

# PA (2233 bp)

Nature: cRNA

Source: NC\_002022.1 Influenza A virus (A/Puerto Rico/8/1934(H1N1)) segment 3

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AGCGAAAGCAGGTACTGATCCAAAATGGAAGATTTTGTGCGACAATGCTTCAATCCGATGATTGTCGAGC
TTGCGGAAAAACAATGAAAGAGTATGGGGAGGACCTGAAAATCGAAACAAACAAATTTGCAGCAATATG
CACTCACTTGGAAGTATGCTTCATGTATTTCAGATTTCCACTTCATCAATGAGCAAGGCGAGTCAATAATC
GTAGAACTTGGTGATCCTAATGCACATTTTGAAGCACAGATTTGAAATAATCGAGGGGAAGAGATCGCACAA
TGGCCTGGACAGTAGTAAACAGTATTTGCAACACTACAGGGGCTGAGAAAACCAAAGTTTCTACCAGATTT
GTATGATTACAAGGAAAATAGATTTCATCGAAATTGGAGTAACAAGGAGAGAAGTTCACATATACTATCTG
GAAAAGGCCAATAAAATTAATCTGAGAAAACACACATCCACATTTTCTCGTTCACTGGGGAAGAAATGG
CCACAAAGGCCGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAAACCAGGCTATTACCATAAG
ACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCTTTTCGTCACTCCGAGAGAGGAGAAGAGACAATTGAA
GAAAGGTTTGAAATCACAGGAACAATGCGCAAGCTTGCCGACCAAAGTCTCCCGCCGAACCTTCTCCAGCC
TTGAAAATTTTAGAGCCTATGTGGATGGATTTCGAACCGAACGGCTACATTGAGGGCAAGCTGTCTCAAAT
GTCCAAAGAAGTAAATGCTAGAATTGAACCTTTTTTTGAAAACAACACCACGACCACTTAGACTTCCGAAT
GGGCCTCCCTGTTCTCAGCGGTCCAAATTCCTGCTGATGGATGCCTTAAAAATTAAGCATTGAGGACCCAA
GTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAAATGCATGAGAACATTCTTTGGATGGAAGGA
ACCCAATGTTGTTAAACCACACGAAAAGGGAATAAATCCAAATTATCTTCTGTCATGGAAGCAAGTACTG
GCAGAACTGCAGGACATTGAGAATGAGGAGAAAAATTCCAAAGACTAAAAATATGAAAAAACAAAGTCAGC
TAAAGTGGGCACTTGGTGAGAACATGGCACCAGAAAAGGTAGACTTTGACGACTGTAAAGATGTAGGTGA
TTTGAAGCAATATGATAGTGATGAACCAGAATTGAGGTCGCTTGCAAGTTGGATTGAGAATGAGTTCAAC
AAGGCATGCGAACTGACAGATTCAAGCTGGATAGAGCTTGATGAGATTGGAGAAGATGTGGCTCCAATTG
AACACATTGCAAGCATGAGAAGGAATTATTTACATCAGAGGTGTCTCACTGCAGAGCCACAGAATACAT
AATGAAGGGGGTGTACATCAATACTGCCTTACTTAATGCATCTTGTGCAGCAATGGATGATTTCCAATTA
ATTCCAATGATAAGCAAGTGTAAGTAAGGAGGGAAGGCGAAAAGACCAACTTGATGGTTTCATCATAA
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CCCAAGACTTGAAACCACACAAATGGGAGAAGTACTGTGTTCTTGAGATAGGAGATATGCTTCTAAGAAGT
GCCATAGGCCAGGTTTCAAGGCCCATGTTCTTGTATGTGAGGACAAATGGAACCTCAAAAATTAATGA
AATGGGGAATGGAGATGAGGCGTTGTCTCCTCCAGTCACTTCAACAAATTGAGAGTATGATTGAAGCTGA
GTCCTCTGTCAAAGAGAAAGACATGACCAAAGAGTTCTTTGAGAACAAATCAGAAACATGGCCCATTTGA
GAGTCTCCCAAAGGAGTGGAGGAAAGTTCCATTGGGAAGGTCTGCAGGACTTTATTAGCAAAGTCGGTAT
TTAACAGCTTGTATGCATCTCCACAACCTAGAAGGATTTTCAGCTGAATCAAGAAAACCTGCTTCTTATCGT
TCAGGCTCTTAGGGACAATCTGGAACCTGGGACCTTTGATCTTGGGGGGCTATATGAAGCAATTGAGGAG
TGCCTAATTAATGATCCCTGGGTTTTGCTTAATGCTTCTTGGTTCAACTCCTTCCTTACACATGCATTGA
GTTAGTTGTGGCAGTGCTACTATTTGCTATCCATACTGTCCAAAAAAGTACCTTGTTTCTACT
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# PA protein

Source: NP\_040986.1 (716 aa)

Sequence: 25 - 2175

MEDFVRQCFNPMIVELAECTMKEYGEDLKIETNKFAAICTHLEVCFMYSDFHFINEQGESIIVELGDPNA  
LLKHRFEIIIEGRDRTMAWTVVNSICNTTGAEKPKFLPDLYDYKENRFIEIGVTRREVHIYYLEKANKIKS  
EKTHIHIFSFTGEEMATKADYTLDEESRARIKTRLFTIRQEMASRGLWDSFRQSERGEETIEERFEITGT  
MRKLADQSLPPNFSSLENFRAYVDGFEPNGYIEGKLSQMSKEVNARIEPFLKTTTPRPLRLPNGPPCSQRS  
KFLLM DALKLSIEDPSHEGEGIPLYDAIKCMRTFFGWKEPNVVKPHEKGINPNYLLSWKQVLAELQDIEN  
EEKIPKTKNMKKTSQ LK WALGENMAPEKVDFDDCKDVGD LKQYDSDEPELRS LASWIQNEFNKACELTDS  
SWIELDEIGEDVAPIEH IASMR RNYFTSEVSHCRATEYIMKGVYINTALLNASCAAMDDFQLIPMISKCR  
TKEGRRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTDPRLEPHKWEKYCVLEIGDMLLRSAIGQVSRP  
MFLYVRTNGTSKIKMKWGMEMRCLLQSLQQIESMIEAESSVKEKDMTKEFFENKSETWP IGESPKGV EE  
SSIGKVCRTLLAKSVFNSLYASPQLEGFSAESRKL LLLIVQALRDNLEPGTFDLGGLYEAIEECLINDPWV  
LLNASWFNSFLTHALS

# PA-X protein

Source: YP\_006495785.1 (252 aa)

Sequence: 25 - 784

MEDFVRQCFNPMIVELAECTMKEYGEDLKIETNKFAAICTHLEVCFMYSDFHFINEQGESIIVELGDPNA  
LLKHRFEIIIEGRDRTMAWTVVNSICNTTGAEKPKFLPDLYDYKENRFIEIGVTRREVHIYYLEKANKIKS  
EKTHIHIFSFTGEEMATKADYTLDEESRARIKTRLFTIRQEMASRGLWDSFVSPREEKRQLKKGLKSQEQ  
CASLP TKVSRRTSPALKILEPMWMDSNRTATLRASCLKCPKK

# PA (2233 bp)

Nature: vRNA

Source: Illumina sequences from virus stocks\_RPS2022

NNNNNAAGCAGGTACTGATCCAAAATGGAAGATTTTGTGCGACAATGCTTCAATCCGATGAT  
TGTCGAGCTTGCGGAAAAACAATGAAAGAGTATGGGGAGGACCTGAAAATCGAAACAAACA  
AATTTGCAGCAATATGCACTCACTTGGAAGTATGCTTCATGTATTCAGATTTTCACTTCATC  
AATGAGCAAGGCGAGTCAATAATCGTAGAACTTGGTGATCCAAATGCACTTTTGAAGCACAG  
ATTTGAAATAATCGAGGGAAGAGATCGCACAAATGGCCTGGACAGTAGTAAACAGTATTTGCA  
ACACTACAGGGGCTGAGAAACCAAAGTTTCTACCAGATTTGTATGATTACAAGGAGAATAGA  
TTCATCGAAATTGGAGTAACAAGGAGAGAAGTTCACATATACTATCTGGAAAAGGCCAATAA  
AATTAAATCTGAGAAAACACACATCCACATTTTCTCGTTCACTGGGGAAGAAATGGCCACAA  
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AGACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCCTTTCGTCAGTCCGAGAGAGGAGAAGA  
GACAATTGAAGAAAGGTTTGAAATCACAGGAACAATGCGTAAGCTTGCCGACCAAAGTCTCC  
CGCCGAACCTTCTCCAGCCTTGAAAATTTTAGAGCCTATGTGGATGGATTCTGAACCGAACGGC  
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TCCTGCTGATGGATGCCTTAAAATTAAGCATTGAGGACCCAAGTCATGAAGGAGAGGGAATA  
CCGCTATATGATGCAATCAAATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGT  
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GGATTCAGAATGAGTTTAAACAAGGCATGCGAACTGACAGATTCAAGCTGGATAGAGCTCGAT  
GAGATTGGAGAAGATGTGGCTCCAATTGAACACATTGCAAGCATGAGAAGGAATTATTTTAC  
ATCAGAGGTGTCTCACTGCAGAGCCACAGAATACATAATGAAGGGAGTGATACATCAATACTG  
CCTTGCTTAATGCATCTTGTGCAGCAATGGATGATTTCCAATTAATTCCAATGATAAGCAAG  
TGTAGAACTAAGGAGGGAAGGCGAAAAGACCAACTTGTATGGTTTCATCATAAAAGGAAGATC  
CCACTTAAGGAATGACACCGACGTGGTAAACTTTGTGAGCATGGAGTTTTTCTCTCACTGACC  
CAAGACTTGAACCACATAAATGGGAGAAGTACTGTGTTCTTGAGATAGGAGATATGCTTATA  
AGAAGTGCCATAGGCCAGGTTTCAAGGCCCATGTTCTTGTATGTGAGAACAAATGGAACCTC  
AAAAATTAAAATGAAATGGGGAATGGAGATGAGGCGTTGCCTCCTCCAGTCACTTCAACAAA  
TTGAGAGTATGATTGAAGCTGAGTCCTCTGTCAAAGAGAAAGACATGACCAAAGAGTTCTTT  
GAGAACAAATCAGAAACATGGCCCATTTGGAGAGTCCCCCAAAGGAGTGGAGGAAAGTTCCAT  
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AACTAGAAGGATTTTTCAGCTGAATCAAGAAAAGTCTTCTTATCGTTTCAGGCTCTTAGGGAC  
AACCTGGAACCTGGGACCTTTGATCTTGGGGGGCTATATGAAGCAATTGAGGAGTGCCTGAT  
TAATGATCCCTGGGTTTTGCTTAATGCTTCTTGGTTCAACTCCTTCCTTACACATGCATTGA  
GTTAGTTGTGGCAGTGCTACTATTTGCTATCCATACTGTCCAAAAAAGTACCTTGTTTNNNN  
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# PA (2233 bp)

Nature: cDNA\_pHW2000

Source: GATC sequences from Maxiprep\_RPS\_2023

AGCGAAAGCAGGTACTGATCCAAA**ATG**GAAAGATTTTGTGCGACAATGCTTCAATCCGATGAT  
TGTCGAGCTTGCGGAAAAACAATGAAAGAGTATGGGGAGGACCTGAAAATCGAAACAAACA  
AATTTGCAGCAATATGCACTCACTTGGAAGTATGCTTCATGTATTCAGATTTTCACTTCATC  
AATGAGCAAGGCGAGTCAATAATCGTAGAACTTGGTGATCCAAATGCACTTTTGAAGCACAG  
ATTTGAAATAATCGAGGGAAGAGATCGCACAAATGGCCTGGACAGTAGTAAACAGTATTTGCA  
ACACTACAGGGGCTGAGAAACCAAAGTTTCTACCAGATTTGTATGATTACAAGGAGAATAGA  
TTCATCGAAATTGGAGTAACAAGGAGAGAAGTTCACATATACTATCTGGAAAAGGCCAATAA  
AATTAAATCTGAGAAAACACACATCCACATTTTCTCGTTCACTGGGGAAGAAATGGCCACAA  
AGGCAGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAACCAGACTATTCACCATA  
AGACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCCTTTCGTCAGTCCGAGAGAGGAGAAGA  
GACAATTGAAGAAAGGTTTGAAATCACAGGAACAATGCGTAAGCTTGCCGACCAAAGTCTCC  
CGCCGAACCTTCTCCAGCCTTGAAAATTTTAGAGCCTATGTGGATGGATTCTGAACCGAACGGC  
TACATTGAGGGCAAGCTGTCTCAAATGTCCAAAGAAGTAAATGCTAGAATTGAACCTTTTTT  
GAAAACAACACCACGACCACTTAGACTTCCGAATGGGCCTCCCTGTTCTCAGCGGTCCAAAT  
TCCTGCTGATGGATGCCTTAAAATTAAGCATTGAGGACCCAAGTCATGAAGGAGAGGGAATA  
CCGCTATATGATGCAATCAAATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGT  
TAAACCACACGAAAAGGGAATAAATCCAAATTATCTTCTGTCATGGAAGCAAGTACTGGCAG  
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CAGCTAAAGTGGGCACTTGGTGAGAACATGGCACCAGAAAAGGTAGACTTTGACGACTGTAA  
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GAGATTGGAGAAGATGTGGCTCCAATTGAACACATTGCAAGCATGAGAAGGAATTATTTTAC  
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CCTTGCTTAATGCATCTTGTGCAGCAATGGATGATTTCCAATTAATTCCAATGATAAGCAAG  
TGTAGAACTAAGGAGGGAAGGCGAAAAGACCAACTTGTATGGTTTCATCATAAAAGGAAGATC  
CCACTTAAGGAATGACACCGACGTGGTAAACTTTGTGAGCATGGAGTTTTCTCTCACTGACC  
CAAGACTTGAACCACATAAATGGGAGAAGTACTGTGTTCTTGAGATAGGAGATATGCTTATA  
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AAAAATTAAAATGAAATGGGGAATGGAGATGAGGCGTTGCCTCCTCCAGTCACTTCAACAAA  
TTGAGAGTATGATTGAAGCTGAGTCCTCTGTCAAAGAGAAAAGACATGACCAAAGAGTTCTTT  
GAGAACAAATCAGAAACATGGCCCATTTGGAGAGTCCCCCAAAGGAGTGAGGAAAGTTCCAT  
TGGGAAGGTCTGCAGGACTTTATTAGCAAAGTCGGTATTCAACAGCTTGTATGCATCTCCAC  
AACTAGAAGGATTTTTCAGCTGAATCAAGAAAAGTCTTCTTATCGTTTCAGGCTCTTAGGGAC  
AACCTGGAACCTGGGACCTTTGATCTTGGGGGGCTATATGAAGCAATTGAGGAGTGCCTGAT  
TAATGATCCCTGGGTTTTGCTTAATGCTTCTTGGTTCAACTCCTTCCTTACACATGCATTGA  
GTTAGTTGTGGCAGTGCTACTATTTGCTATCCATACTGTCCAAAAAAGTACCTTGTTTCTAC  
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LUSTAL 0(1.2.4) multiple sequence alignment			
PR8_PA_NCB1	AGCGAAAGCAGGTACTGATCCAAAATGGAAGATTTTGTGCGACAATGCTTCAATCCGATG	60	
PR8_PA_illumina	NNNNNAAGCAGGTACTGATCCAAAATGGAAGATTTTGTGCGACAATGCTTCAATCCGATG	60	
PR8_PA_pHW2000	AGCGAAAGCAGGTACTGATCCAAAATGGAAGATTTTGTGCGACAATGCTTCAATCCGATG	60	
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PR8_PA_NCB1	ATTGTCGAGCTTGC GGAAAAACAATGAAAGAGTATGGGAGGACCTGAAAAATCGAAAAACA	120	
PR8_PA_illumina	ATTGTCGAGCTTGC GGAAAAACAATGAAAGAGTATGGGAGGACCTGAAAAATCGAAAAACA	120	
PR8_PA_pHW2000	ATTGTCGAGCTTGC GGAAAAACAATGAAAGAGTATGGGAGGACCTGAAAAATCGAAAAACA	120	
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PR8_PA_NCB1	AACAAATTTGCAGCAATATGCACTCACTTGGAAGTATGCTTCATGTATTCAGATTTGCAC	180	
PR8_PA_illumina	AACAAATTTGCAGCAATATGCACTCACTTGGAAGTATGCTTCATGTATTCAGATTTGCAC	180	
PR8_PA_pHW2000	AACAAATTTGCAGCAATATGCACTCACTTGGAAGTATGCTTCATGTATTCAGATTTGCAC	180	
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PR8_PA_NCB1	TTCATCAATGAGCAAGCGAGTCAATAATCGTAGAACTTGGTGATCCTAATGCACTTT	240	
PR8_PA_illumina	TTCATCAATGAGCAAGCGAGTCAATAATCGTAGAACTTGGTGATCCAAATGCACTTT	240	
PR8_PA_pHW2000	TTCATCAATGAGCAAGCGAGTCAATAATCGTAGAACTTGGTGATCCAAATGCACTTT	240	
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PR8_PA_NCB1	AAGCACAGATTTGAAATAATCGAGGGAAGAGATCGCACAATGGCCTGGACAGTAGTA AAC	300	
PR8_PA_illumina	AAGCACAGATTTGAAATAATCGAGGGAAGAGATCGCACAATGGCCTGGACAGTAGTA AAC	300	
PR8_PA_pHW2000	AAGCACAGATTTGAAATAATCGAGGGAAGAGATCGCACAATGGCCTGGACAGTAGTA AAC	300	
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PR8_PA_NCB1	AGTATTTGCAACACTACAGGGGCTGAGAAACCAAAGTTTCTACCAGATTTGTATGATTAC	360	
PR8_PA_illumina	AGTATTTGCAACACTACAGGGGCTGAGAAACCAAAGTTTCTACCAGATTTGTATGATTAC	360	
PR8_PA_pHW2000	AGTATTTGCAACACTACAGGGGCTGAGAAACCAAAGTTTCTACCAGATTTGTATGATTAC	360	
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PR8_PA_NCB1	AAGGAAATAGATTTCATCGAAATTGGAGTAACAAGGAGAGAAGTTCACATATACTATCTG	420	
PR8_PA_illumina	AAGGAAATAGATTTCATCGAAATTGGAGTAACAAGGAGAGAAGTTCACATATACTATCTG	420	
PR8_PA_pHW2000	AAGGAAATAGATTTCATCGAAATTGGAGTAACAAGGAGAGAAGTTCACATATACTATCTG	420	
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PR8_PA_NCB1	GAAAAGGCCAATAAAATTAATCTGAGAAAAACACATCCACATTTTCTCGTTCACTGGG	480	
PR8_PA_illumina	GAAAAGGCCAATAAAATTAATCTGAGAAAAACACATCCACATTTTCTCGTTCACTGGG	480	
PR8_PA_pHW2000	GAAAAGGCCAATAAAATTAATCTGAGAAAAACACATCCACATTTTCTCGTTCACTGGG	480	
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PR8_PA_NCB1	GAAGAAATGCCACA AAGGCAGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAA	540	
PR8_PA_illumina	GAAGAAATGCCACA AAGGCAGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAA	540	
PR8_PA_pHW2000	GAAGAAATGCCACA AAGGCAGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAA	540	
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PR8_PA_NCB1	ACCAGGCTATTTCACCATAAGACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCCCTTCGT	600	
PR8_PA_illumina	ACCAGGCTATTTCACCATAAGACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCCCTTCGT	600	
PR8_PA_pHW2000	ACCAGGCTATTTCACCATAAGACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCCCTTCGT	600	
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PR8_PA_NCB1	CAGTCCGAGAGAGGAGAAGAGACAATTGAAGAAAGGTTTGAANACACAGGAACAATGCG	660	
PR8_PA_illumina	CAGTCCGAGAGAGGAGAAGAGACAATTGAAGAAAGGTTTGAANACACAGGAACAATGCG	660	
PR8_PA_pHW2000	CAGTCCGAGAGAGGAGAAGAGACAATTGAAGAAAGGTTTGAANACACAGGAACAATGCG	660	
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PR8_PA_NCB1	AAGCTTGCCGACCAAAGTCTCCGCCGAACCTTCTCCAGCCTTGAAAAATTTAGAGCCTAT	720	
PR8_PA_illumina	AAGCTTGCCGACCAAAGTCTCCGCCGAACCTTCTCCAGCCTTGAAAAATTTAGAGCCTAT	720	
PR8_PA_pHW2000	AAGCTTGCCGACCAAAGTCTCCGCCGAACCTTCTCCAGCCTTGAAAAATTTAGAGCCTAT	720	
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PR8_PA_NCB1	GTGGATGGATTCGAACCGAACGGCTACATTGAGGGCAAGCTGTCTCAAATGTCCAAAGAA	780	
PR8_PA_illumina	GTGGATGGATTCGAACCGAACGGCTACATTGAGGGCAAGCTGTCTCAAATGTCCAAAGAA	780	
PR8_PA_pHW2000	GTGGATGGATTCGAACCGAACGGCTACATTGAGGGCAAGCTGTCTCAAATGTCCAAAGAA	780	
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PR8_PA_NCB1	GTAAATGCTAGAATTGAACCTTTTTTTGAAAAACAACACACGACCACTTAGACTTCGGAAT	840	
PR8_PA_illumina	GTAAATGCTAGAATTGAACCTTTTTTTGAAAAACAACACACGACCACTTAGACTTCGGAAT	840	
PR8_PA_pHW2000	GTAAATGCTAGAATTGAACCTTTTTTTGAAAAACAACACACGACCACTTAGACTTCGGAAT	840	
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PR8_PA_NCB1	GGGCCTCCCTGTTCTCAGCGGTCCAAATTCCTGCTGATGGATGCCTTAAAAATTAAGCATT	900	
PR8_PA_illumina	GGGCCTCCCTGTTCTCAGCGGTCCAAATTCCTGCTGATGGATGCCTTAAAAATTAAGCATT	900	
PR8_PA_pHW2000	GGGCCTCCCTGTTCTCAGCGGTCCAAATTCCTGCTGATGGATGCCTTAAAAATTAAGCATT	900	
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PR8_PA_NCB1	GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAAATGCATGAGA	960	
PR8_PA_illumina	GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAAATGCATGAGA	960	
PR8_PA_pHW2000	GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAAATGCATGAGA	960	
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PR8_PA_NCB1	ACATTCTTTGGATGGAAGGAACCCCAATGTTGTTAAACCACACGAAAAGGGAATAAAATCCA	1020	
PR8_PA_illumina	ACATTCTTTGGATGGAAGGAACCCCAATGTTGTTAAACCACACGAAAAGGGAATAAAATCCA	1020	
PR8_PA_pHW2000	ACATTCTTTGGATGGAAGGAACCCCAATGTTGTTAAACCACACGAAAAGGGAATAAAATCCA	1020	
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PR8_PA_NCB1	AATTATCTTCTGTCAATGGAAGCAAGTACTGGCAGAACTGCAGGACATTGAGAATGAGGAG	1080	
PR8_PA_illumina	AATTATCTTCTGTCAATGGAAGCAAGTACTGGCAGAACTGCAGGACATTGAGAATGAGGAG	1080	
PR8_PA_pHW2000	AATTATCTTCTGTCAATGGAAGCAAGTACTGGCAGAACTGCAGGACATTGAGAATGAGGAG	1080	
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PR8_PA_NCB1	AAAAATCCAAGACTAAAAATATGA AAAAAACAAGTCAGCTAAAGTGGGCACCTTGGTGAG	1140	
PR8_PA_illumina	AAAAATCCAAGACTAAAAATATGA AAAAAACAAGTCAGCTAAAGTGGGCACCTTGGTGAG	1140	
PR8_PA_pHW2000	AAAAATCCAAGACTAAAAATATGA AAAAAACAAGTCAGCTAAAGTGGGCACCTTGGTGAG	1140	
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PR8_PA_NCB1	AACATGGCACCAGAAAAGSTAGACTTTGACGACTGTA AAGATGTAGGTGATTTGAAGCAA	1200	
PR8_PA_illumina	AACATGGCACCAGAAAAGSTAGACTTTGACGACTGTA AAGATGTAGGTGATTTGAAGCAA	1200	
PR8_PA_pHW2000	AACATGGCACCAGAAAAGSTAGACTTTGACGACTGTA AAGATGTAGGTGATTTGAAGCAA	1200	
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PR8_PA_NCB1	TATGATAGTGATGAACCAGAATTGAGGTCGCTTGCAAGTTGGATTGAGAAATGAGTTCAAC	1260	
PR8_PA_illumina	TATGATAGTGATGAACCAGAATTGAGGTCGCTTGCAAGTTGGATTGAGAAATGAGTTCAAC	1260	
PR8_PA_pHW2000	TATGATAGTGATGAACCAGAATTGAGGTCGCTTGCAAGTTGGATTGAGAAATGAGTTCAAC	1260	
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PR8_PA_NCB1	AAGGCATGCGAACTGACAGATTCAAGCTGGATAGAGCTGATGAGATTTGGAGAAGATGTG	1320	
PR8_PA_illumina	AAGGCATGCGAACTGACAGATTCAAGCTGGATAGAGCTGATGAGATTTGGAGAAGATGTG	1320	
PR8_PA_pHW2000	AAGGCATGCGAACTGACAGATTCAAGCTGGATAGAGCTGATGAGATTTGGAGAAGATGTG	1320	
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PR8_PA_NCB1	GCTCCAATTGAACACATTGCAAGCATGAGAAGGAATTATTTACATCAGAGGTGTCTCAC	1380	
PR8_PA_illumina	GCTCCAATTGAACACATTGCAAGCATGAGAAGGAATTATTTACATCAGAGGTGTCTCAC	1380	
PR8_PA_pHW2000	GCTCCAATTGAACACATTGCAAGCATGAGAAGGAATTATTTACATCAGAGGTGTCTCAC	1380	
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PR8_PA_NCB1	TGCAGAGCCACAGAATACATAATGAAGGGGTGTACATCAATACTGCCTTACTTAATGCA	1440	
PR8_PA_illumina	TGCAGAGCCACAGAATACATAATGAAGGGGTGTACATCAATACTGCCTTACTTAATGCA	1440	
PR8_PA_pHW2000	TGCAGAGCCACAGAATACATAATGAAGGGGTGTACATCAATACTGCCTTACTTAATGCA	1440	
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PR8_PA_NCB1	TC TTGTGCAGCAATGGATGATTTCCAATTAATTTCCAATGATAAGCAAGGTGAGAACTAAG	1500	
PR8_PA_illumina	TC TTGTGCAGCAATGGATGATTTCCAATTAATTTCCAATGATAAGCAAGGTGAGAACTAAG	1500	
PR8_PA_pHW2000	TC TTGTGCAGCAATGGATGATTTCCAATTAATTTCCAATGATAAGCAAGGTGAGAACTAAG	1500	
*****			
PR8_PA_NCB1	GAGGGAAGGCGAAAGACCAACTTGTATGGTTTCATCATAAAAGGAAGATCCCACCTTAAGG	1560	
PR8_PA_illumina	GAGGGAAGGCGAAAGACCAACTTGTATGGTTTCATCATAAAAGGAAGATCCCACCTTAAGG	1560	
PR8_PA_pHW2000	GAGGGAAGGCGAAAGACCAACTTGTATGGTTTCATCATAAAAGGAAGATCCCACCTTAAGG	1560	
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PR8_PA_NCB1	AATGACACCGACGTGGTAAACTTTGTGAGCATGGAGTTTCTCTCACTGACCCAAGACTT	1620	
PR8_PA_illumina	AATGACACCGACGTGGTAAACTTTGTGAGCATGGAGTTTCTCTCACTGACCCAAGACTT	1620	
PR8_PA_pHW2000	AATGACACCGACGTGGTAAACTTTGTGAGCATGGAGTTTCTCTCACTGACCCAAGACTT	1620	
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PR8_PA_NCB1	GAACCACA A AATGGGAGAAGTACTGTGTTCTTGAGATAGGAGATATGCTTTAAGAAGT	1680	
PR8_PA_illumina	GAACCACA A AATGGGAGAAGTACTGTGTTCTTGAGATAGGAGATATGCTTTAAGAAGT	1680	
PR8_PA_pHW2000	GAACCACA A AATGGGAGAAGTACTGTGTTCTTGAGATAGGAGATATGCTTTAAGAAGT	1680	
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PR8_PA_NCB1	GCCATAGGCCAGGTTTCAAGGCCCATGTTCTTGATGTGAGACAAATGGAACCTCAAAA	1740	
PR8_PA_illumina	GCCATAGGCCAGGTTTCAAGGCCCATGTTCTTGATGTGAGACAAATGGAACCTCAAAA	1740	
PR8_PA_pHW2000	GCCATAGGCCAGGTTTCAAGGCCCATGTTCTTGATGTGAGACAAATGGAACCTCAAAA	1740	
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PR8_PA_NCB1	ATTAAAAATGAAATGGGGAATGGAGATGAGGCGTTGCTCCTCCAGTCACTTCAACAAATT	1800	
PR8_PA_illumina	ATTAAAAATGAAATGGGGAATGGAGATGAGGCGTTGCTCCTCCAGTCACTTCAACAAATT	1800	
PR8_PA_pHW2000	ATTAAAAATGAAATGGGGAATGGAGATGAGGCGTTGCTCCTCCAGTCACTTCAACAAATT	1800	
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PR8_PA_NCB1	GAGAGTATGATTGAAGCTGAGTCCCTCTGTCAAAGAGAAAACATGACCAAAGAGTCTTT	1860	
PR8_PA_illumina	GAGAGTATGATTGAAGCTGAGTCCCTCTGTCAAAGAGAAAACATGACCAAAGAGTCTTT	1860	
PR8_PA_pHW2000	GAGAGTATGATTGAAGCTGAGTCCCTCTGTCAAAGAGAAAACATGACCAAAGAGTCTTT	1860	
*****			
PR8_PA_NCB1	GAGAACA AATCAGAAAACATGGCCCATGGAGAGTC CCAAAGGAGTGGAGGAAAGTTCC	1920	
PR8_PA_illumina	GAGAACA AATCAGAAAACATGGCCCATGGAGAGTC CCAAAGGAGTGGAGGAAAGTTCC	1920	
PR8_PA_pHW2000	GAGAACA AATCAGAAAACATGGCCCATGGAGAGTC CCAAAGGAGTGGAGGAAAGTTCC	1920	
*****			
PR8_PA_NCB1	ATTGGGAAGGTCTGCAGGACTTTTATTAGCAAAGTCGGTATTCAACAGCTTGTATGCATCT	1980	
PR8_PA_illumina	ATTGGGAAGGTCTGCAGGACTTTTATTAGCAAAGTCGGTATTCAACAGCTTGTATGCATCT	1980	
PR8_PA_pHW2000	ATTGGGAAGGTCTGCAGGACTTTTATTAGCAAAGTCGGTATTCAACAGCTTGTATGCATCT	1980	
*****			
PR8_PA_NCB1	CCACAAC TAGAAGGATTTTCAGCTGAATCAAGAAAACGCTTCTTATCGTTCAGGCTCTT	2040	
PR8_PA_illumina	CCACAAC TAGAAGGATTTTCAGCTGAATCAAGAAAACGCTTCTTATCGTTCAGGCTCTT	2040	
PR8_PA_pHW2000	CCACAAC TAGAAGGATTTTCAGCTGAATCAAGAAAACGCTTCTTATCGTTCAGGCTCTT	2040	
*****			
PR8_PA_NCB1	AGGGACA A ACTGGAACCTGGGACCTTTGATCTTGGGGGCTATATGAAGCAATTGAGGAG	2100	
PR8_PA_illumina	AGGGACA A ACTGGAACCTGGGACCTTTGATCTTGGGGGCTATATGAAGCAATTGAGGAG	2100	
PR8_PA_pHW2000	AGGGACA A ACTGGAACCTGGGACCTTTGATCTTGGGGGCTATATGAAGCAATTGAGGAG	2100	
*****			
PR8_PA_NCB1	TGCCTA AATATGATCCCTGGGTTTTGCTTAAATGCTTCTTGGTTCAACTCCTTCCTTACA	2160	
PR8_PA_illumina	TGCCTA AATATGATCCCTGGGTTTTGCTTAAATGCTTCTTGGTTCAACTCCTTCCTTACA	2160	
PR8_PA_pHW2000	TGCCTA AATATGATCCCTGGGTTTTGCTTAAATGCTTCTTGGTTCAACTCCTTCCTTACA	2160	
*****			
PR8_PA_NCB1	CATGCATTGAGTTAGTTGTGGCAGTGCTACTATTTGCTATCCATACTGTCCAAAAAGTA	2220	
PR8_PA_illumina	CATGCATTGAGTTAGTTGTGGCAGTGCTACTATTTGCTATCCATACTGTCCAAAAAGTA	2220	
PR8_PA_pHW2000	CATGCATTGAGTTAGTTGTGGCAGTGCTACTATTTGCTATCCATACTGTCCAAAAAGTA	2220	
*****			
PR8_PA_NCB1	CCTTGT TTCTACT	2233	
PR8_PA_illumina	CCTTGT TTNNNNN	2233	
PR8_PA_pHW2000	CCTTGT TTCTACT	2233	
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PA_NCB1	-----MEDFVRQCFNPMIVELAEKTMKEYGEDLKIETNKFAAICTHLEVCFMYSDFH	52
PA_pHW2000	SESRY*SKMEDFVRQCFNPMIVELAEKTMKEYGEDLKIETNKFAAICTHLEVCFMYSDFH	59
	*****	
PA_NCB1	FINEQGESIIIVELGDPNALLKHRFEIIIEGRDRTMAWTVVNSICNTTGAEKPKFLPDLYDY	112
PA_pHW2000	FINEQGESIIIVELGDPNALLKHRFEIIIEGRDRTMAWTVVNSICNTTGAEKPKFLPDLYDY	119
	*****	
PA_NCB1	KENRFIEIGVTRREVHIYYLEKANKIKSEKTHIHIFSFTGEEMATKADYTLDEESRARIK	172
PA_pHW2000	KENRFIEIGVTRREVHIYYLEKANKIKSEKTHIHIFSFTGEEMATKADYTLDEESRARIK	179
	*****	
PA_NCB1	TRLFTIRQEMASRGLWDSFRQSERGEETIEERFEITGTMRKLADQSLPPNFSSLENFRAY	232
PA_pHW2000	TRLFTIRQEMASRGLWDSFRQSERGEETIEERFEITGTMRKLADQSLPPNFSSLENFRAY	239
	*****	
PA_NCB1	VDGFEPNGYIEGKLSQMSKEVNARIEPFLKTTPRPLRLPNGPPCSQRSKFLMDALKLSI	292
PA_pHW2000	VDGFEPNGYIEGKLSQMSKEVNARIEPFLKTTPRPLRLPNGPPCSQRSKFLMDALKLSI	299
	*****	
PA_NCB1	EDPSHEGEGIPLYDAIKCMRTFFGWKEPNVVKPHEKGINPNYLLSWKQVLAELQDIENEE	352
PA_pHW2000	EDPSHEGEGIPLYDAIKCMRTFFGWKEPNVVKPHEKGINPNYLLSWKQVLAELQDIENEE	359
	*****	
PA_NCB1	KIPKTKNMKKTSQLKWALGENMAPEKVDFDDCKDVGDLKQYDSDEPELRSIASWIQNEFN	412
PA_pHW2000	KIPKTKNMKKTSQLKWALGENMAPEKVDFDDCKDVGDLKQYDSDEPELRSIASWIQNEFN	419
	*****	
PA_NCB1	KACELTDSSWIELDEIGEDVAPIEHIASMRRNYFTSEVSHCRATEYIMKGVYINTALLNA	472
PA_pHW2000	KACELTDSSWIELDEIGEDVAPIEHIASMRRNYFTSEVSHCRATEYIMKGVYINTALLNA	479
	*****	
PA_NCB1	SCAAMDDFQLIPMISKCRTKEGRRKTNLYGFI IKGRSHLRNDTDVVNFVSMEFSLTDPRL	532
PA_pHW2000	SCAAMDDFQLIPMISKCRTKEGRRKTNLYGFI IKGRSHLRNDTDVVNFVSMEFSLTDPRL	539
	*****	
PA_NCB1	EPHKWEKYCVLEIGDMLLRSAIGQVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQI	592
PA_pHW2000	EPHKWEKYCVLEIGDMLIRSAIGQVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQI	599
	*****	
PA_NCB1	ESMIEAESSVKEKDMTKEFFENKSETWPIGESPKGVEESSIGKVCRTLLAKSVFNSLYAS	652
PA_pHW2000	ESMIEAESSVKEKDMTKEFFENKSETWPIGESPKGVEESSIGKVCRTLLAKSVFNSLYAS	659
	*****	
PA_NCB1	PQLEGFSAESRLLLLIVQALRDNLEPGTFDLGGLYEAIIECLINDPWVLLNASWFNSFLT	712
PA_pHW2000	PQLEGFSAESRLLLLIVQALRDNLEPGTFDLGGLYEAIIECLINDPWVLLNASWFNSFLT	719
	*****	
PA_NCB1	HALS-----	716
PA_pHW2000	HALS*LWQCYLLSILSKKVPCFY	742
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