NP (1565 bp)

Nature: cRNA

Source: NC_002019.1 Influenza A virus (A/Puerto Rico/8/1934(H1N1)) segment 5

AGCAAAAGCAGGGTAGATAATCACTCACTGAGTGACATCAAAATCATGGCGTCCCAAGGCACCAAACGGT
CTTACGAACAGATGGAGACTGATGGAGAACGCCAGAATGCCACTGAAATCAGAGCATCCGTCGGAAAAAT
GATTGGTGGAATTGGACGATTCTACATCCAAATGTGCACAGAACTTAAACTCAGTGATTATGAGGGACGG
TTGATCCAAAACAGCTTAACAATAGAGAGAATGGTGCTCTCTGCTTTTGACGAAAGGAGAAATAAATACC
TGGAAGAACATCCCAGTGCGGGGAAGGATCCTAAGAAAACTGGAGGACCTATATACAGAAGAGTAAACGG
AAAGTGGATGAGAGAACTCATCCTTTATGACAAAGAAGAAATAAGGCGAATCTGGCGCCAAGCTAATAAT
GGTGACGATGCAACGGCTGGTCTGACTCACATGATGATCTGGCATTCCAATTTGAATGATGCAACTTATC
AGAGGACAAGGGCTCTTGTTCGCACCGGAATGGATCCCAGGATGTGCTCTCTGATGCAAGGTTCAACTCT
CCCTAGGAGGTCTGGAGCCGCAGGTGCTGCAGTCAAAGGAGTTGGAACAATGGTGATGGAATTGGTCAGG
ATGATCAAACGTGGGATCAATGATCGGAACTTCTGGAGGGGTGAGAATGGACGAAAAACAAGAATTGCTT
ATGAAAGAATGTGCAACATTCTCAAAGGGAAATTTCAAACTGCTGCACAAAAAGCAATGATGGATCAAGT
GAGAGAGAGCCGGGACCCAGGGAATGCTGAGTTCGAAGATCTCACTTTTCTAGCACGGTCTGCACTCATA
TTGAGAGGGTCGGTTGCTCACAAGTCCTGCCTGCCTGCCTGTGTGTATGGACCTGCCGTAGCCAGTGGGT
ACGACTTTGAAAGAGAGGGATACTCTCTAGTCGGAATAGACCCTTTCAGACTGCTTCAAAACAGCCAAGT
GTACAGCCTAATCAGACCAAATGAGAATCCAGCACACAAGAGTCAACTGGTGTGGATGGCATGCCATTCT
GCCGCATTTGAAGATCTAAGAGTATTGAGCTTCATCAAAGGGACGAAGGTGGTCCCAAGAGGGAAGCTTT
CCACTAGAGGAGTTCAAATTGCTTCCAATGAAAATATGGAGACTATGGAATCAAGTACACTTGAACTGAG
AAGCAGGTACTGGGCCATAAGGACCAGAAGTGGAGGAAACACCAATCAACAGAGGGCATCTGCGGGCCAA
ATCAGCATACAACCTACGTTCTCAGTACAGAGAAATCTCCCTTTTGACAGAACAACCGTTATGGCAGCAT
TCACTGGGAATACAGAGGGGAGAACATCTGACATGAGGACCGAAATCATAAGGATGATGGAAAGTGCAAG
ACCAGAAGATGTGTCTTTCCAGGGGCGGGGAGTCTTCGAGCTCTCGGACGAAAAGGCAGCGAGCCCGATC
GTGCCTTCCTTTGACATGAGTAATGAAGGATCTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATT
AAAGAAAAATACCCTTGTTTCTACT

NP protein

Source: NP_040982.1 (566 aa)

Sequence: 46 - 1542

MASQGTKRSYEQMETDGERQNATEIRASVGKMIGGIGRFYIQMCTELKLSDYEGRLIQNSLTIERMVLSA
FDERRNKYLEEHPSAGKDPKKTGGPIYRRVNGKWMRELILYDKEEIRRIWRQANNGDDATAGLTHMMIWH
SNLNDATYQRTRALVRTGMDPRMCSLMQGSTLPRRSGAAGAAVKGVGTMVMELVRMIKRGINDRNFWRGE
NGRKTRIAYERMCNILKGKFQTAAQKAMMDQVRESRDPGNAEFEDLTFLARSALILRGSVAHKSCLPACV
YGPAVASGYDFEREGYSLVGIDPFRLLQNSQVYSLIRPNENPAHKSQLVWMACHSAAFEDLRVLSFIKGT
KVVPRGKLSTRGVQIASNENMETMESSTLELRSRYWAIRTRSGGNTNQQRASAGQISIQPTFSVQRNLPF
DRTTVMAAFTGNTEGRTSDMRTEIIRMMESARPEDVSFQGRGVFELSDEKAASPIVPSFDMSNEGSYFFG
DNAEEYDN

NP (1566 bp)

Nature: vRNA

Source: Illumina sequences from virus stocks_RPS2022

NNNNNAAGCAGGGTAGATAATCACTCACTGAGTGACATCAAAATCATGGCGTCTCAAGGCAC
CAAACGATCTTACGAACAGATGGAGACTGATGGAGAACGCCAGAATGCCACTGAAATCAGAG
CATCCGTCGGAAAAATGATTGGTGGAATTGGACGATTCTACATCCAAATGTGCACCGAACTC
AAACTCAGTGATTATGAGGGACGGTTGATCCAAAACAGCTTAACAATAGAGAGAATGGTGCT
CTCTGCTTTTGACGAAAGGAGAAATAAATACCTTGAAGAACATCCCAGTGCGGGGAAAGATC
CTAAGAAAACTGGAGGACCTATATACAGGAGAGTAAACGGAAAGTGGATGAGAGAACTCATC
CTTTATGACAAAGAAGAAATAAGGCGAATCTGGCGCCAAGCTAATAATGGTGACGATGCAAC
GGCTGGTCTGACTCACATGATGATCTGGCATTCCAATTTGAATGATGCAACTTATCAGAGGA
CAAGAGCTCTTGTTCGCACCGGAATGGATCCCAGGATGTGCTCTCTGATGCAAGGTTCAACT
CTCCCTAGGAGGTCTGGAGCCGCAGGTGCTGCAGTCAAAGGAGTTGGAACAATGGTGATGGA
ATTGGTCAGAATGATCAAACGTGGGATCAATGATCGGAACTTCTGGAGGGGTGAGAATGGAC
GAAAAACAAGAATTGCTTATGAAAGAATGTGCAACATTCTCAAAGGGAAATTTCAAACTGCT
GCACAAAAAGCAATGATGGATCAAGTGAGAGAGAGCCGGAACCCAGGGAATGCTGAGTTCGA
AGATCTCACTTTTCTAGCACGGTCTGCACTCATATTGAGAGGGTCGGTTGCTCACAAGTCCT
GCCTGCCTGCCTGTGTGTATGGACCTGCCGTAGCCAGTGGGTACGACTTTGAAAGGGAGGGA
TACTCTCTAGTCGGAATAGACCCTTTCAGACTGCTTCAAAACAGCCAAGTGTACAGCCTAAT
CAGACCAAATGAGAATCCAGCACACAAGAGTCAACTGGTGTGGATGGCATGCCATTCTGCCG
CATTTGAAGATCTAAGAGTATTAAGCTTCATCAAAGGGACGAAGGTGCTCCCAAGAGGGAAG
CTTTCCACTAGAGGAGTTCAAATTGCTTCCAATGAAAATATGGAGACTATGGAATCAAGTAC
ACTTGAACTGAGAAGCAGGTACTGGGCCATAAGGACCAGAAGTGGAGGAAACACCAATCAAC
AGAGGGCATCTGCGGGCCAAATCAGCATACAACCTACGTTCTCAGTACAGAGAAATCTCCCT
TTTGACAGAACAACCATTATGGCAGCATTCAATGGGAATACAGAGGGGAGAACATCTGACAT
GAGGACCGAAATCATAAGGATGATGGAAAGTGCAAGACCAGAAGATGTGTCTTTCCAGGGGC
GGGGAGTCTTCGAGCTCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCTTCCTTTGACATG
AGTAATGAAGGATCTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTAAAGAAAAAT
ACCCTTGNNNNNNNN

NP (1566 bp)

Nature: cDNA_pHW2000

Source: GATC sequences from Maxiprep_RPS_2023

AGCAAAAGCAGGGTAGATAATCACTCACTGAGTGACATCAAAATCATGGCGTCTCAAGGCAC
CAAACGATCTTACGAACAGATGGAGACTGATGGAGAACGCCAGAATGCCACTGAAATCAGAG
CATCCGTCGGAAAAATGATTGGTGGAATTGGACGATTCTACATCCAAATGTGCACCGAACTC
AAACTCAGTGATTATGAGGGACGGTTGATCCAAAACAGCTTAACAATAGAGAGAATGGTGCT
CTCTGCTTTTGACGAAAGGAGAAATAAATACCTTGAAGAACATCCCAGTGCGGGGAAAGATC
CTAAGAAAACTGGAGGACCTATATACAGGAGAGTAAACGGAAAGTGGATGAGAGAACTCATC
CTTTATGACAAAGAAGAAATAAGGCGAATCTGGCGCCAAGCTAATAATGGTGACGATGCAAC
GGCTGGTCTGACTCACATGATGATCTGGCATTCCAATTTGAATGATGCAACTTATCAGAGGA
CAAGAGCTCTTGTTCGCACCGGAATGGATCCCAGGATGTGCTCTCTGATGCAAGGTTCAACT
CTCCCTAGGAGGTCTGGAGCCGCAGGTGCTGCAGTCAAAGGAGTTGGAACAATGGTGATGGA
ATTGGTCAGAATGATCAAACGTGGGATCAATGATCGGAACTTCTGGAGGGGTGAGAATGGAC
GAAAAACAAGAATTGCTTATGAAAGAATGTGCAACATTCTCAAAGGGAAATTTCAAACTGCT
GCACAAAAAGCAATGATGGATCAAGTGAGAGAGAGCCGGAACCCAGGGAATGCTGAGTTCGA
AGATCTCACTTTTCTAGCACGGTCTGCACTCATATTGAGAGGGTCGGTTGCTCACAAGTCCT
GCCTGCCTGCCTGTGTGTATGGACCTGCCGTAGCCAGTGGGTACGACTTTGAAAGGGAGGGA
TACTCTCTAGTCGGAATAGACCCTTTCAGACTGCTTCAAAACAGCCAAGTGTACAGCCTAAT
CAGACCAAATGAGAATCCAGCACACAAGAGTCAACTGGTGTGGATGGCATGCCATTCTGCCG
CATTTGAAGATCTAAGAGTATTAAGCTTCATCAAAGGGACGAAGGTGCTCCCAAGAGGGAAG
CTTTCCACTAGAGGAGTTCAAATTGCTTCCAATGAAAATATGGAGACTATGGAATCAAGTAC
ACTTGAACTGAGAAGCAGGTACTGGGCCATAAGGACCAGAAGTGGAGGAAACACCAATCAAC
AGAGGGCATCTGCGGGCCAAATCAGCATACAACCTACGTTCTCAGTACAGAGAAATCTCCCT
TTTGACAGAACAACCATTATGGCAGCATTCAATGGGAATACAGAGGGGAGAACATCTGACAT
GAGGACCGAAATCATAAGGATGATGGAAAGTGCAAGACCAGAAGATGTGTCTTTCCAGGGGC
GGGGAGTCTTCGAGCTCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCTTCCTTTGACATG
AGTAATGAAGGATCTTATTTCTTCGGAGACAATGCAGA**G**GAGTACGACAATTAA**A**G**AAAAA**T
ACCCTTGTTTCTACT

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CLUSTAL O(1.2.4) multiple sequence alignment


PR8_NP_NCBI          AGCAAAAGCAGGGTAGATAATCACTCACTGAGTGACATCAAAATCATGGCGTCCCAAGGC       60
PR8_NP_Illumina      NNNNNAAGCAGGGTAGATAATCACTCACTGAGTGACATCAAAATCATGGCGTCTCAAGGC       60
PR8_NP_pHW2000       AGCAAAAGCAGGGTAGATAATCACTCACTGAGTGACATCAAAATCATGGCGTCTCAAGGC       60
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PR8_NP_NCBI          ACCAAACGGTCTTACGAACAGATGGAGACTGATGGAGAACGCCAGAATGCCACTGAAATC       120
PR8_NP_Illumina      ACCAAACGATCTTACGAACAGATGGAGACTGATGGAGAACGCCAGAATGCCACTGAAATC       120
PR8_NP_pHW2000       ACCAAACGATCTTACGAACAGATGGAGACTGATGGAGAACGCCAGAATGCCACTGAAATC       120
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PR8_NP_NCBI          AGAGCATCCGTCGGAAAAATGATTGGTGGAATTGGACGATTCTACATCCAAATGTGCACA       180
PR8_NP_Illumina      AGAGCATCCGTCGGAAAAATGATTGGTGGAATTGGACGATTCTACATCCAAATGTGCACC       180
PR8_NP_pHW2000       AGAGCATCCGTCGGAAAAATGATTGGTGGAATTGGACGATTCTACATCCAAATGTGCACC       180
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PR8_NP_NCBI          GAACTTAAACTCAGTGATTATGAGGGACGGTTGATCCAAAACAGCTTAACAATAGAGAGA       240
PR8_NP_Illumina      GAACTCAAACTCAGTGATTATGAGGGACGGTTGATCCAAAACAGCTTAACAATAGAGAGA       240
PR8_NP_pHW2000       GAACTCAAACTCAGTGATTATGAGGGACGGTTGATCCAAAACAGCTTAACAATAGAGAGA       240
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PR8_NP_NCBI          ATGGTGCTCTCTGCTTTTGACGAAAGGAGAAATAAATACCTGGAAGAACATCCCAGTGCG       300
PR8_NP_Illumina      ATGGTGCTCTCTGCTTTTGACGAAAGGAGAAATAAATACCTTGAAGAACATCCCAGTGCG       300
PR8_NP_pHW2000       ATGGTGCTCTCTGCTTTTGACGAAAGGAGAAATAAATACCTTGAAGAACATCCCAGTGCG       300
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PR8_NP_NCBI          GGGAAGGATCCTAAGAAAACTGGAGGACCTATATACAGAAGAGTAAACGGAAAGTGGATG       360
PR8_NP_Illumina      GGGAAAGATCCTAAGAAAACTGGAGGACCTATATACAGGAGAGTAAACGGAAAGTGGATG       360
PR8_NP_pHW2000       GGGAAAGATCCTAAGAAAACTGGAGGACCTATATACAGGAGAGTAAACGGAAAGTGGATG       360
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PR8_NP_NCBI          AGAGAACTCATCCTTTATGACAAAGAAGAAATAAGGCGAATCTGGCGCCAAGCTAATAAT       420
PR8_NP_Illumina      AGAGAACTCATCCTTTATGACAAAGAAGAAATAAGGCGAATCTGGCGCCAAGCTAATAAT       420
PR8_NP_pHW2000       AGAGAACTCATCCTTTATGACAAAGAAGAAATAAGGCGAATCTGGCGCCAAGCTAATAAT       420
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PR8_NP_NCBI          GGTGACGATGCAACGGCTGGTCTGACTCACATGATGATCTGGCATTCCAATTTGAATGAT       480
PR8_NP_Illumina      GGTGACGATGCAACGGCTGGTCTGACTCACATGATGATCTGGCATTCCAATTTGAATGAT       480
PR8_NP_pHW2000       GGTGACGATGCAACGGCTGGTCTGACTCACATGATGATCTGGCATTCCAATTTGAATGAT       480
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PR8_NP_NCBI          GCAACTTATCAGAGGACAAGGGCTCTTGTTCGCACCGGAATGGATCCCAGGATGTGCTCT       540
PR8_NP_Illumina      GCAACTTATCAGAGGACAAGAGCTCTTGTTCGCACCGGAATGGATCCCAGGATGTGCTCT       540
PR8_NP_pHW2000       GCAACTTATCAGAGGACAAGAGCTCTTGTTCGCACCGGAATGGATCCCAGGATGTGCTCT       540
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PR8_NP_NCBI          CTGATGCAAGGTTCAACTCTCCCTAGGAGGTCTGGAGCCGCAGGTGCTGCAGTCAAAGGA       600
PR8_NP_Illumina      CTGATGCAAGGTTCAACTCTCCCTAGGAGGTCTGGAGCCGCAGGTGCTGCAGTCAAAGGA       600
PR8_NP_pHW2000       CTGATGCAAGGTTCAACTCTCCCTAGGAGGTCTGGAGCCGCAGGTGCTGCAGTCAAAGGA       600
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PR8_NP_NCBI          GTTGGAACAATGGTGATGGAATTGGTCAGGATGATCAAACGTGGGATCAATGATCGGAAC       660
PR8_NP_Illumina      GTTGGAACAATGGTGATGGAATTGGTCAGAATGATCAAACGTGGGATCAATGATCGGAAC       660
PR8_NP_pHW2000       GTTGGAACAATGGTGATGGAATTGGTCAGAATGATCAAACGTGGGATCAATGATCGGAAC       660
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PR8_NP_NCBI          TTCTGGAGGGGTGAGAATGGACGAAAAACAAGAATTGCTTATGAAAGAATGTGCAACATT       720
PR8_NP_Illumina      TTCTGGAGGGGTGAGAATGGACGAAAAACAAGAATTGCTTATGAAAGAATGTGCAACATT       720
PR8_NP_pHW2000       TTCTGGAGGGGTGAGAATGGACGAAAAACAAGAATTGCTTATGAAAGAATGTGCAACATT       720
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PR8_NP_NCBI          CTCAAAGGGAAATTTCAAACTGCTGCACAAAAAGCAATGATGGATCAAGTGAGAGAGAGC       780
PR8_NP_Illumina      CTCAAAGGGAAATTTCAAACTGCTGCACAAAAAGCAATGATGGATCAAGTGAGAGAGAGC       780
PR8_NP_pHW2000       CTCAAAGGGAAATTTCAAACTGCTGCACAAAAAGCAATGATGGATCAAGTGAGAGAGAGC       780
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PR8_NP_NCBI          CGGGACCCAGGGAATGCTGAGTTCGAAGATCTCACTTTTCTAGCACGGTCTGCACTCATA       840
PR8_NP_Illumina      CGGAACCCAGGGAATGCTGAGTTCGAAGATCTCACTTTTCTAGCACGGTCTGCACTCATA       840
PR8_NP_pHW2000       CGGAACCCAGGGAATGCTGAGTTCGAAGATCTCACTTTTCTAGCACGGTCTGCACTCATA       840
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PR8_NP_NCBI          TTGAGAGGGTCGGTTGCTCACAAGTCCTGCCTGCCTGCCTGTGTGTATGGACCTGCCGTA       900
PR8_NP_Illumina      TTGAGAGGGTCGGTTGCTCACAAGTCCTGCCTGCCTGCCTGTGTGTATGGACCTGCCGTA       900
PR8_NP_pHW2000       TTGAGAGGGTCGGTTGCTCACAAGTCCTGCCTGCCTGCCTGTGTGTATGGACCTGCCGTA       900
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PR8_NP_NCBI          GCCAGTGGGTACGACTTTGAAAGAGAGGGATACTCTCTAGTCGGAATAGACCCTTTCAGA       960
PR8_NP_Illumina      GCCAGTGGGTACGACTTTGAAAGGGAGGGATACTCTCTAGTCGGAATAGACCCTTTCAGA       960
PR8_NP_pHW2000       GCCAGTGGGTACGACTTTGAAAGGGAGGGATACTCTCTAGTCGGAATAGACCCTTTCAGA       960
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PR8_NP_NCBI          CTGCTTCAAAACAGCCAAGTGTACAGCCTAATCAGACCAAATGAGAATCCAGCACACAAG       1020
PR8_NP_Illumina      CTGCTTCAAAACAGCCAAGTGTACAGCCTAATCAGACCAAATGAGAATCCAGCACACAAG       1020
PR8_NP_pHW2000       CTGCTTCAAAACAGCCAAGTGTACAGCCTAATCAGACCAAATGAGAATCCAGCACACAAG       1020
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PR8_NP_NCBI          AGTCAACTGGTGTGGATGGCATGCCATTCTGCCGCATTTGAAGATCTAAGAGTATTGAGC       1080
PR8_NP_Illumina      AGTCAACTGGTGTGGATGGCATGCCATTCTGCCGCATTTGAAGATCTAAGAGTATTAAGC       1080
PR8_NP_pHW2000       AGTCAACTGGTGTGGATGGCATGCCATTCTGCCGCATTTGAAGATCTAAGAGTATTAAGC       1080
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PR8_NP_NCBI          TTCATCAAAGGGACGAAGGTGGTCCCAAGAGGGAAGCTTTCCACTAGAGGAGTTCAAATT       1140
PR8_NP_Illumina      TTCATCAAAGGGACGAAGGTGCTCCCAAGAGGGAAGCTTTCCACTAGAGGAGTTCAAATT       1140
PR8_NP_pHW2000       TTCATCAAAGGGACGAAGGTGCTCCCAAGAGGGAAGCTTTCCACTAGAGGAGTTCAAATT       1140
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PR8_NP_NCBI          GCTTCCAATGAAAATATGGAGACTATGGAATCAAGTACACTTGAACTGAGAAGCAGGTAC       1200
PR8_NP_Illumina      GCTTCCAATGAAAATATGGAGACTATGGAATCAAGTACACTTGAACTGAGAAGCAGGTAC       1200
PR8_NP_pHW2000       GCTTCCAATGAAAATATGGAGACTATGGAATCAAGTACACTTGAACTGAGAAGCAGGTAC       1200
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PR8_NP_NCBI          TGGGCCATAAGGACCAGAAGTGGAGGAAACACCAATCAACAGAGGGCATCTGCGGGCCAA       1260
PR8_NP_Illumina      TGGGCCATAAGGACCAGAAGTGGAGGAAACACCAATCAACAGAGGGCATCTGCGGGCCAA       1260
PR8_NP_pHW2000       TGGGCCATAAGGACCAGAAGTGGAGGAAACACCAATCAACAGAGGGCATCTGCGGGCCAA       1260
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PR8_NP_NCBI          ATCAGCATACAACCTACGTTCTCAGTACAGAGAAATCTCCCTTTTGACAGAACAACCGTT       1320
PR8_NP_Illumina      ATCAGCATACAACCTACGTTCTCAGTACAGAGAAATCTCCCTTTTGACAGAACAACCATT       1320
PR8_NP_pHW2000       ATCAGCATACAACCTACGTTCTCAGTACAGAGAAATCTCCCTTTTGACAGAACAACCATT       1320
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PR8_NP_NCBI          ATGGCAGCATTCACTGGGAATACAGAGGGGAGAACATCTGACATGAGGACCGAAATCATA       1380
PR8_NP_Illumina      ATGGCAGCATTCAATGGGAATACAGAGGGGAGAACATCTGACATGAGGACCGAAATCATA       1380
PR8_NP_pHW2000       ATGGCAGCATTCAATGGGAATACAGAGGGGAGAACATCTGACATGAGGACCGAAATCATA       1380
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PR8_NP_NCBI          AGGATGATGGAAAGTGCAAGACCAGAAGATGTGTCTTTCCAGGGGCGGGGAGTCTTCGAG       1440
PR8_NP_Illumina      AGGATGATGGAAAGTGCAAGACCAGAAGATGTGTCTTTCCAGGGGCGGGGAGTCTTCGAG       1440
PR8_NP_pHW2000       AGGATGATGGAAAGTGCAAGACCAGAAGATGTGTCTTTCCAGGGGCGGGGAGTCTTCGAG       1440
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PR8_NP_NCBI          CTCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCTTCCTTTGACATGAGTAATGAAGGA       1500
PR8_NP_Illumina      CTCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCTTCCTTTGACATGAGTAATGAAGGA       1500
PR8_NP_pHW2000       CTCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCTTCCTTTGACATGAGTAATGAAGGA       1500
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PR8_NP_NCBI          TCTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTAAAGAAAAATACCCTTGTTT       1560
PR8_NP_Illumina      TCTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTAAAGAAAAATACCCTTGNNN       1560
PR8_NP_pHW2000       TCTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTAAAGAAAAATACCCTTGTTT       1560
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PR8_NP_NCBI          CTACT      1565
PR8_NP_Illumina      NNNNN      1565
PR8_NP_pHW2000       CTACT      1565
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CLUSTAL O(1.2.4) multiple sequence alignment


NP_NCBI         ---------------MASQGTKRSYEQMETDGERQNATEIRASVGKMIGGIGRFYIQMCT    45
NP_pHW2000      SKSRVDNHSLSDIKIMASQGTKRSYEQMETDGERQNATEIRASVGKMIGGIGRFYIQMCT    60
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NP_NCBI         ELKLSDYEGRLIQNSLTIERMVLSAFDERRNKYLEEHPSAGKDPKKTGGPIYRRVNGKWM    105
NP_pHW2000      ELKLSDYEGRLIQNSLTIERMVLSAFDERRNKYLEEHPSAGKDPKKTGGPIYRRVNGKWM    120
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NP_NCBI         RELILYDKEEIRRIWRQANNGDDATAGLTHMMIWHSNLNDATYQRTRALVRTGMDPRMCS    165
NP_pHW2000      RELILYDKEEIRRIWRQANNGDDATAGLTHMMIWHSNLNDATYQRTRALVRTGMDPRMCS    180
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NP_NCBI         LMQGSTLPRRSGAAGAAVKGVGTMVMELVRMIKRGINDRNFWRGENGRKTRIAYERMCNI    225
NP_pHW2000      LMQGSTLPRRSGAAGAAVKGVGTMVMELVRMIKRGINDRNFWRGENGRKTRIAYERMCNI    240
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NP_NCBI         LKGKFQTAAQKAMMDQVRESRDPGNAEFEDLTFLARSALILRGSVAHKSCLPACVYGPAV    285
NP_pHW2000      LKGKFQTAAQKAMMDQVRESRNPGNAEFEDLTFLARSALILRGSVAHKSCLPACVYGPAV    300
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NP_NCBI         ASGYDFEREGYSLVGIDPFRLLQNSQVYSLIRPNENPAHKSQLVWMACHSAAFEDLRVLS    345
NP_pHW2000      ASGYDFEREGYSLVGIDPFRLLQNSQVYSLIRPNENPAHKSQLVWMACHSAAFEDLRVLS    360
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NP_NCBI         FIKGTKVVPRGKLSTRGVQIASNENMETMESSTLELRSRYWAIRTRSGGNTNQQRASAGQ    405
NP_pHW2000      FIKGTKVLPRGKLSTRGVQIASNENMETMESSTLELRSRYWAIRTRSGGNTNQQRASAGQ    420
                *******:****************************************************

NP_NCBI         ISIQPTFSVQRNLPFDRTTVMAAFTGNTEGRTSDMRTEIIRMMESARPEDVSFQGRGVFE    465
NP_pHW2000      ISIQPTFSVQRNLPFDRTTIMAAFNGNTEGRTSDMRTEIIRMMESARPEDVSFQGRGVFE    480
                ******************:****.**********************************

NP_NCBI         LSDEKAASPIVPSFDMSNEGSYFFGDNAEEYDN--------       498
NP_pHW2000      LSDEKAASPIVPSFDMSNEGSYFFGDNAEEYDN*RKIPLFL       520
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