

	10	20	30	40	50	60	70	
1								gi_6434141
1								gi_1825234
1								gi_4105985
1								gi_1862007
1	ATGGGATTTGAGATTGCAAAGACCAACTCAATCTTATCAAAATTGGCTACTAATGAAGAGCATGGCGAAA							gi_7220183
1	-----							gi_9241836
								consensus
	80	90	100	110	120	130	140	
1								gi_6434141
1								gi_1825234
1								gi_4105985
1								gi_1862007
-1	ACTCGCCATATTTTGATGGGTGGAAAGCATACGATAGTGATCCTTTCCACCCTCTAAAAAACCCCAACGG							gi_7220183
1	-----							gi_9241836
								consensus
	150	160	170	180	190	200	210	
1								gi_6434141
1								gi_1825234
1								gi_4105985
1								gi_1862007
70	AGTTATCCAAATGGGTCTTGCTGAAAATCAGGTAATTAATTATCCTTTATTTATATATTTTTGCAGTTTGA							gi_7220183
1	-----							gi_9241836
								consensus
	220	230	240	250	260	270	280	
1								gi_6434141
1								gi_1825234
1								gi_4105985
1								gi_1862007
140	CCAAACAGACTATTATAATTTTTTTCTGAAACCTCGATGGTGTTAAATTTCTTTTGTAGCTTTGTTTAGA							gi_7220183
1	-----							gi_9241836
								consensus
	290	300	310	320	330	340	350	
1								gi_6434141
1								gi_1825234
1								gi_4105985
1								gi_1862007
210	CTTGATAGAAGATTGGATTAAGAGAAAACCCAAAAGGTTCAATTTGTTCTGAAGGAATCAAATCATTCAAG							gi_7220183
1	-----							gi_9241836
								consensus
	360	370	380	390	400	410	420	
1								gi_6434141
1								gi_1825234
1								gi_4105985
1								gi_1862007
280	GCCATTGCCAACTTTCAAGATTATCATGGCTTGCCTGAATTCAGAAAAGTACATATCGTACTATAGTCAG							gi_7220183
1	-----							gi_9241836
								consensus

```

          430          440          450          460          470          480          490
1
1
1
1
350 TTAAATTATATTGATAGTATAAAAAATTCGTTAATATATTTAACTAACGAGTTTATTTAATCAGGCGATTG
1
-----

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gi_6434141
gi_1825234
gi_4105985
gi_1862007
gi_7220183
gi_9241836
consensus

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          500          510          520          530          540          550          560
1
1
1
1
420 CGAAATTTATGGAGAAAACAAGAGGAGGAAGAGTTAGATTTGATCCAGAAAAGAGTTGTTATGGCTGGTGG
1
-----

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gi_6434141
gi_1825234
gi_4105985
gi_1862007
gi_7220183
gi_9241836
consensus

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```

          570          580          590          600          610          620          630
1
1
1
1
490 TGCCACTGGAGCTAATGAGACAATTATATTTTTGTTTGGCTGATCCTGGCGATGCATTTTTAGTACCTTCA
1
-----

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gi_6434141
gi_1825234
gi_4105985
gi_1862007
gi_7220183
gi_9241836
consensus

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```

          640          650          660          670          680          690          700
1
1
1
1
560 CCATACTACCCAGCGTAAGTATATTTAATTATATATGTGTAATAAAAAAAAAATTAATAATCATCAAAATCATTTTT
1
-----

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gi_6434141
gi_1825234
gi_4105985
gi_1862007
gi_7220183
gi_9241836
consensus

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```

          710          720          730          740          750          760          770
1
1
1
1
630 TTTATTTGTATTACCAAATAAATTGTCTAATTTTCAAGATTGTAACACATTCATCAAAGTACCTAATAAT
1
-----

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gi_6434141
gi_1825234
gi_4105985
gi_1862007
gi_7220183
gi_9241836
consensus

```

```

          780          790          800          810          820          830          840
1
1
1
1
700 ATAAACGATTCAGTATATTAACGATGTATATAATTTAATTCCTTTGGCGGATTTGTCTTTTTATGTTGGG
1
-----

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gi_6434141
gi_1825234
gi_4105985
gi_1862007
gi_7220183
gi_9241836
consensus

```

850 860 870 880 890 900 910

1 AAATACACATCGG.....ATCTGTTTTGGTTTGTGCCTTGATAATAATCGT gi_6434141
 1 gi_1825234
 1 gi_4105985
 1 ATAACACAATTCTA...CAAGAAAAACATACACTTTTACTATATC..T.....ATAAGTAT gi_1862007
 770 CCATCAGAAGAACATTCTGGTGTATTAATTAATTAATTAATTAATAATAGATG..TGTTGTCAATCTTTT gi_7220183
 1 gi_9241836

 consensus

920 930 940 950 960 970 980

1 TA.....GAGC..TCAGCTAAATAATTCAAATTCAAATT... gi_6434141
 49 CGAAAGCGAAAACCGTTTAGCACAGTAAGACTACCTAAAACCTTAG..AGATCTAGCTCCTCTACTCTCC gi_1825234
 1 AAGCAACCAGCTTTTCTAT.AGACAGAAGTAGTAGTCACATATCTATATATTTGATACTTTTATTTT. gi_4105985
 55 TTGAAGCACTACAAA TACTTT. CATCTT....CTTAATTCTCTTCAATATTTAATTTCTTCACTTTTA gi_1862007
 838 TTAAGACAGCGAGAGTTTAATT.AGTCTTAATTACTGGATTATCAGC..CAAGCTCTTTCTTGAATTTTA gi_7220183
 1 gi_9241836
 ---aaa--a--a---t-----ag-----tgg--tc-c-t--a-at-t---ttcttc--tttt--
 consensus

990 1000 1010 1020 1030 1040 1050

35TCAAGCTTCTCTAGCCATAACACAATA.....AAAAA TACTGACCTTTTTTTCTTT gi_6434141
 117 ATAGACTTTGAT.AGATTCCTCACTGCATTGCAAGG.....ATTTT TTAGGCATTTAA gi_1825234
 66CTCCAATAT...TTTTTCACTTTAAACTCGTTAAGA..... gi_4105985
 119TTAAGCTCATTAAGGA AAAAAAATGGGATTTGAGTGTGCA..... gi_1862007
 905 TTATTCTTATATTAAACACATGATAGCATAATATCTTTCTTTTGTGGAATCAGCTTGTTCGTGAAGCTT gi_7220183
 1 gi_9241836
 -----t-aac-c-t-----at-a-a-a-----c-----t-tt-----
 consensus

1060 1070 1080 1090 1100 1110 1120

87 CGCATAC AAGATTACTAAGAAAGAGACAATGGGAATCTTGTCTAAGATTGCTACAACAATGGCCACGGCG gi_6434141
 169 AAAATGGGTTTACTTTGAGCAACCAACAGCAACTGTTGTCTAAGATTGGCAACAGGCGATGGCCACGGCG gi_1825234
 100 AAAATGGGATTGAGAATGAGAAGAACAACCTC GATCTTGTCTAAGCTCGCTACTAATGAAGAACATGCTG gi_4105985
 160AAGAACAACGCAATCTTGTCA AAGCTGGCTACTAACGAAGAACATGGCG gi_1862007
 975 TGTATTCACACTTATAAAAACAACAAAAATAA AATCTGGTGGTAATTGATTAAAGAGAGAAAATATAAAA gi_7220183
 1 gi_9241836
 -g-at--a---t-----a--aagaa-aa---aatcttgctc-aag-t-gctac-aacga-ga-catggcg
 consensus

1130 1140 1150 1160 1170 1180 1190

157 AAGACTCGGCTTACTTCGACGGGTGGAAGGCATTTGATAGGAACCCCTTTTCACCCAACTCAAAAATCCTGG gi_6434141
 239 AAAACTCTCCGTACTTTGATGGCTGGAAGGCTTATGACAGTGATCCTTTTCACCCCAACAAGAACCTAA gi_1825234
 170 AAAACTCGCCGATTTTCGATGGATGGAAGGCATACGATAACGATCCTTTTCACCCTTTGAAGAACCTAA gi_4105985
 209 AAAACTCCCATATTTTGTGGTGGAAAGCATACGATAACGATCCTTTTCACCCCTTGAAGAACCTAA gi_1862007
 1045 AATAATAGTCAAAATAGACTAATAAGGAAAGAAATAAA...AATAACA..CAAAATACTAAAAA AAAGAA gi_7220183
 1 gi_9241836
 aaaactc-ccatattttgatggatggaaagcat-cgataa-gatccttttcacc--t-aagaaccctaa
 consensus

1200 1210 1220 1230 1240 1250 1260

227 GGGTGTCAATCAACTTTGGTCTTGCAGAGAATCAGCTTTGCTTCGATTTGATCAAGGATTTGGATTACCAAA gi_6434141
 309 TGGGGTTATCCAGATGGGTCTTCGAGAAAATGAAAATGTGTTTTGATTTGATCCAAGAGTGGGTTCTGAAC gi_1825234
 240 TGGTGTATCCAAATGGGTCTTGTGAAAATCAGCTTTGTTTTGACTTGTATAGAGGAATGGATTAAAGAGA gi_4105985
 279 TGGAGTTATCCAGATGGCCCTTGTGAAAATCAGCTTTGTTTTGACTTGTATAGAAAGTGGATTAAAGAGA gi_1862007
 1110 TTAAGGTATAGTGGTCT.....ATTATTGAGAACTTTTTTTGAAGAATTGAAACCCACTTTAATTCTTGC gi_7220183
 1 gi_9241836
 tgg-gttatccagat-ggtcttgc-gaaaat-agctttgTTTTgacttgat--aaga-tggatt---ag-
 consensus

297 AACCCATATGCATCAATTGACACAG...CTGAAGGTGTTGAAGTC TTCAAAGA TATTGCTATCTTTCAGGA gi_6434141
 379 AATCCAGAAAGCCTCAATTGACACAG...CAGCAGGAGTAAATGAA TTCAAAGA CATAGCCATCTTTCAGGA gi_1825234
 310 AATCCAAACGCTTCAATTGACACCA...CTGAAGGAATCAAATCTTTCAGGGCCATTGCCAACTTTCAGA gi_4105985
 349 AACCCAAAAGCCTTCAATTGTTCCA...ATGAAGGAATCAAATCATTTCAAAGGCATTGCCAACTTTCAGA gi_1862007
 1175 TTGACC...CGTGACCATTGCTTATTCGAGGTAAAAATAAAATTTCAAACATTGACATATGACTTGTTAGAGAG gi_7220183
 1 aacca-a-gc-tc-atttgc-c-a----gaagg-at-aa--c-ttcaagg-cattgcc-a-ctttcagga gi_9241836
 consensus

365 CTATCATGGCCTCCCGGAATTTAGACAGGCCGTGGCAAAGTTTATGGGAAAGGAGAGAGGC...A gi_6434141
 447 TTATCATGGATTGCCAGAATTCAGAAATGCTGTTACAAACTTTATGGGAAAGAGTGAAGGAAAT...C gi_1825234
 378 TTATCACGGCCTACCTGAATTCAGAAAGACTATTGCAAAAATTTATGGAAAAAACAA...GAGGGGAAA gi_4105985
 417 TTATCACGGCTTGCCTGAATTCAGAAAGACTATTGCGAAGTTTATGGAGAA...AACAAAGAGGGGAA gi_1862007
 1243 TAATTACCACAAAGTCAAAATTTGTTACTCTGTCTCGTTATTTTCATTAGGATCGATAAAGATAACATCTAA gi_7220183
 1 ttatcacggcttgcc-gaattcaga-a-gctggttgcaaaatztatggagaa---a-aa-a-ga-----a gi_9241836
 consensus

430 GGGTAACATTTGATCCAGAT.....CGTATAGTTATGGTGG.....CGGAGCAAAGTG gi_6434141
 512 GTGTACATTTGACGCCGAC.....CGGATTGTTATGAGCGG.....AGGAGCTACCG gi_1825234
 443 GAGTTACGTTTATCCAGAG.....AGAGTAGTTATGGCTGGTGGTGCA...ACTGGA... gi_4105985
 482 GAGTTAGATTTGATCCAGAA.....AGAGTAGTTATGGCTGGTGGTGCC...ACTGGAGGCAA gi_1862007
 1313 CATATATATCTTTTTTATTAGTACTTGTATTTTTTAGTAAAAGCACGTTATACATTTTAAATAGTCAA gi_7220183
 1 gagttacatttgatccaga-----g-gtagttatgg-tgg-----a--ag---c-a gi_9241836
 consensus

478 GAGCTAACGAGCTTATCATGTTTTGCTTAGCCAATCTGGCGATGCTTTTCTTGTGCCTTCACTTATTA gi_6434141
 560 GAGCTCATGAGACGATCGCTTTTTGCTTGGCTGATCTGGGGATGCATTTCTGGTGCCTGTTCCTTATTA gi_1825234
 493 .GCAAACGAAAATAATATTTTTGTTTGGCTGATGCAGGGCGATGCATTTTAGTACCTTCACTATACTA gi_4105985
 537 TGAATC.....AATATATTTTTGTTTGGCTGATCAGGGCGATGCATTTTAGTACCTTCACTATACTA gi_1862007
 1383 TTGTTGCATATATAGTATATATTTT....GCTAAGTCTAATAACAATAATTTTGGCAATGACTA gi_7220183
 1 --gct---a--t-attatattttgtttgctgat-c-ggcgatgcatttttagtacct-cacc-tacta gi_9241836
 consensus

548 TGCAGCATTGACCGTGATCTGTCATGGCGCCTGGGGTACAAAATTGTCCAGTTCAGTGCAGCATCTCC gi_6434141
 630 TCCAGGTTTTGACAGAGATTTGGGTGGCGAACGGGAGTGCAACTGATACAGTTCCTGTGACAGCTCC gi_1825234
 561 CCCAGCATTAAACCGGGACTTAAGATGGAGAAGCTGGAGTACAACCTATTCCAATTCCTGCGACAGCTCC gi_4105985
 600 CCCAGCATTAAACAGAGATCTAAGATGGAGAAGCTGGTGTACAACCTATTCCAATTCAGTGTGAGAGCTCC gi_1862007
 1449 ATGCAGATTAAACAGAGATTTAAGATGGAGAAGCTGGAGTACAACCTATTCCAATTCAGTGTGAGAGCTCC gi_7220183
 1 ATTTAAACAGAGATTTAAGATGGAGAAGCTGGAGTACAACCTATTCCAATTCAGTGTGAGAGCTCC gi_9241836
 cccag-aTTtAACaGaGAttTaagaTGGaGaActGGaGTaCAAcTtAtTCCaATTcactGtGA-AgCTCC consensus

618 AACCACTTCAAAATAACGAGAGAAGCACCTGGAGGCAGCTTACGAAAGGGCCCAAGAAAGCAGCATCAACA gi_6434141
 700 AACCAATTTGAAAGTACCAGAGCAGCTTTGGAAGCTGCCATATGAGAAAGCTCAGAAGGGCAAACATCAGAG gi_1825234
 631 AACCAATTTCAAATCACTACAAAAGCTGTGAATGAAGCAATATGAAAATGCCAGAAATCAAACATCAAAG gi_4105985
 670 AACCAATTTCAAATCACTACAAAAGCAGTAAAAGAAGCTATGAAAATGCCAAAAATCAAACATCAAAG gi_1862007
 1519 AATAATTTCAAAATTACTTCAAAGCAGTAAAAGAAGCAATATGAAAATGCCAAAAATCAAACATCAAAG gi_7220183
 65 AATAATTTCAAAATTACTTCAAAGCAGTAAAAGAAGCAATATGAAAATGCCAAAAATCAAACATCAAAG gi_9241836
 AACAAAtTTCaAAAtTActacAaaAGCagTaaAaGaaGC-TAtGaaAatGCcCAaaAatCaAaCATCAaag consensus

1690 1700 1710 1720 1730 1740 1750

688 TCAAAGGCTTGATCAATAACA AACCC TCGAATCCACTAGGCACA AACTTTGGACAGAGACACACTTAAAAAG gi_6434141
770 TAAAGGCTTGCTCATTACCAACCCCTCAAATCCCTTGGGTACTGTCCCTTGACCGAGATACCTCAGAAAG gi_1825234
701 TCAAAGGCTTGATTTTGACCAACCCATCAAATCCATTAGGCACCCTTTGGACAGAGACACACTGAAAAA gi_4105985
740 TAAAGGCTTGATTTTGACCAACCCATCAAATCCACTAGGCACCCTTTGGACAAAACACACACTGAAAAAG gi_1862007
1589 TAAAGGCTTGATTTTGACCAATCCATCAAATCCATTGGGCACCCTTTGGACAAAAGACACACTGAAAAAG gi_7220183
135 TAAAGGCTTGATTTTGACCAATCCATCAAATCCATTGGGCACCCTTTGGACAAAAGACACACTGAAAAAG gi_9241836
TaAAaGGcTTGaTttTgACcAAcCCaTcAaATCCatTgGGcACcacttTgGACaaAgAcACaCTgAaAAg consensus

1760 1770 1780 1790 1800 1810 1820

758 CTTAGTGAGCTTTCATCAATGACAAGAACATTCACCTTGTATGCGACGAGATTTATGCGGCCACTGCCCTC gi_6434141
840 TTCAGTGACATTCATCAACGAAAAGAAAATCCACCTAGTCTGCGATGAAATCTATGCTGCCACCGTGTTTC gi_1825234
771 TTTCTTGACCCTTCCACCAACCAACACAACATCCACCTCGTCTGCGACGAAATTTACGCGCAACTGTCTTT gi_4105985
810 TCTCTTGAACTTCCACCAACCAACACAACCTCCACCTTGTGTGCGACGAAATCTACGCTGCCACTGTCTTT gi_1862007
1659 TGTCTTGAGTTTCCACCAACCAACACAACATCCACCTTGTGTGACGAAATCTACGAGCCACTGTCTTT gi_7220183
205 TGTCTTGAGTTTCCACCAACCAACACAACATCCACCTTGTGTGACGAAATCTACGAGCCACTGTCTTT gi_9241836
tttctTGAgcTTCaCaaAccAacAcAAcaTcCACCTtGtTtGcGAcGAAATcTAcGC-GCcAcTgTctTt consensus

1830 1840 1850 1860 1870 1880 1890

828 AGCTCTCCTAAGTTACAGAGCGTGTGCTGAAGTCAATCAAGAAA.....TGGACTGCAATCGTGACC gi_6434141
910 AGTCAGCCAAAGTTTCATAAGCATAGCCGAGATCATAGAGGA.....AAACATCGGATGCAACCGCAATC gi_1825234
841 AATACACCTCAATTCGTCAGCATGCTGAAATCTCAACG...ACGAAATGAGCCATTGCAACAAAAGATT gi_4105985
880 GACATGGCTCAATTCGTCAGTATGCTGAAATCCTAGAAACAACGAAATGAGTCAATGCAACAAAAGATT gi_1862007
1729 GACACGCCTCAATTCGTCAGTATGCTGAAATCCTCGATGAACAGGAAATGACTTACTGCAACAAAAGATT gi_7220183
275 GACACGCCTCAATTCGTCAGTATGCTGAAATCCTCGATGAACAGGAAATGACTTACTGCAACAAAAGATT gi_9241836
gacacgCCTcaaTTCgtcAGcaT-GCtGAaATccTcgA-Ga--a-gaaatgacttacTGCAACaaagAtt consensus

1900 1910 1920 1930 1940 1950 1960

889 TCATTCATATCATTTACAGCTTGTCTAAGGACATGGGGCTCCCTGGCTTTAGAGTTGGCATTGTGTACTC gi_6434141
974 TTATTCACATTGTGTACAGTCTTTCAAAGACATGGGGTTCCTGGCTTTCAGGGTTGGCATTGTTATATTC gi_1825234
908 TGGTTCAATATTGTATACAGTCTTTCAAAGACATGGGGTTCCTGGATTTAGAGTCGGAATCGTGTATTC gi_4105985
950 TGGTCCACATTGTCTATAGTCTTTCAAAGACATGGGGTTCACAGGATTTAGAAATGGAATATATATTC gi_1862007
1799 TAGTTACATCGCTACAGTCTTTCAAAGACATGGGGTTCACAGGATTTAGAGTCGGAATCATATATTC gi_7220183
345 TAGTTACATCGCTACAGTCTTTCAAAGACATGGGGTTCACAGGATTTAGAGTCGGAATCATATATTC gi_9241836
TagTtCaATcgTcTAcAGtcTtTcAAaGACATGGGgtTaCC-GGaTTtAGagTcGGaATcaTaTATTC consensus

1970 1980 1990 2000 2010 2020 2030

959 GTTTAATGATACAGCTGTGAATTGCGGCCGCAAGATGTCGAGCTTCGGTTAGTCTCTTCGCAGACTCAG gi_6434141
1044 CTACAATGACGCTGTGTTAATTGCGCACGAAAGATGTCGAGTTTGGATTGGTTTCGACACAACCTCAG gi_1825234
978 ATTCACGATGCCGTGTTAATTGTGCTAGAAAAATGTCGAGTTTCGGTTAGTTCCACTCAAAACAAA gi_4105985
1020 TTTCAACGATGCTGTGTTAGTTGCTAGAAAAATGTCGAGCTTCGGTTAGTTTCACGCAGAGGCAG gi_1862007
1869 TTTTAAACGACGATGTCGTTAATTGTGCTAGAAAAATGTCGAGTTTCGGTTAGTTATCTACACAACGCAA gi_7220183
415 TTTTAAACGACGATGTCGTTAATTGTGCTAGAAAAATGTCGAGTTTCGGTTAGTTATCTACACAACGCAA gi_9241836
tTttAAcGAcgctGtcGTTaATtGtGctaGaAAaATGTCGAGtTtCGGtTtAGTtTcTcaCaCAaACgCAa consensus

2040 2050 2060 2070 2080 2090 2100

1029 TACTTGCTTGCTTCAATGCTCTCTGATGATGAGTTTGTGCGATAACTTTCTCGTGGAGACTCTCAAGAGGT gi_6434141
1114 CATCTGATTGCATCAATGCTGTGACACAATGAGTTTGTGGAGAGATTTATAGCACAAAGTGTAAAAAGGC gi_1825234
1048 TATTTGCTCGCTGAGATGTTATCYGACGAAAAATTCGTCTCAAAATTTCTAGCTGAAAAGCTCAAAAGAGGT gi_4105985
1090 CATTTCCTCGCTGCGATGCTCAACGACGAAAAATTCGTCTCAATTAACCTCGCAGAAAAGTGGAGGAGGC gi_1862007
1939 TATTTTAAAGCGCAATGCTATCGGACGAAAAATTCGTCTCAATTTCTAAGAGAAAAGCGCGATGAGGT gi_7220183
485 TATTTTAAAGCGCAATGCTATCGGACGAAAAATTCGTCTCAATTTTCTAAGAGAAAAGCGCGATGAGGT gi_9241836
tAttt-cTcGC-gcaATGcTatc-GAcgAaaAaTtCgTcgatAatTttcTagcagAaAgcgCgAagAGGT consensus

2110 2120 2130 2140 2150 2160 2170
 1099 TAGCTAAGAGACACATAATTTACCAAGGGACTTGAACAAGTGGAAATCAAC TGCTTGAAAAACAATGC gi_6434141
 1184 TGAACAACAGGCACATGCGCTTCAATGAGCTTGGCTCAAGTGGCAACAAGCTGCTTGAAAGACAATGC gi_1825234
 1118 TGGCGAAAAGGCACAAACATTTACTAACGGACTCGAAGAAGTGGAAATTAATGCTTGAGAAACAATGC gi_4105985
 1160 TAGATAATAGGCACAAACATTTACCGATGGACTAGAGGAAGTAGGCATTAATGCTTAAAAACAATGC gi_1862007
 2009 TAGGTAAGGCACAAACATTTACTAATGGACTTGAAGTAGTGGAAATTAATGCTTGAAAAATAATGC gi_7220183
 555 TAGGTAAGGCACAAACATTTACTAATGGACTTGAAGTAGTGGAAATTAATGCTTGAAAAATAATGC gi_9241836
 TaggtAaaAGgCACAaacatTTtACTaatGgaCTtGaagaAGT-GGAAttAaaTGCTTgAaaAacAATGc consensus

2180 2190 2200 2210 2220 2230 2240
 1169 GGGTCTTTTTTTTGGATGGACTTGCCTATCTGCTTAAGGAAAAACAATTAGAAGGTGAAATGCTCTG gi_6434141
 1254 CGGTCTTTTTCGTATGGATGGACTTGCCTAGGCTGCTCAAGGAGCAGACGTTCGAAGCTGAGATGGATTG gi_1825234
 1188 TGGACTTTTCTGTTGGATGGATTTGCGAACCCTTTTGAACAGTCAAAATTTTCGACGCTGAAATGTCATTA gi_4105985
 1230 AGGACTTTTTTGTGGATGGACTTGCAAAACCTTTTAAAGGACTCCACATTCGATTCGAAATGTCGTTA gi_1862007
 2079 GGGGCTTTTTTGTGGATGGATTTGCCTCCACTTTTAAAGGAAATCGACTTTTCGATAGCGAAATGTCGTTA gi_7220183
 625 GGGGCTTTTTTGTGGATGGATTTGCCTCCACTTTTAAAGGAAATCGACTTTTCGATAGCGAAATGTCGTTA gi_9241836
 gGGgCTTTTTtgtTGGATGGAtTTGCgtc-aCTttTaAgggAatcgAc-TTcGAtg-cGAaATgtcgtTa consensus

2250 2260 2270 2280 2290 2300 2310
 1239 TGGCGCACCAATTGTCACAGGATGTGAAGCTCAATGTTTCGCTGGCTCTTCGTTTCAGTGTACTGAGCGTG gi_6434141
 1324 TGGCGTACAAATAATCCATGAAGTTAAGCTCAATGTGTCAACAGGTTCTTCGTTTCACTGCCCGAGCCGG gi_1825234
 1258 TGGAAAGTTATTATAAACGACGTGAAGCTTAATGTCTCGCTGGATCTTCAATTTGATGTCAAGAGCCAG gi_4105985
 1300 TGGAGGGTATTATAAACGATGTGAAGCTCAATGTCTCGCCAGGATCTTCAATTTGATGTCAAGAACCGG gi_1862007
 2149 TGGAGAGTTATTATAAACGATGTGAAGCTTAACGTCTCGCTGGATCTTCGTTTGAATGTCAAGAGCCAG gi_7220183
 695 TGGAGAGTTATTATAAACGATGTGAAGCTTAACGTCTCGCTGGATCTTCGTTTGAATGTCAAGAGCCAG gi_9241836
 TGGagagttATtaTaaAcGAtGT-AAGCTtAAtGTcTCgCCtGGaTCTTCgTTTgA-TGtcaaGAgCCaG consensus

2320 2330 2340 2350 2360 2370 2380
 1309 GTTGGTTTAAAGGTTTGTTCCTTTCCTAACATGGATGATGACACATGCAAGTTGCACTAAACCGAATTGCCGC gi_6434141
 1394 GCTGGTTCAAGAGTTTGTTCCTTTCCTAACATGGATGACAAGACCATGGAAGTTGCTTTGACACGAATCCGAAC gi_1825234
 1328 GATTTTTCAGAGTTTGTTCCTTTCCTAACATGGATGATGAAACTGTGGATATTGCATTAGCGAGGATTCGGAG gi_4105985
 1370 GATGGTTCAAGGTTTGTTCCTTTCCTGAATATGGATGATGAAACAGTGGATATCGCGCTCCCGAGGATTCGGAG gi_1862007
 2219 GGTGGTTCAAGAGTTTGTTCCTTTCCTAACATGGATGATGAAACGGTTGATATTGCGCTCCCGAGGATTCGGAG gi_7220183
 765 GGTGGTTCAAGAGTTTGTTCCTTTCCTAACATGGATGATGAAACGGTTGATATTGCGCTCCCGAGGATTCGGAG gi_9241836
 GgTggtTtC-GaGTTTgtTTtGC-AAATATGGATGAtggaACggTggAataTtGCgcT-gcgaGgAttcggag consensus

2390 2400 2410 2420 2430 2440 2450
 1379 ATTTGTCAACAGGATAAGGAAAGTGAGAAACCAACCAAGAAACGTTGGC.....ACCAAG gi_6434141
 1464 CTTTGTGCTACAAGACAAGGAAGCAATTTGTGCCGAGGAAAGCAAC.....AGGTTATGGAAGC gi_1825234
 1398 GTTTGTGGTGTAAAGGAAAGTGGAGATGAGACAACCGCATGGAGAAGAAGCAGCAATGGAAAGAAGC gi_4105985
 1440 GTTTGTAGGTGTTAAGAAAAGTGGAGATGAATCGAATGCGATGGAAAAGAAGCAACAATGGAAGAAAGAAAT gi_1862007
 2289 GTTTCGTAGGTGTTGAGAAAAGTGGAGATAAATCGAGTTCGATGGAAAAGAAGCAACAATGGAAGAAAGAAAT gi_7220183
 835 GTTTCGTAGGTGTTGAGAAAAGTGGAGATAAATCGAGTTCGATGGAAAAGAAGCAACAATGGAAGAAAGAAAT gi_9241836
 gTTtGTaggtgttGAgAaaagtggagataaatCgAgtgcGAtggaaaagaagcaacaatggaagaAgaat consensus

2460 2470 2480 2490 2500 2510 2520
 1434 AATCTTCGCTCAGCTTCTCATCGA.GGATCTACGAAACAGGTGTGATGTCGCCGCACATGATGCTCCT gi_6434141
 1524 AACCTTAGGCTCAGCTTTTTCAGTCTCGCGCAATGGATGACAACATGATGCTCCTCGTGCATGATGCTCCT gi_1825234
 1468 AATTTACGACTTAGTTTCCCAAAA....AGAATGTACGATGAAAAGTGTAAATA...ATTTGTCACCACTT gi_4105985
 1510 AATTTACGACTTAGTTTTCGAAA....AGAATGTACGATGAAAAGTGTTTT.....GTCACCACTT gi_1862007
 2359 AATTTACGACTTAGTTTTCGAAA....AGAATGTATGATGAAAAGTGTTTT.....GTCACCACTT gi_7220183
 905 AATTTACGACTTAGTTTTCGAAA....AGAATGTATGATGAAAAGTGTTTT.....GTCACCACTT gi_9241836
 AAttTg-GacTtAGtTTtTtCgaaa----agaatgtAtgAtgaaagtgtTttt-----GtcacCaCtT consensus

1503 CACTCTCCAATTCCCCAGTCGCCTCTCGTCCGGGCAAGGACTTAAAAAGAGGAAATATTATATTATTCTAT gi_6434141
 1594 CATAcaccGATACCCcAGTCGCCTCTTGTTCGAGCCACTTAGA GAAGTGA CTGATCTCCcAGCTACAAAAT gi_1825234
 1531 TCATCTCTTATCCCTCACTCACCACTCGTTTCGAGCTAGAAATTAAAAcGGAGGAATTAGTATTATTTTT gi_4105985
 1567 TCGTCACC AATTCCCAATCCCCATTAGTTTCGCTAGAAA..TTAAAAcGGAAAGGAAGAATATTAAATTTTT gi_1862007
 2416 TCGTCACC TATCCCTCCCTCACCAATTAGTTTCGTTAAG..... gi_7220183
 962 TCGTCACC TATCCCTCCCTCACCAATTAGTTTCGTTAAG..... gi_9241836
 tcgtCaCC-ATtCctCacTCaCCatT-GTtCG---aa-----aaaa-gg--g-----t--t---t consensus

1573 CTAC.....TCAAAAAATAAGTGGTGATTCCA.....CGAAGTAACTGTCATTTTTTCCcAGTA gi_6434141
 1664 GTTG.....ATCATGATGCATTTA.....TTCC..... gi_1825234
 1601 ATTTTT...ATATAAGAAGAAGA.....TAAAGGAAAAAGAAAAGAAGAAGGTAGTAGAA gi_4105985
 1635 GTTTTTTATATGTAAAACAAAAATAGTATACTAATAGTAATTAAGAAGATAAAAAATAAGAATGTAGGAGGA gi_1862007
 2453 gi_7220183
 999 gi_9241836
 -t-----a----- consensus

1627 GCG.TGGGTTCTGTCAcCTTTTTTGTGGGACTG....CTAGATTTAAATTAGCGTGTTTTcACTGCGAAAA gi_6434141
 1687 CCCTTAGTTTCTGGATTAATAATTGTTTCATT.....ATTTCCTCGTGG.....AATTTTGAG.. gi_1825234
 1652 TGATTCCTTTCAGAAAAAATTTGTTATATAGTATGATTTACTGTACTGAT.....CTATTGTGAC.. gi_4105985
 1705 GGATTCCTTTCAGAAAAAATTTGTTGTTAGCATCT.ATATGTATTTACTACTGATCTATGTACTTTGAC.. gi_1862007
 2453 gi_7220183
 999 gi_9241836
 ----t---ttc-g---t-----t-----a-----t-t-t-----act-tga--- consensus

1691 GCTAGGGGTGGTAcCTTCTTTAAATTTAATTGATAATTGAACTTTTGTGTTTCATATATGATGATGT.... gi_6434141
 1739 ...TGGTGGATACCTTCTTTcATAGGAAAAAaaaaa gi_1825234
 1713 ...ATC...ATAATTTGTCTAATTAGATGCAAAAAGTCATGTGATCTGATTATGACTGAGGATTTGTTAG gi_4105985
 1772 ...ATCATTATTGCTAGCTAATTGAAATGCAAAAATTAAGTTATGTTACGACCCTT gi_1862007
 2453 gi_7220183
 999 gi_9241836
 -----a---tct--ct-at--aa---a-aa----- consensus

1756TTGATTGTG.....TAATTCATCATA.....TATAGTGGAAAGT gi_6434141
 1771 gi_1825234
 1777 GAAATCAGAAAATGTTCTCAATGATCCTGGAATCTTTTAATTTCTTCGACTTTCTGGATTTGGTACAGGT gi_4105985
 1826 gi_1862007
 2453 gi_7220183
 999 gi_9241836
 ----- consensus

1789 AATAGAATTTCAAAAAAATTT gi_6434141
 1771 gi_1825234
 1847 AGAGTTATGTAACAAGGCTACTTCTAGTTGATAAAATATACTCCAGTTTTTATTTTGGACGTGTGCTGGTA gi_4105985
 1826 gi_1862007
 2453 gi_7220183
 999 gi_9241836
 ----- consensus

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          2950      2960      2970      2980      2990      3000      3010
1810
1771
1917 TGGGATTCCACAATTACTCCTGAAAATCTACATTCATCAACAGCGTATATATTAGTACATCAATCCACGT
1826 .....
2453 .....
999 -----
                                     gi_6434141
                                     gi_1825234
                                     gi_4105985
                                     gi_1862007
                                     gi_7220183
                                     gi_9241836
                                     consensus

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          3020      3030      3040      3050
1810
1771
1987 GTACGCCTAATCCACATCTCAAATCTCAATAAAAAGTACTATCAAAC
1826 .....
2453 .....
999 -----
                                     gi_6434141
                                     gi_1825234
                                     gi_4105985
                                     gi_1862007
                                     gi_7220183
                                     gi_9241836
                                     consensus

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- X non conserved
- X similar
- X conserved
- X all match