009724389.1 AYWVPRASANIGCNHTGVVGEGSEGLNDNLLEILQKEKVNINIVGDFKLNEEIAIILASF 480

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YP\_009724389.1 SASTSAFVETVKGLDYKAFKQIVESCGNFKVTKGKAKKGAWNIGEQKSILSPLYAFASEA 540

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YP\_009724389.1 ARVVRSIFSRTLETAQNSVRVLQKAAITILDGISQYSLRLIDAMMFTSDLATNNLVVMAY 600

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YP\_009724389.1 GGQIVTCAKEIKESVQTFFKLVNKFLALCADSIIIGGAKLKALNLGETFVTHSKGLYRKC 720

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YP\_009724389.1 TPVCINGLMLLEIKDTEKYCALAPNMMVTNNTFTLKGGAPTKVTFGDDTVIEVQGYKSVN 840

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YP\_009724389.1 SMATYYLFDESGEFKLASHMYCSFYPPDEDEEEGDCEEEEFEPSTQYEYGTEDDYQGKPL 960

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YP\_009724389.1 EFGATSAALQPEEEQEEDWLDDDSQQTVGQQDGSEDNQTTTIQTIVEVQPQLEMELTPVV 1020

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YP\_009724389.1 QTIEVNSFSGYLKLTDNVYIKNADIVEEAKKVKPTVVVNAANVYLKHGGGVAGALNKATN 1080

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YP\_009724389.1 NAMQVESDDYIATNGPLKVGGSCVLSGHNLAKHCLHVVGPNVNKGEDIQLLKSAYENFNQ 1140

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YP\_009724389.1 HEVLLAPLLSAGIFGADPIHSLRVCVDTVRTNVYLAVFDKNLYDKLVSSFLEMKSEKQVE 1200

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YP\_009724389.1 QKIAEIPKEEVKPFITESKPSVEQRKQDDKKIKACVEEVTTTLEETKFLTENLLLYIDIN 1260

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YP\_009724389.1 GNLHPDSATLVSDIDITFLKKDAPYIVGDVVQEGVLTAVVIPTKKAGGTTEMLAKALRKV 1320

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YP\_009724389.1 FIETISLAGSYKDWSYSGQSTQLGIEFLKRGDKSVYYTSNPTTFHLDGEVITFDNLKTLL 1560

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YP\_009724389.1 LPNDDTLRVEAFEYYHTTDPSFLGRYMSALNHTKKWKYPQVNGLTSIKWADNNCYLATAL 1680

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YP\_009724389.1 LDSCKRVLNVVCKTCGQQQTTLKGVEAVMYMGTLSYEQFKKGVQIPCTCGKQATKYLVQQ 1800

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YP\_009724389.1 ESPFVMMSAPPAQYELKHGTFTCASEYTGNYQCGHYKHITSKETLYCIDGALLTKSSEYK 1860

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YP\_009724389.1 GPITDVFYKENSYTTTIKPVTYKLDGVVCTEIDPKLDNYYKKDNSYFTEQPIDLVPNQPY 1920

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YP\_009724389.1 PNASFDNFKFVCDNIKFADDLNQLTGYKKPASRELKVTFFPDLNGDVVAIDYKHYTPSFK 1980

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YP\_009724389.1 KGAKLLHKPIVWHVNNATNKATYKPNTWCIRCLWSTKPVETSNSFDVLKSEDAQGMDNLA 2040

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YP\_009724389.1 CEDLKPVSEEVVENPTIQKDVLECNVKTTEVVGDIILKPANNSLKITEEVGHTDLMAAYV 2100

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YP\_009724389.1 DNSSLTIKKPNELSRVLGLKTLATHGLAAVNSVPWDTIANYAKPFLNKVVSTTTNIVTRC 2160

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YP\_009724389.1 LNRVCTNYMPYFFTLLLQLCTFTRSTNSRIKASMPTTIAKNTVKSVGKFCLEASFNYLKS 2220

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YP\_009724389.1 PNFSKLINIIIWFLLLSVCLGSLIYSTAALGVLMSNLGMPSYCTGYREGYLNSTNVTIAT 2280

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QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 LGLAAIMQLFFSYFAVHFISNSWLMWLIINLVQMAPISAMVRMYIFFASFYYVWKSYVHV 2400

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 VDGCNSSTCMMCYKRNRATRVECTTIVNGVRRSFYVYANGGKGFCKLHNWNCVNCDTFCA 2460

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YP\_009724389.1 GSTFISDEVARDLSLQFKRPINPTDQSSYIVDSVTVKNGSIHLYFDKAGQKTYERHSLSH 2520

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 FVNLDNLRANNTKGSLPINVIVFDGKSKCEESSAKSASVYYSQLMCQPILLLDQALVSDV 2580

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YP\_009724389.1 GDSAEVAVKMFDAYVNTFSSTFNVPMEKLKTLVATAEAELAKNVSLDNVLSTFISAARQG 2640

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YP\_009724389.1 FVDSDVETKDVVECLKLSHQSDIEVTGDSCNNYMLTYNKVENMTPRDLGACIDCSARHIN 2700

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YP\_009724389.1 AQVAKSHNIALIWNVKDFMSLSEQLRKQIRSAAKKNNLPFKLTCATTRQVVNVVTTKIAL 2760

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YP\_009724389.1 KGGKIVNNWLKQLIKVTLVFLFVAAIFYLITPVHVMSKHTDFSSEIIGYKAIDGGVTRDI 2820

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YP\_009724389.1 ASTDTCFANKHADFDTWFSQRGGSYTNDKACPLIAAVITREVGFVVPGLPGTILRTTNGD 2880

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YP\_009724389.1 FLHFLPRVFSAVGNICYTPSKLIEYTDFATSACVLAAECTIFKDASGKPVPYCYDTNVLE 2940

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YP\_009724389.1 GSVAYESLRPDTRYVLMDGSIIQFPNTYLEGSVRVVTTFDSEYCRHGTCERSEAGVCVST 3000

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YP\_009724389.1 CPRHVICTSEDMLNPNYEDLLIRKSNHNFLVQAGNVQLRVIGHSMQNCVLKLKVDTANPK 3360

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YP\_009724389.1 WFLNRFTTTLNDFNLVAMKYNYEPLTQDHVDILGPLSAQTGIAVLDMCASLKELLQNGMN 3540

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YP\_009724389.1 GRTILGSALLEDEFTPFDVVRQCSGVTFQSAVKRTIKGTHHWLLLTILTSLLVLVQSTQW 3600

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YP\_009724389.1 VYYGNALDQAISMWALIISVTSNYSGVVTTVMFLARGIVFMCVEYCPIFFITGNTLQCIM 3780

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YP\_009724389.1 LVYCFLGYFCTCYFGLFCLLNRYFRLTLGVYDYLVSTQEFRYMNSQGLLPPKNSIDAFKL 3840

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YP\_009724389.1 AKDTTEAFEKMVSLLSVLLSMQGAVDINKLCEEMLDNRATLQAIASEFSSLPSYAAFATA 3960

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YP\_009724389.1 PANSTVLSFCAFAVDAAKAYKDYLASGGQPITNCVKMLCTHTGTGQAITVTPEANMDQES 4320

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YP\_009724389.1 FGGASCCLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPVGFTLKNTVCTVCGMWKGYG 4380

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YP\_009724389.1 CSCDQLREPMLQSADAQSFLNRVCGVSAARLTPCGTGTSTDVVYRAFDIYNDKVAGFAKF 4440

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YP\_009724389.1 DMVPHISRQRLTKYTMADLVYALRHFDEGNCDTLKEILVTYNCCDDDYFNKKDWYDFVEN 4560

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YP\_009724389.1 PDILRVYANLGERVRQALLKTVQFCDAMRNAGIVGVLTLDNQDLNGNWYDFGDFIQTTPG 4620

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YP\_009724389.1 SGVPVVDSYYSLLMPILTLTRALTAESHVDTDLTKPYIKWDLLKYDFTEERLKLFDRYFK 4680

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YP\_009724389.1 YWDQTYHPNCVNCLDDRCILHCANFNVLFSTVFPPTSFGPLVRKIFVDGVPFVVSTGYHF 4740

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YP\_009724389.1 RELGVVHNQDVNLHSSRLSFKELLVYAADPAMHAASGNLLLDKRTTCFSVAALTNNVAFQ 4800

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YP\_009724389.1 TVKPGNFNKDFYDFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYYRYNLPTMCDIRQ 4860

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YP\_009724389.1 LLFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNKWGKARLYYDSMSYEDQDALF 4920

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YP\_009724389.1 AYTKRNVIPTITQMNLKYAISAKNRARTVAGVSICSTMTNRQFHQKLLKSIAATRGATVV 4980

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YP\_009724389.1 IGTSKFYGGWHNMLKTVYSDVENPHLMGWDYPKCDRAMPNMLRIMASLVLARKHTTCCSL 5040

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YP\_009724389.1 SHRFYRLANECAQVLSEMVMCGGSLYVKPGGTSSGDATTAYANSVFNICQAVTANVNALL 5100

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 STDGNKIADKYVRNLQHRLYECLYRNRDVDTDFVNEFYAYLRKHFSMMILSDDAVVCFNS 5160

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 TYASQGLVASIKNFKSVLYYQNNVFMSEAKCWTETDLTKGPHEFCSQHTMLVKQGDDYVY 5220

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 LPYPDPSRILGAGCFVDDIVKTDGTLMIERFVSLAIDAYPLTKHPNQEYADVFHLYLQYI 5280

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 RKLHDELTGHMLDMYSVMLTNDNTSRYWEPEFYEAMYTPHTVLQAVGACVLCNSQTSLRC 5340

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 GACIRRPFLCCKCCYDHVISTSHKLVLSVNPYVCNAPGCDVTDVTQLYLGGMSYYCKSHK 5400

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 PPISFPLCANGQVFGLYKNTCVGSDNVTDFNAIATCDWTNAGDYILANTCTERLKLFAAE 5460

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 TLKATEETFKLSYGIATVREVLSDRELHLSWEVGKPRPPLNRNYVFTGYRVTKNSKVQIG 5520

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 EYTFEKGDYGDAVVYRGTTTYKLNVGDYFVLTSHTVMPLSAPTLVPQEHYVRITGLYPTL 5580

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 NISDEFSSNVANYQKVGMQKYSTLQGPPGTGKSHFAIGLALYYPSARIVYTACSHAAVDA 5640

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 LCEKALKYLPIDKCSRIIPARARVECFDKFKVNSTLEQYVFCTVNALPETTADIVVFDEI 5700

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 SMATNYDLSVVNARLRAKHYVYIGDPAQLPAPRTLLTKGTLEPEYFNSVCRLMKTIGPDM 5760

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 FLGTCRRCPAEIVDTVSALVYDNKLKAHKDKSAQCFKMFYKGVITHDVSSAINRPQIGVV 5820

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 REFLTRNPAWRKAVFISPYNSQNAVASKILGLPTQTVDSSQGSEYDYVIFTQTTETAHSC 5880

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 NVNRFNVAITRAKVGILCIMSDRDLYDKLQFTSLEIPRRNVATLQAENVTGLFKDCSKVI 5940

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 TGLHPTQAPTHLSVDTKFKTEGLCVDIPGIPKDMTYRRLISMMGFKMNYQVNGYPNMFIT 6000

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 REEAIRHVRAWIGFDVEGCHATREAVGTNLPLQLGFSTGVNLVAVPTGYVDTPNNTDFSR 6060

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 VSAKPPPGDQFKHLIPLMYKGLPWNVVRIKIVQMLSDTLKNLSDRVVFVLWAHGFELTSM 6120

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 KYFVKIGPERTCCLCDRRATCFSTASDTYACWHHSIGFDYVYNPFMIDVQQWGFTGNLQS 6180

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 NHDLYCQVHGNAHVASCDAIMTRCLAVHECFVKRVDWTIEYPIIGDELKINAACRKVQHM 6240

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 VVKAALLADKFPVLHDIGNPKAIKCVPQADVEWKFYDAQPCSDKAYKIEELFYSYATHSD 6300

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 KFTDGVCLFWNCNVDRYPANSIVCRFDTRVLSNLNLPGCDGGSLYVNKHAFHTPAFDKSA 6360

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 FVNLKQLPFFYYSDSPCESHGKQVVSDIDYVPLKSATCITRCNLGGAVCRHHANEYRLYL 6420

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 DAYNMMISAGFSLWVYKQFDTYNLWNTFTRLQSLENVAFNVVNKGHFDGQQGEVPVSIIN 6480

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 NTVYTKVDGVDVELFENKTTLPVNVAFELWAKRNIKPVPEVKILNNLGVDIAANTVIWDY 6540

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 KRDAPAHISTIGVCSMTDIAKKPTETICAPLTVFFDGRVDGQVDLFRNARNGVLITEGSV 6600

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 KGLQPSVGPKQASLNGVTLIGEAVKTQFNYYKKVDGVVQQLPETYFTQSRNLQEFKPRSQ 6660

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 MEIDFLELAMDEFIERYKLEGYAFEHIVYGDFSHSQLGGLHLLIGLAKRFKESPFELEDF 6720

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 IPMDSTVKNYFITDAQTGSSKCVCSVIDLLLDDFVEIIKSQDLSVVSKVVKVTIDYTEIS 6780

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 FMLWCKDGHVETFYPKLQSSQAWQPGVAMPNLYKMQRMLLEKCDLQNYGDSATLPKGIMM 6840

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 NVAKYTQLCQYLNTLTLAVPYNMRVIHFGAGSDKGVAPGTAVLRQWLPTGTLLVDSDLND 6900

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 FVSDADSTLIGDCATVHTANKWDLIISDMYDPKTKNVTKENDSKEGFFTYICGFIQQKLA 6960

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 LGGSVAIKITEHSWNADLYKLMGHFAWWTAFVTNVNASSSEAFLIGCNYLGKPREQIDGY 7020

QIH55230.1 ------------------------------------------------------------ 107

YP\_009724389.1 VMHANYIFWRNTNPIQLSSYSLFDMSKFPLKLRGTAVMSLKEGQINDMILSLLSKGRLII 7080

QIH55230.1 ---------------- 107

YP\_009724389.1 RENNRVVISSDVLVNN 7096