

**Bacteria - non redundant**

>tdbD00010839 Buchnera\_aphidicola\_str.\_APS (Acyrtosiphon\_pisum) 107806 Val GAC  
-ACGTTTCGTAGCTCAATT-GGTT-AGAGCGCTACCATGACATGGTAGAA-----GTTAGTGGTTCAAGTCCACTCGAACGTA---  
>tdbD00010840 Buchnera\_aphidicola\_str.\_APS (Acyrtosiphon\_pisum) 107806 Val TAC  
-GGGTGATTAGCTCAGTT-GGT--AGAGCTCCTCCTTTACACGGAGAA-----GTCGGCGGTTTCGAGTCCGTCATCACCCA---  
>tdbD00011132 Buchnera\_aphidicola\_str.\_Bp (Baizongia\_pistaciae) 224915 Val GAC  
-ATGTCCGTAACCTCAGTCAGGT--AGAGTGCCATCATGACATGATGGAA-----GTCAGTGGTTCAATTCCTCGGACATACCA  
>tdbD00011131 Buchnera\_aphidicola\_str.\_Bp (Baizongia\_pistaciae) 224915 Val TAC  
-GGGTGATTAGCTCAATT-GGT--AGAGCATCTCCTTTACACGGAGAA-----GTCGGCGGTTTCGAGACCGTCATCACCCA---  
>tdbD00011039 Buchnera\_aphidicola\_str.\_Sg (Schizaphis\_graminum) 198804 Val GAC  
-ACGTTTCGTAGCTCAATA-GGTT-AGAGCATTACCATGACATGGTAGAG-----GTTAGTGGTTCAAGTCCACTCGAACGTA---  
>tdbD00011038 Buchnera\_aphidicola\_str.\_Sg (Schizaphis\_graminum) 198804 Val TAC  
-GGGTGATTAGCTCAGTT-GGT--AGAGCTCCTCCTTTACACGGAGAA-----GTCGGCGGTTTCGAGTCCGTCATCACCTACCA  
>tdbD00011236 Candidatus\_Blochmannia\_floridanus 203907 Val GAC  
-GCGTCTTAGCTCAGTT-GGTT-AGAGTGCTACCCTGACATGGTAGAG-----GTCGATGGTTTCGAGTCCATTAGAAGCA---  
>tdbD00011237 Candidatus\_Blochmannia\_floridanus 203907 Val TAC  
-GGGTGATTAGCTCAATA-GGT--AGAGTATCTCTTACACGGAGAA-----GTCGGCGGTTCAATCCGCCATCACCTA---  
>tdbD00011030 Chlorobium\_tepidum TLS 194439 Val TAC  
-GGGTCTTAGCTCAGTT-GGTT-AGAGCGACTGGTTTACACCCAGTAG-----GTCGGGGGTTTCGAATCCCTCGGACCCA---  
>tdbD00011127 Coxiella\_burnetii RSA 493 227377 Val TAC  
-GGGTGCTTAGCTCAGTT-GGT--AGAGCTCGCCCTTACAAGCGAAT-----GTCGGGGGTTTCGAATCCCTCAGCACCCA---  
>tdbD00003122 Escherichia\_coli 562 Val GAC  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACACCTTGACATGGTGGGG-----GTCGGTGGTTTCGAGTCCACTCGGACGCACCA  
>tdbD00003123 Escherichia\_coli 562 Val GAC  
-GCGTTCATAGCTCAGTT-GGTT-AGAGCACACCTTGACATGGTGGGG-----GTCGTTGGTTTCGAGTCCAATTGAACGCACCA  
>tdbD00003121 Escherichia\_coli 562 Val TAC  
-GGGTGATTAGCTCAGTT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GTCGGCGGTTTCGATCCCGTCATCACCCACCA  
>tdbD00010864 Escherichia\_coli\_O157H7 83334 Val TAC:  
-GGGTGATTAGCTCAGTT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GGCGGCGGTTTCGATCCCGTCATCACCCACCA  
>tdbD00010845 Neisseria\_meningitidis MC58 122586 Val TAC  
-GGGTGATTAGCTCAGTT-GGT--AGAGTGTCTGCCTTACAAGCAGAAT-----GTCGGCGGTTTCGACTCCGTCATCACCCACCA  
>tdbD00010846 Neisseria\_meningitidis MC58 122586 Val TAC  
-GGGTGATTAGCTCAGTT-GGT--AGAGCGTCTGCCTTACAAGCAGAAT-----GTCGGCGGTTTCGACTCCGTCATCACCCACCA  
>tdbD00011152 Nitrosomonas\_europaea ATCC 19718 228410 Val TAC  
-GGGTGCTTAGCTCAGTT-GGT--AGAGCGTCCCTTACAAGCGAAT-----GTCGGGGGTTTCGATCCCTCAGCACCCACCA  
>tdbD00010893 Pseudomonas\_aeruginosa PAO1 208964 Val TAC  
-GGGTGATTAGCTCAGTT-GGG--AGAGCATCTGCCTTACAAGCAGAGG-----GTCGGCGGTTTCGATCCCGTCATCACCCACCA  
>tdbD00011157 Pseudomonas\_syringae pv. tomato str. DC3000 223283 Val TAC  
-GGGTGATTAGCTCAGTT-GGG--AGAGCAGCTGCCTTACAAGCAGCGG-----GTCGGCGGTTTCGATCCCGTCATCACCCACCA  
>tdbD00010935 Ralstonia\_solanacearum GMI1000 267608 Val CAC  
-GGGTGGTTAGCTCAGC--GGT--AGAGCACTGCCTTACACCGGAGGG-----GTCACAGGTTCAATCCCTGTACCACCCACCA  
>tdbD00010934 Ralstonia\_solanacearum GMI1000 267608 Val TAC  
-GGGTGCTTAGCTCAGTT-GGT--AGAGCGGCGCCCTTACAAGGCGTAG-----GTCGGGAGTTTCGAGCCTCTCAGCACCCACCA  
>tdbD00010920 Rickettsia\_conorii str. Malish 7 272944 Val GAC  
-GGGTGATTAGCTCAGTT-GGTT-AGAGCATTACGTTGACATCGTAAAG-----GTCGGTGGTTTCGAGCCCACTATCACTACCA  
>tdbD00011041 Rickettsia\_prowazekii str. Madrid E 272947 Val GAC  
-GGGTGATTAGCTCAGTT-GGTT-AGAGCATTACGTTGACATCGTAAAG-----GTCAGTGGTTTCGAGTCCACTATCACCCACCA  
>tdbD00011191 Rickettsia\_typhi str. Wilmington 257363 Val GAC  
-GGGTGATTAGCTCAGTT-GGTT-AGAGTATTACGTTGACATCGTAAAG-----GTCAGTGGTTTCGAACCCACTATCACCCACCA  
>tdbD00010943 Salmonella\_enterica subsp. enterica serovar Typhi str. CT18 220341 Val GAC  
-GCGTCTAGCTCAGTT-GGTT-AGAGCACCACTTGACATGGTGGGG-----GTCGATGGTTTCGAGTCCACTTCAGACGCACCA  
>tdbD00010944 Salmonella\_enterica subsp. enterica serovar Typhi str. CT18 220341 Val TAC  
-GGGTGATTAGCTCAGTT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GTCGGCGGTTTCGATACCCTCAGCACCCACCA  
>tdbD00011096 Shigella\_flexneri 2a str. 301 198214 Val GAC  
-GCGTTCATAGCTCAGTT-GGTT-AGAGCACCACTTGACATGGTGGGG-----GTCGGTGGTTTCGAGTCCACTCGGACGCACCA  
>tdbD00010896 Thermotoga\_maritima MSB8 243274 Val CAC  
-GGGTGCGTAGCTCAGG--GGG--AGAGCGCTTCCCTCAGGAGGAGAG-----GTCGAGGTTTCGAATCCCTGCCGCACCCACCA  
>tdbD00010897 Thermotoga\_maritima MSB8 243274 Val GAC  
-GGGTGCGTAGCTCAGT--GGG--AGAGCGCTTCCCTCAGGAGGAGAG-----GTCGAGGTTTCGAATCCCTGCCGCACCCACCA  
>tdbD00010849 Vibrio\_cholerae O1 biovar El\_Tor str. N16961 243277 Val GAC  
-GCGTCTATAGCTCAGTT-GGTT-AGAGCACCACTTGACATGGTGGGG-----GTCGGTGGTTTCGAGTCCACTTCAGACGCACCA  
>tdbD00011225 Wolbachia\_endosymbiont\_of Drosophila\_melanogaster 163164 Val GAC  
-GGGTAATTAGCTCAGTT-GGT--AGAGCACTTGCCTGACGTGCAAGCG-----GTCGTTGGTTTCGAACCCAGTGTACCCA---  
>tdbD00011061 Xanthomonas\_axonopodis pv. citri str. 306 190486 Val TAC  
-GGGTGCTTAGCTCAGC--GGT--AGAGCGTCTCCCTTACAAGGAGAGG-----GTCGGGGGTTTCGAAACCCTCAGCACCCACCA  
>tdbD00010901 Xylella\_fastidiosa 9a5c 160492 Val TAC  
-GGGTGCTTAGCTCAGC--GGT--AGAGCGTCTCCCTTACAAGGAGAGG-----GTCGGGGGTTTCGAAACCCTCAGCACCCACCA  
>tdbD00011118 Xylella\_fastidiosa Temecula 183190 Val TAC  
-GGGTGCTTAGCTCAGC--GGT--AGAGCGTCTCCCTTACAAGGAGAGG-----GCCGGGGGTTTCGAAACCCTCAGCACCCACCA  
>tdbD00011197 Yersinia\_pestis biovar Microtus str. 91001 229193 Val GAC  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACTTGACATGGTGGGG-----GTCGATGGTTTCGAGTCCACTTCGACGCACCA  
>tdbD00011198 Yersinia\_pestis biovar Microtus str. 91001 229193 Val GAC  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACTTGACATGGTGGGG-----GTCGATGGTTTCGAGTCCACTTCGACGCACCA  
>tdbD00011201 Yersinia\_pseudotuberculosis IP\_32953 273123 Val GAC

-GGCTTCTTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGATGGTTCGAGTCCATTAGAACGCACCA  
>tdbD00001132 Acetobacter acetii 435 Ile GAT  
-GGGCTAGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCCCTCCCTGGCCCACCA  
>tdbD00001140 Acholeplasma laidlawii 2148 Ile CAT  
-GGACCCGTAGCTCAGTT-GGTT-AGAGCTACCGGCTCATAACCGGTGCG-----GTCGTTGGTTCGAGTCCAACCGGGTCCACCA  
>tdbD00001161 Acidithiobacillus ferrooxidans 920 Ile GAT  
-GGGCTATAGCTCAGCT-GGCT-AGAGCACACGCTTGATAAGCGTGAG-----GTCAGTGGTTCGAGTCCACTTGGGCCACCA  
>tdbD00005896 Agrobacterium tumefaciens\_str.\_C58 176299 Ile GAT  
-GGGCCCCTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGTAGTTCGAGTCTACCCGGGCCACCA  
>tdbD00005876 Aquifex aeolicus VF5 224324 Ile GAT  
-GGGCTCTAGCTCAGCT-GGTT-AGAGCGTGCCCTGATAAGGGCAAG-----GTCCAGGTTTCGAGTCTGGGAGGCCA---  
>tdbD00005999 Bacillus anthracis\_str.\_Ames 198094 Ile GAT  
-GGGCTATAGCTCAGCT-GGTT-AGAGCGCACGCTTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTTAGGCCACCA  
>tdbD00005972 Bacillus halodurans\_C-125 272558 Ile GAT  
-GGGCTGTAGCTCAGCT-GGTT-AGAGCGCACGCTTGATAAGCGTGAG-----GTCGGTGGTTCGAGTCCACTCAGGCCACCA  
>tdbD00005973 Bacillus halodurans\_C-125 272558 Ile GAT  
-GGGCTGTAGCTCAGCT-GGTT-AGAGCGCACGCTTGATAAGCGTGAG-----GTCGGTGGTTCGAGTCCACTCAGGCCACCA  
>tdbD00001156 Bacillus subtilis 1423 Ile CAT  
-GGACCTTCTAGCTCAGTT-GGTT-AGAGCAGACGGCTCATAACCGTCCG-----GTCGTAGTTCGAGTCTTACAAGGTCCACCA  
>tdbD00001155 Bacillus subtilis 1423 Ile GAT  
-GGGCTGTAGCTCAGCT-GGTT-AGAGCGCACGCTTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTCAGGCCACCA  
>tdbD00001124 Bartonella bacilliformis 774 Ile GAT  
-GGGCTGTAGCTCAGTT-GGTT-AGAGCGCGCTTGATAAGCGTGAG-----GTCGGAGGTTCAAGTCCCTCCAGGCCACCA  
>tdbD00001126 Bartonella henselae 38323 Ile GAT  
-GGGCTGTAGCTCAGTT-GGTT-AGAGCGCGCTTGATAAGCGTGAG-----T-CGGAGGTTCAAGTCCCTCCAGGCCACCA  
>tdbD00001127 Bartonella quintana 803 Ile GAT  
-GGGCTGTAGCTCAGCT-GGTT-AGAGCGCGCTTGATAAGCGTGAG-----GTCGGAGGTTCAAGTCCCTCCAGGCCACCA  
>tdbD00006002 Bdellovibrio bacteriovorus HD100 264462 Ile GAT  
-GGGCTGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAAGTTCGAGTCTTCCAGGCCACCA  
>tdbD00005974 Bradyrhizobium japonicum\_USDA\_110 224911 Ile GAT  
-GGGCTGTAGCTCAGTT-GGTT-AGAGCGCGCTTGATAAGCGTGAG-----GTCGGAAGTTCGAGTCTTCCAGGCCACCA  
>tdbD00001182 Brucella abortus 235 Ile GAT  
-GGGCTGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCCCTCCAGGCCACCA  
>tdbD00001183 Brucella abortus 235 Ile GAT  
-GGGCTGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCCCTCCAGGCCACCA  
>tdbD00005847 Buchnera aphidicola\_str.\_APS\_(Acyrtosiphon\_pisum) 107806 Ile GAT  
-AGGCTGTAGCTCAGTT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCGAGTCCACTCAGGCCCTACCA  
>tdbD00005989 Buchnera aphidicola\_str.\_Bp\_(Baizongia\_pistaciae) 224915 Ile GAT  
-AGGCTGTAGCTCAGCTTGCT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCGAGTCCACTCAGGCCCTA---  
>tdbD00005947 Buchnera aphidicola\_str.\_Sg\_(Schizaphis\_graminum) 198804 Ile GAT  
-AGGCTGTAGCTCAGTT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCGAGTCCACTCAGGCCCTACCA  
>tdbD00001177 Campylobacter jejuni 197 Ile GAT  
-GGGCTATAGCTCAGCT-GGTT-AGAGTGACACCCCTGATAAGGGTGAG-----GTCACAAGTTCGAGTCTTGTAGGCCACCA  
>tdbD00006039 Candidatus Blochmannia floridanus 203907 Ile GAT  
-AGGCTGTAGCTCAGCT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCGAGTCCACTCAGGCCCTA---  
>tdbD00005866 Caulobacter crescentus\_CB15 190650 Ile GAT  
-AGGCTGTAGCTCAGTT-GGTT-AGAGCGTACGCTGATAAGCGTAAAG-----GTCGGCAGTTCGAGTCTGCCAGGCCCTACCA  
>tdbD00001179 Caulobacter vibrioides 155892 Ile GAT  
-AGGCTGTAGCTCAGTT-GGTT-AGAGCGTACGCTGATAAGCGTAAAG-----GTCGGCAGTTCGAGTCTGCCAGGCCCTACCA  
>tdbD00005943 Chlorobium tepidum\_TLS 194439 Ile GAT  
-GGGCTGTAGCTCAGTT-GGTT-AGAGCGCACGCTTGATAAGCGTGAG-----GTCAGTGGTTCGAGTCCACTCAGGCCACCA  
>tdbD00005975 Clostridium tetani\_E88 212717 Ile GAT  
-GGGCTATAGCTCAGCT-GGTT-AGAGCGCACGCTTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTTAGGCCACCA  
>tdbD00006027 Desulfovibrio vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough 882 Ile GAT  
-GGGCTGTAGCTCAGTT-GGTT-AGAGCGCACGCTTGATAAGCGTGAG-----GTCGGAAGTTCGAGTCTTCCAGGCCACCA  
>tdbD00005976 Enterococcus faecalis\_V583 226185 Ile GAT  
-GGGCTATAGCTCAGCT-GGTT-AGAGCGCACGCTTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTTAGGCCA---  
>tdbD00001164 Escherichia coli 562 Ile CAT  
-GGCCCTTAGCTCAGTT-GGTT-AGAGCAGGCGACTCATAATCGCTTG-----GTCGTTGGTTCGAGTCCAGCGGGGCCACCA  
>tdbD00001163 Escherichia coli 562 Ile GAT  
-AGGCTGTAGCTCAGTT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCGAGTCCACTCAGGCCCTACCA  
>tdbD00006012 Geobacter sulfurreducens\_PCA 243231 Ile GAT  
-GGGCTGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAATCGTGAG-----GTCGTTGGTTCGAGTCCAGCCAGGCCACCA  
>tdbD00001133 Gluconacetobacter europaeus 33995 Ile GAT  
-GGGCTAGTATCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGCGGTTCAACTCCCTCCCTGGGCCACCA  
>tdbD00001139 Gluconacetobacter liquefaciens 89584 Ile GAT  
-GGGCTAGTACCTCAGTT-GGTT-AGAGCACGCGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCCCTCCCTGGGCCACCA  
>tdbD00001142 Gluconacetobacter xylinus 28448 Ile GAT  
-GGGCTAGTACCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCCCTCCCTGGGCCACCA  
>tdbD00001188 Haemophilus influenzae 727 Ile CAT  
-CCCCCTTAGCTCAGTT-GGTT-AGAGCAGGCGACTCATAATCGCTTG-----GTCAGTGGTTCGAGTCCGCTAGGGGGGACCA  
>tdbD00001152 Helicobacter pylori 210 Ile GAT  
-GGGCTATAGCTCAGTT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGAGGTTCAACTCCCTCCTAAGGCCACCA  
>tdbD00001158 Lactobacillus casei 1582 Ile GAT  
-GGGCTATAGCTCAGTT-GGTT-AGAGCGCACGCTTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTCAGGCCA---

>tdbD00001151 *Lactobacillus delbrueckii* subsp. *bulgaricus* 1585 Ile GAT  
-GGGCCTGTAGCTCAGCT-GGTT-AGAGCGCAGCCTTGATAAGCGTGAG-----GTCGATGGTTCAAGTCCATCCAGGCCA---  
>tdbD00001162 *Lactobacillus helveticus* 1587 Ile GAT  
-GGGCCTATAGCTCAGCT-GGTTTAGAGCGCAGCCTGATAAGCGTGAG-----GTCGATGGTTCAAGTCCATTTAGGCCA---  
>tdbD00006013 *Lactobacillus johnsonii* NCC\_533 257314 Ile GAT  
-GGGCCTATAGCTCAGCT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGATGGTTCAAGTCCATTTAGGCCA---  
>tdbD00005965 *Leptospira interrogans* serovar *Lai* str. 56601 189518 Ile GAT  
-GGGCCTGTAGCTCAGCT-GGTT-AGAGCACAGCCTGATAAGCGTGGG-----GTCATGTGTTCAAATCACATCAGGCCA---  
>tdbD00001128 *Mycoplasma capricolum* 2095 Ile CAT  
-GGACCTTTAGCTCAGTT-GGTT-AGAGCATCCGGCTCATAACCCGGACG-----GTCATGTGTTCAAGTCCAATAAGGTCCACCA  
>tdbD00001167 *Mycoplasma* sp. 2108 Ile GAT  
-GGGCCTATAGCTCAGTT-GGTT-AGAGCACAGCCTGATAAGCGTGAG-----GTCGGTGGTTCAAGTCCGCTTAGGCCACCA  
>tdbD00005894 *Nostoc* sp. PCC\_7120 103690 Ile GAT  
-GGCCTATTAGCTCAGGT-GGTT-AGAGCGCACCCCTGATAAGCGTGAG-----GTCCCTGGTTTCGAGTCCAGGATGGGCCA---  
>tdbD00006004 *Onion yellows phytoplasma* OY-M 262768 Ile GAT  
-GGGCCTATAGCTCAGTT-GGTT-AGAGCACAGCCTGATAAGCGTGAG-----GTCGGTGGTTCAAGTCCATTTAGGCCACCA  
>tdbD00005898 *Sinorhizobium meliloti* 1021 266834 Ile GAT  
-GGCCCGTAGCTCAGTT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGCAGTTTCGAGTCTGCCCGGGCCACCA  
>tdbD00001143 *Spiroplasma melliferum* 2134 Ile CAT  
-GGACCTTAGCTCAGTT-GGTT-AGAGCATCCGGCTCATAACCCGGATG-----GTCACTGGTTCAAGTCCAGTAGGGTCCACCA  
>tdbD00001150 *Staphylococcus aureus* 1280 Ile CAT  
-GGACCTTTAGCTCAGTT-GGTT-AGAGCTAACGGCTCATAACCCGTCG-----GTCGCGAGTTTCGAGTCTGCAAGGTCCA---  
>tdbD00006008 *Staphylococcus aureus* subsp. *aureus* MRSA252 282458 Ile GAT  
-GGGCCTATAGCTCAGCT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGTGGTTTCGAGTCCACTTAGGCCACCA  
>tdbD00005970 *Streptococcus agalactiae* 2603V/R 208435 Ile GAT  
-GGCGCGTAGCTCAGTT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGTGGTTTCGAGTCCACTCGTGCCCA---  
>tdbD00005971 *Streptococcus mutans* UA159 210007 Ile GAT  
-GGCGCGTAGCTCAGCT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGTGGTTTCGAGTCCACTCGTGCCCA---  
>tdbD00005882 *Streptococcus pyogenes* M1 GAS 160490 Ile GAT  
-GGCGCGTAGCTCAGTT-GGTT-AGAGTGACGCTGATAAGCGTGAG-----GTCGGTGGTTTCGAGTCCACTCGTGCCCA---  
>tdbD00001193 *Synechococcus elongatus* PCC 6301 269084 Ile GAT  
-GGGCTATTAGCTCAGGT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCCCTGGTTCAAGTCCAGGATGGGCCA---  
>tdbD00001195 *Synechocystis* sp. 1143 Ile GAT  
-GGGCTATTAGCTCAGTT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCTCTGGTTCAAGTCCAGAATGGGCCA---  
>tdbD00005955 *Thermoanaerobacter tengcongensis* MB4 273068 Ile GAT  
-GGGCTTATAGCTCAGTT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGATGGTTCAAGTCCATCTAAGGCCACCA  
>tdbD00005874 *Thermotoga maritima* MSB8 243274 Ile GAT  
-GGGCTCGTAGCTCAGTT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGTGGTTTCGAGTCCACCCGAGGCCACCA  
>tdbD00006031 *Thermus thermophilus* HB27 262724 Ile GAT  
-GGGCGATTAGCTCAGCT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGTGGTTCAAGTCCACCATCGGCCACCA  
>tdbD00001166 *Trichodesmium* sp. 1207 Ile GAT  
-GGGCTATTAGCTCAGTT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCCCTGGTTCAAGTCCAGGATAGGCCA---  
>tdbD00001507 *Acholeplasma laidlawii* 2148 Leu CAA  
-CCCGTGTGGCGAAAT--GGTA-GACGCGCTTGACTCAAAATCAAGTAGT-----GAAG-----ACTGTGTGGTTTCGAGTCCGGTACGGGGACCA  
>tdbD00001509 *Acholeplasma laidlawii* 2148 Leu TAA  
-GCCCGGTGGTGAATC-GGTA-GACACGCAGGACTTAAATCCTGTGGCA-----TAAA-----AGCATGTGGTTCAAGTCCGACCCGGGCACCA  
>tdbD00001508 *Acholeplasma laidlawii* 2148 Leu TAG  
-GCGGGTGTGGCGAAAT--GGTA-GACGCACTAGACTTAGGATCTAGCGCT-----TTAC-----GGCATGCAGTTCAAGTCCCTGTACCCGCACCA  
>tdbD00007209 *Acinetobacter* sp. ADP1 62977 Leu CAA  
-CCCAGGTGGTGAATC-GGTA-GACGCGGTGACTCAAAATCCACTGTTT-----GAGA-----GAACGTGTGGTTTCGAGTCCGACCCCTGGGACCA  
>tdbD00007210 *Acinetobacter* sp. ADP1 62977 Leu GAG  
-GCGGTGGTGGTGAATC-GGTA-GACACGCTACCTTGAGGTGGTAGTGT-----TTCG-----GGCGTGGGGTTCAAGTCCCCCTTCCGCACCA  
>tdbD00007211 *Acinetobacter* sp. ADP1 62977 Leu TAA  
-GCCCGGTGGTGAATA-GGTA-GACACAGGGGATTTAAATCCCCCGCC-----TCA-----AAGCGTGCCGTTTCGAGTCCGGCCCGGGCACCA  
>tdbD00007212 *Acinetobacter* sp. ADP1 62977 Leu TAG  
-GGGGCGTGGCGAAAT--GGTA-GACGCACTGGATTTAGGTTCACGCGCC-----GCAA-----GGTGTAAAGTTTCGAGTCTCTTCGCCCCACCA  
>tdbD00001541 *Aeromonas hydrophila* 644 Leu CAG  
-GCGAAGGTGGCGAAT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGCC-----CCC-----GGGTGTGAGGGTTTCGAGTCCCTCTCTTCGCACCA  
>tdbD00006660 *Agrobacterium tumefaciens* str. C58 176299 Leu CAA  
-GCGGGTGTGGTGAAT--GGTA-GACGCGCCGACTCAAAATCCGGTTCC-----GAAA-----GGAGTGTGGTTTCGACCCCGACCACCCGCACCA  
>tdbD00006658 *Agrobacterium tumefaciens* str. C58 176299 Leu CAG  
-GCCAGATGGCGAAT--GGTA-GACGCGCCAGCTTCAGGTGCTGGTACT-----GAAA-----GGGTGTGGAGTTTCGAGTCCCTCTCTTCGGGCACCA  
>tdbD00006661 *Agrobacterium tumefaciens* str. C58 176299 Leu GAG  
--CGGTCTGGCGAAT--GGTA-GACGCGCAGCCTTGAGGTGCTGTGGGG-----CAA-----CCCG-TGGAAGTTTCGAGTCTCTTCGACCCGCACCA  
>tdbD00006659 *Agrobacterium tumefaciens* str. C58 176299 Leu TAA  
-GCCCGCATGGTGAAT--GGTA-AACACATCGACTTAAATGCGCCGCC-----TCT-----GGCTTGCCGTTCAAGTCCGGCTGCGGGCACCA  
>tdbD00006662 *Agrobacterium tumefaciens* str. C58 176299 Leu TAG  
--CGGTATGGCGAAT--GGTA-GACGCATTGGTTTTAGGTACCAACGC-----TTCG-----GCGTGGGAGTTTCGAGTCTCTTACCCGCACCA  
>tdbD00006580 *Aquifex aeolicus* VF5 224324 Leu CAA  
-GCCGTGTGGCGAAT--GGTA-GACGCGGGGATTTAAATCCCTGCCCT-----TCA-----CGGGCGTGGGGTTTCGACTCCCGCCACCCGCACCA  
>tdbD00006581 *Aquifex aeolicus* VF5 224324 Leu CAG  
-GCGGGTGTGGCGAAT--GGTA-GACGCGCCGACTCAGGATCCGGTGCC-----GCAA-----GGGCGTGGGGTTTCGACTCCCGCCACCCGCACCA  
>tdbD00006582 *Aquifex aeolicus* VF5 224324 Leu GAG  
-GCCGAGTGGCGAAT--GGTA-GACGCGCGCTTTCGAGGGGACGGTGCCCT-----TTA-----CGGGCGTGGGGTTTCGACTCCCGCTCCGGCACCA  
>tdbD00006583 *Aquifex aeolicus* VF5 224324 Leu TAA

-GGGGGTGTGGCGGAATT-GGCA-GACGCGGGGACTTAAAAATCCCCTGGGCG-AAA-AGCCCGTGAGGGTTCGACTCCCTCCACCCACCA  
>tdbD00006584 Aquifex aeolicus\_VF5\_224324 Leu TAG  
-GCGGGTGTGGCGGAATT-GGCA-GACGCGCGGACTTAGGATCCGGTGCCC-GTAA-GGGCGTGGGGTTCGACTCCCGCCACCCGACCA  
>tdbD00001543 Azococcus\_sp.\_BH72\_62928 Leu TAA  
-GCCGGGTGGCGGAATC-GGTA-GACACAACGGATTTAAAAATCCTGCGGTAG-GTGA-CTACCGTGCCGGTTCAGTCCGGCCCTCGGCA-  
>tdbD00007213 Bacillus anthracis\_str.\_A2012\_191218 Leu CAA  
-GCCGATGTGGCGGAATT-GGCA-GACGCGCAGACTCAAAAATCGTGTTC-TTCG-GGAGTGTGGTTCGACCCCGACCATCGGTACCA  
>tdbD00007066 Bacillus anthracis\_str.\_Ames\_198094 Leu CAA  
-GCCGATGTGGCGGAATT-GGCA-GACGCGCAGACTCAAAAATCGTGTTC-TTCG-GGAGTGTGGTTCGACCCCGACCATCGGTACCA-  
>tdbD00007065 Bacillus anthracis\_str.\_Ames\_198094 Leu GAG  
-GCGGTGTGGCGGAAC-GGCA-GACGCGCTAGGTTGAGGGCCTAGTGGGG-AAA-CCCG-TGGAGGTTCAAGTCTCTCGGCCGCA-  
>tdbD00007068 Bacillus anthracis\_str.\_Ames\_198094 Leu TAA  
-GCCGGGTGGCGGAACA-GGCA-GACGCGCAGACTTAAAAATCCTGCGGTGG-GTGA-CCACCGTGCCGGTTCGACCCCGCCCTCGGCACCA  
>tdbD00007067 Bacillus anthracis\_str.\_Ames\_198094 Leu TAG  
-GCGGGTGTGGCGGAATT-GGCA-GACGCGCTAGACTTAGGATCTAGCGCC-TTT-GGCGTGGGGTTCGACTCCCTTCACCCGCA-  
>tdbD00007069 Bacillus anthracis\_str.\_Ames\_198094 Leu TAG  
-GCGGGTGTGGCGGAATT-GGCA-GACGCGCAGACTTAGGATCTGGCGCC-TTT-GGCGTGGGGTTCGACTCCCTTCACCCGCA-  
>tdbD00006955 Bacillus\_halodurans\_C-125\_272558 Leu CAA  
-GCCGGTGTGGCGGAATT-GGCA-GACGCGCAGACTCAAAAATCGTGTTC-TTCG-TGGAGTGTGGTTCGACCCCGACCATCGGTACCA  
>tdbD00006956 Bacillus\_halodurans\_C-125\_272558 Leu GAG  
-GCGGTGTGGCGGAAT-GGCA-GACGCGCTAGGTTGAGGGCCTAGTGGGG-TTGA-CCCG-TGGAGGTTTCAGTCTCTCAACCGCA-  
>tdbD00006957 Bacillus\_halodurans\_C-125\_272558 Leu TAA  
-GCCGGGTGTGGGAATT-GGCA-GACACACAGACTTAAAAATCCTGCGGTAG-GTGA-CTACCGTGCCGGTTCAGTCCGGCCCTCGGCACCA  
>tdbD00006958 Bacillus\_halodurans\_C-125\_272558 Leu TAA  
-GCCGGGTGTGGGAATT-GGCA-GACACACAGACTTAAAAATCCTGCGGTAG-GTGA-CTACCGTGCCGGTTCAGTCCGGCCCTCGGCACCA  
>tdbD00006959 Bacillus\_halodurans\_C-125\_272558 Leu TAG  
-GCGGGTGTGGCGGAATT-GGCA-GACGCGCTAGACTTAGGATCTAGTGTCC-TTG-TGACGTGGGGTTCGACTCCCTTCACCCGCA-  
>tdbD00006960 Bacillus\_halodurans\_C-125\_272558 Leu TAG  
-GCGGGTGTGGCGGAATT-GGCA-GACGCGCTAGACTTAGGATCTAGTGTCC-TTG-TGACGTGGGGTTCGACTCCCTTCACCCGACCA  
>tdbD00001530 Bacillus\_subtilis\_1423 Leu CAA  
-GCCGGTGTGGCGGAATT-GGCA-GACGCGCAGACTCAAAAATCGTGTTC-TTCT-GGAGTGTGGTTCGACCCCGACCATCGGTACCA  
>tdbD00001527 Bacillus\_subtilis\_1423 Leu CAG  
-GCCGATGTGGCGGAATT-GGCA-GACGCGCTAGAAATCAGGCTCTAGTGTCT-TTAC-AGACGTGGGGTTCAGTCCCTTCATCCGCACCA  
>tdbD00001532 Bacillus\_subtilis\_1423 Leu GAG  
-GCGGTGTGGCGGAAT-GGCA-GACGCGCTAGGTTGAGGGCCTAGTGGGTAGT-GGTATAACCCG-TGGAGGTTCAAGTCTCTCGGCCGCA-  
>tdbD00001528 Bacillus\_subtilis\_1423 Leu TAA  
-GCCGGGTGTGGGAATT-GGCA-GACACACAGACTTAAAAATCCTGCGGTAG-GTGA-CTACCGTGCCGGTTCAGTCCGGCCCTCGGCA-  
>tdbD00001531 Bacillus\_subtilis\_1423 Leu TAG  
-GCCGGTGTGGCGGAATT-GGCA-GACGCGCTAGACTTAGGATCTAGTGTCT-TTA-TGACGTGGGGTTCAGTCCCTTCACCCGCA-  
>tdbD00006447 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308 Leu CAA  
-GCCGGTGTGGCGGAATT-GGCA-GCGCGCAGACTCAAAAATCGTGTTC-TTCT-GGAGTGTGGTTCGACCCCGACCATCGGTACCA  
>tdbD00006449 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308 Leu GAG  
-GCGGTGTGGCGGAAT-GGCA-GACGCGCTAGGTTGAGGGCCTAGTGGGTG-AAT-AACCGTGGAGGTTCAAGTCTCTCGGCCGCA-  
>tdbD00006453 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308 Leu TAG  
-GCGGGTGTGGCGGAATT-GGCA-GACGCGCTAGACTTAGGATCTAGTGTCT-TTAC-GACGTGGGGTTCGAGTCCCTTCACCCGCA-  
>tdbD00007215 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27\_281309 Leu GAG  
-GCGGTGTGGCGGAAT-GGCA-GACGCGCTAGGTTGAGGGCCTAGTGGGG-AAA-CCCG-TGGAGGTTCAAGTCTCTCGGCCGACCA  
>tdbD00007057 Bacteroides\_thetaiotaomicron\_VPI-5482\_226186 Leu CAA  
-GCCAGATGGCGGAATC-GGTA-GACGCGCTGGTCTCAAACACAGTGGAT-TCAC-TTCCATCCCGGTTTCGACCCCGGTTCTGGGTACCA  
>tdbD00007055 Bacteroides\_thetaiotaomicron\_VPI-5482\_226186 Leu CAG  
-GCCAGATGGCGGAAT-GGTA-GACGCGCAGCTTTTCAGGTGCGTGTGC-GAGA-GGCATGCAGGTTTCGAGTCTCTCTGTTGGA-  
>tdbD00007056 Bacteroides\_thetaiotaomicron\_VPI-5482\_226186 Leu GAG  
-GGAGAGGTGGCGGAATT-GGTA-GACGCGCTACTTTGAGGGGGTAGTGACA-GTTA-TGTCGTGGGAGTTCGAGTCTCTCTCTCA-  
>tdbD00007059 Bacteroides\_thetaiotaomicron\_VPI-5482\_226186 Leu TAA  
-GCTCGAATGGTGAAT-GGTA-GACACGAGGACTTAAAAATCCTTGGCCA-TTG-CGGTGTGGGGTTCAGTCCCGCTTCGAGTA-  
>tdbD00007058 Bacteroides\_thetaiotaomicron\_VPI-5482\_226186 Leu TAG  
-GCCGATGTGGCGTAAT-GGTA-GCCGCGCCAGACTTAGGATCTGGTGCC-GTGA-GGCGTGTAGGTTTCGAGTCTATCATCCGCA-  
>tdbD00007074 Bartonella\_henselae\_str.\_Houston-1\_283166 Leu CAA  
-GCGGTGTGGTGAAT-GGTA-GACGCGCCAGACTCAAAAATCTGGTTC-GAGA-GGAGTGTGGTTCGAGTCCGACCCCGACCA  
>tdbD00007073 Bartonella\_henselae\_str.\_Houston-1\_283166 Leu CAG  
-GCCAGATGGCGGAAT-GGTA-GACGCGCAGGTTTCAGGTACCTGTGCC-GCAA-GGCGTGGAGGTTTCGAGTCTCTTTGGGCACCA  
>tdbD00007071 Bartonella\_henselae\_str.\_Houston-1\_283166 Leu GAG  
-GCGGTGTGGCGGAAT-GGTA-GACGCGCAGGTTGAGGTCGCTGTGGGG-CAC-CCCG-TGGAAGTTCGAGTCTCTTCGACCCGACCA  
>tdbD00007072 Bartonella\_henselae\_str.\_Houston-1\_283166 Leu TAA  
-GCGGACGTGATGAAATC-GGTA-AACATAGCAGACTTAAAAATCTGCGGGTCC-TAA-GACCTTGGGGTTCAGTCCCGCTTCGACCA  
>tdbD00007070 Bartonella\_henselae\_str.\_Houston-1\_283166 Leu TAG  
-GCGGATGTGGCGAAAT-GGTA-GACGCGCAGACTTAAAGTTCTGGCGGG-AGA-CCG-TGGGGTTCGAGTCCCTCCATCCGACCA  
>tdbD00007225 Bartonella\_quintana\_str.\_Toulouse\_283165 Leu CAG  
-GCCAGATGGCGGAAT-GGTA-GACGCGCAGGTTTCAGGTACCTGTGCC-GTAA-GGCGTGGAGGTTTCGAGTCTCTTTGGGCACCA  
>tdbD00007226 Bartonella\_quintana\_str.\_Toulouse\_283165 Leu GAG  
-GCGGTGTGGCGGAAT-GGTA-GACGCGCAGGTTGAGGTCGCTGTGGGG-CAA-CCCG-TGGAAGTTCGAGTCTCTTCGACCCGACCA  
>tdbD00007227 Bartonella\_quintana\_str.\_Toulouse\_283165 Leu TAA  
-GCCGATGTGATGAAATC-GGTA-AACATAGCAGACTTAAAAATCTGCGGGTCC-TAA-GACCTTGGGGTTCAGTCCCGCTTCGACCA  
>tdbD00007228 Bartonella\_quintana\_str.\_Toulouse\_283165 Leu TAG  
-GCGGATGTGGCGAAAT-GGTA-GACGCGCAGACTTAAAGTTCTGGCGGG-AGA-CTG-TGGGGTTCGAGTCCCTCCATCCGACCA

>tdbD00007076 *Bdellovibrio bacteriovorus* HD100 264462 Leu CAA  
-GCGGTGTGGTGAAT--GGTA-GACACAGGAGACTCAAAATCTCCCGC-----GAAA-----GCATGGGGGTTCAAGTCCCTCCACCCGCACCA  
>tdbD00007078 *Bdellovibrio bacteriovorus* HD100 264462 Leu CAG  
-GCGGGGTGGTGAAT--GGTA-GACACAGGAGTCTCAGAAGCCTGTGGGA-----GAAA-----TCCTGTGGGGGTTCAAGTCCCTCCCGGCACCA  
>tdbD00007079 *Bdellovibrio bacteriovorus* HD100 264462 Leu GAG  
-GCGGGATGGTGAAT--GGTA-GACACAGGAGTCTCAGAAGCCTGTGGGA-----GAAA-----TCCTGTGGGGGTTCAAGTCCCTCCCGGCACCA  
>tdbD00007077 *Bdellovibrio bacteriovorus* HD100 264462 Leu TAA  
-GCCCCGGTGGCGAAATC--GGTA-GACGACAGGACTTAAATCCTGAGCTTCGT--TTAA--ACGGGCG--TGCCGGTTCAAGTCCGGCCCGGGGCACCA  
>tdbD00007075 *Bdellovibrio bacteriovorus* HD100 264462 Leu TAG  
-GCCCCGGTGGCGAAAT--GGTA-GACACAGTACTTAGGATCTAGTGC-----GCAA-----GCGTGGGGGTTCAAGTCCCTCCGGGGCACCA  
>tdbD00006905 *Bifidobacterium longum* NCC2705 206672 Leu CAA  
-GCCCTCGTATCCCAATT--GGTA-GAGGAAGCAGCCTCAAAATCTGCGC-----AGTGTGGGTTTCGAGTCCCACCGAGGGCA---  
>tdbD00006903 *Bifidobacterium longum* NCC2705 206672 Leu CAG  
-GCCCGGTGGCGAAAT--GGTA-GACGCGTGTCTTCAGGTTGAGTGC-----GTAT----GCTCGTGGGGGTTCAACTCCCCCACTCGCACCA  
>tdbD00006904 *Bifidobacterium longum* NCC2705 206672 Leu GAG  
-GCCCCGGTGGCGAAAT--GGTA-GACGCGTACTTAGGTTGAGTGC-----TTA--TACAGGCGTACGGGTTCAAGTCCCGTCTCGGGCA---  
>tdbD00006906 *Bifidobacterium longum* NCC2705 206672 Leu TAA  
-GCTCCGTTGGCGAAAT--GGTA-TACGCGTACTTAGGTTGAGTGC-----TTTCG-----GCTTGTGGGTTTCGAGTCCCACCGAGGGCA---  
>tdbD00006907 *Bifidobacterium longum* NCC2705 206672 Leu TAG  
-GCGCGAGTGGCGAAAT--GGTA-GACGCGCAGGATTTAGGTTCTGTGTC-----TTT-----GACGTGTGGGTTCAAGTCCCATCTCGCGCA---  
>tdbD00001544 *Bordetella pertussis* 520 Leu CAG  
-GCCCCGTTGGCGAAAT--GGTA-GACGCGTACTTAGGTTGAGTGC-----GCAA-----GGTGTGGAGGTTTCGAGTCCCTCTCTGGGCACCA  
>tdbD00001516 *Borrelia burgdorferi* 139 Leu CAA  
-GCCCGTATGGCGGAAT--GGTA-GACGCGCAGACTCAAAATCTGTTGAGG-----GCAA-----CTTCATGTGCGTTTCGACTCCGACTACCGGTA---  
>tdbD00001515 *Borrelia burgdorferi* 139 Leu GAG  
-GCTGTGGTGGTGAAGT--GGTA-GACAGCTAGCTTAGGTTGAGTGC-----GCAA-----GCCCCGTGCTGGTTCAAGTCCAGTTCACAGCA---  
>tdbD00001518 *Borrelia burgdorferi* 139 Leu TAA  
-GCCGAAGTGGTGAAT--GGTA-GACACACAGGACTTAAATCCTGAGGAG-----GAAG-----CTCG--TACCGGTTCAAGTCCGGTCTTCGGTA---  
>tdbD00001517 *Borrelia burgdorferi* 139 Leu TAG  
-CCAGGAGTGGTGAAT--GGTA-GACAGCTAGACTTAGGATCTAGTGC-----TTT-----GGCGTGTGGGTTTCGACTCCCACCTTCTGTA---  
>tdbD00007124 *Borrelia garinii* PBi 290434 Leu CAA  
-GCCCGTATGGCGGAAT--GGTA-GACGCGTACTTAGGTTGAGTGC-----GCAA-----CTTCGTGCTGGTTTCGACTCCGACTACCGGTA---  
>tdbD00007121 *Borrelia garinii* PBi 290434 Leu GAG  
-GCTGTGGTGGTGAAGT--GGTA-GACAGCTAGCTTAGGTTGAGTGC-----GTAA-----GCCCATGCTGGTTCAAGTCCAGTTCACAGCA---  
>tdbD00007123 *Borrelia garinii* PBi 290434 Leu TAA  
-GCCGAAGTGGTGAAGT--GGTA-GACACACAGGACTTAAATCCTGAGGAG-----GAAG-----CTCCGTACCGGTTCAAGTCCGGTCTTCGGTA---  
>tdbD00007122 *Borrelia garinii* PBi 290434 Leu TAG  
-CCAGGAGTGGTGAAT--GGTA-GACAGCTAGACTTAGGATCTAGTGC-----TTT-----GGCGTGTGGGTTTCGACTCCCACCTTCTGTA---  
>tdbD00006962 *Bradyrhizobium japonicum* USDA 110 224911 Leu CAA  
-GCCCTGTGGCGGAAT--GGTA-GACGCGTACTTAGGTTGAGTGC-----GCAA-----GGAGTGTGGGTTTCGATCCGGCCAGGGGCACCA  
>tdbD00006961 *Bradyrhizobium japonicum* USDA 110 224911 Leu CAG  
-GCCAGGTGGTGAAT--GGTA-GACGCGTGGCTTCAGGTTGAGTGC-----TAAC-----GGCCGTGAAGGTTTCGAGTCCCTTCTGGGCACCA  
>tdbD00006964 *Bradyrhizobium japonicum* USDA 110 224911 Leu GAG  
-GCGCTGTGGCGGAAT--GGTA-GACGCGTGGCTTCAGGTTGAGTGC-----AAA-----ATCG--TGGGGGTTTCGAGTCCCTCCGAGCGCACCA  
>tdbD00006965 *Bradyrhizobium japonicum* USDA 110 224911 Leu TAA  
-GCGGGCATGGCGGAAT--GGTA-GACGCAAGGACTTAAATCCTCGGTGC-----GCAA-----GCGCTGTGCCGTTTCGACCCCGGCTGCCCGCACCA  
>tdbD00006963 *Bradyrhizobium japonicum* USDA 110 224911 Leu TAG  
-GCGGGGTGGCGGAAT--GGTA-GACGCGTGGATTTAGGTTCCAGTGC-----GAAA-----GTTGTGGGGGTTTCGAGTCCCTCCGCCCGCACCA  
>tdbD00006620 *Brucella melitensis* 16M 224914 Leu CAA  
-GCGGTGTGGTGAAT--GGTA-GACGCGCGGACTCAAAATCCTCGGTTC-----GAAA-----GGAGTGTGGGTTTCGATCCGACCACCCGCACCA  
>tdbD00006625 *Brucella melitensis* 16M 224914 Leu CAG  
-GCCAGATGGCGGAAT--GGTA-GACGACCACTTCAGGTTGCTGGCGCTC-----GCAA-----GGGCGTGGAGGTTTCGAGTCCCTTCTGGGCACCA  
>tdbD00006621 *Brucella melitensis* 16M 224914 Leu GAG  
-GCGGTATGGCGGAAT--GGTA-GACGCGCAGCTTCAGGTTGCTGTGGGG-----CAA-----CCCG--TGGAAGTTCGAGTCTTCTCGACCGCACCA  
>tdbD00006622 *Brucella melitensis* 16M 224914 Leu GAG  
-GCGGTGTGGCGGAAT--GGTA-GACGCGCAGCTTCAGGTTGCTGTGGGG-----CAA-----CCCG--TGGAAGTTCGAGTCTTCTCGACCGCACCA  
>tdbD00006623 *Brucella melitensis* 16M 224914 Leu TAA  
-GCGGTGTGGCGGAAT--GGTA-TACGCAACGACTTAAATCCTCGTCT-----TTA-----AGACTTGGCGGTTCAAGTCCCGCCGACCGCACCA  
>tdbD00006454 *Buchnera aphidicola* str. APS (*Acyrtosiphon pisum*) 107806 Leu GAG  
-GCCGAGTGGTGAAT--GGTA-GACACGCTATCTTAGGTTGAGTGC-----AAT-----AGCGTGTGGGTTTCGAGTCCCATTTCTCGGTACCA  
>tdbD00006455 *Buchnera aphidicola* str. APS (*Acyrtosiphon pisum*) 107806 Leu TAA  
-GCCCGATGGTGAAT--GGTA-GACACAAGGACTTAAATCCTCGGCC-----TTAT----GGCTTGGCGGTTCAAGTCCCGCTCCGGTA---  
>tdbD00006456 *Buchnera aphidicola* str. APS (*Acyrtosiphon pisum*) 107806 Leu TAG  
-GCGGGAGTGGCGAAAT--GGTA-GACGACCAAGATTTAGGTTCTGGCGCC-----GAAA-----GGTGTGCGAGTTCAAACTCTCGCTCCCGTA---  
>tdbD00007021 *Buchnera aphidicola* str. Bp (*Baizongia pistaciae*) 224915 Leu GAG  
-GCCGAGTGGTGAAT--GGTA-AACACGCTATCTTAGGTTGAGTGC-----TTTT---TAGGTATGCGGGTTCAAACTCCCGTCCCGTA---  
>tdbD00007020 *Buchnera aphidicola* str. Bp (*Baizongia pistaciae*) 224915 Leu TAA  
-GCCCGATGGTGAATC--GGTA-AACACAAGGATTTAAATCCTCGGCC-----TTAT----GGCTTGGCGGTTCAAGTCCCGTCCCGTA---  
>tdbD00007022 *Buchnera aphidicola* str. Bp (*Baizongia pistaciae*) 224915 Leu TAG  
-GCGGAAGTGGCGAAAT--GGTA-AACGACCAAGATTTAGGTTCTGGCGTCA---TAT---TGGCTTGGCGAGTTCAAACTCTCGCTCCCGTACCA  
>tdbD00006839 *Buchnera aphidicola* str. Sg (*Schizaphis graminum*) 198804 Leu GAG  
-ACCAGGTGGTGAAT--GGTA-GACACGCTATCTTAGGTTGAGTGC-----TTTA-----GGCATATGGGTTCAAGTCCCATCTCGGTACCA---  
>tdbD00006838 *Buchnera aphidicola* str. Sg (*Schizaphis graminum*) 198804 Leu TAA  
-GCCCGATGGTGAAT--GGTA-GACACAAGGACTTAAATCCTCGGCTT-----TTA---AAGCTTGGCGGTTCAAGTCCCGTCCCGGTACCA  
>tdbD00006840 *Buchnera aphidicola* str. Sg (*Schizaphis graminum*) 198804 Leu TAG

-GCGGGAGTGGCGAAATA-GGTA-GACGCACCAGATTTAGGTTCTGGCGCC-----GTAA-----GGTGTGCGAGTTCAAATCTCGCCTCCCGTA---  
>tdbD00006529 Campylobacter\_jejuni\_subsp. jejuni\_NCTC\_11168\_192222 Leu CAA  
-GCCCCAGTGGTGAAGT-GGTA-GACGCGCCAGACTCAAAATCTGGTAAGGG---CAA---CCTTG-TGTCGGTTCGAGTCCGACCTCGGGCACCA  
>tdbD00006530 Campylobacter\_jejuni\_subsp. jejuni\_NCTC\_11168\_192222 Leu GAG  
-GCGGTTATGGTGAATTTGGTA-GACACGCATCTTGGAGGGGGTGGTGCGC-----TCC-----GCGTGTGCGAGTTCAAATCTCGCTAACCGCACCA  
>tdbD00006531 Campylobacter\_jejuni\_subsp. jejuni\_NCTC\_11168\_192222 Leu TAA  
-GCCCCGGTGGTGAATTTGGTA-GACACAAGGGACTTAAATCCCTCGGAAT---TTTT---CTTCGTCGCGGTTCAAGTCCGGCCTCGGGCACCA  
>tdbD00006532 Campylobacter\_jejuni\_subsp. jejuni\_NCTC\_11168\_192222 Leu TAG  
-GCGGATGTGGTGAATTTGGTA-GACACGCAGACTTAGGATCTGGTGCA-----GCAA-----TGCGTGAAGGTTCAAGTCCCTTCATCCGCACCA  
>tdbD00007229 Candidatus\_Blochmannia\_floridanus\_203907 Leu CAA  
-GCCGAAGTGGCGGAAA-GGTA-GACGCAATTGATTCAAAATCAATCACT-----GTGA-----GGTGTGTCGGTTCGAGTCCGACCTTCGGTA---  
>tdbD00007230 Candidatus\_Blochmannia\_floridanus\_203907 Leu CAG  
-GCGAAGTGGCGGAAAATA-GGTA-GACGCACTAGCTTCAGGGGTTAGTGTCTTG---TAT---GTAGACGTAAGGGTTCAAATCCCTTCCTTCGTA---  
>tdbD00007231 Candidatus\_Blochmannia\_floridanus\_203907 Leu GAG  
-GCCGAGATGGTGAATTTGGTA-TACACGCTACTTTGAGGGGGTAGTCCGG-----TTA-----ATGGTTGCGGGTTCAAATCCCGTTCCTCGGCA---  
>tdbD00007232 Candidatus\_Blochmannia\_floridanus\_203907 Leu TAA  
-GCCCCGGTGGTGAATTTGGTA-GACACAAGGGACTTAAATCCCTCAGTT-----TTA-----TACTGTACGAGTTCAAGTCTCGTCCCGGGTA---  
>tdbD00007233 Candidatus\_Blochmannia\_floridanus\_203907 Leu TAG  
-ACGGGAGTGGCGGAAAATA-GGTA-GACGCGTCAGAGTTAGAGTCTGATATC-----CTTA-----GATATGCGAGTTCAAATCTCGCCTCCCGTA---  
>tdbD00007095 Candidatus\_Protochlamydia\_amoebophila\_UWE25\_264201 Leu CAA  
-GCCGATGTGGCGGAATTTGGTA-GACGCGGTAGACTCAAAATCTACTTCTA-----GCAA-----TAGAGTGTGGTTCGAGTCCGGTTCATCCGCA---  
>tdbD00007094 Candidatus\_Protochlamydia\_amoebophila\_UWE25\_264201 Leu CAG  
-GCGGCCATGGCGGAATTTGGTA-GACGCGCTAGATTCAGGTTCTAGTCCGG-----GTAA-----CTCGGTGGATGTTTCGAGTTCATCTGGCCGCA---  
>tdbD00007096 Candidatus\_Protochlamydia\_amoebophila\_UWE25\_264201 Leu GAG  
-GCGAAGTGGCGGAAATTTGGTA-TACGCGCTACTTTGAGGTTGGTAGTGAGG-----GTTT---CCTCGTAGGGGTTCAAAGTCCCTTCCTTCGCA---  
>tdbD00007097 Candidatus\_Protochlamydia\_amoebophila\_UWE25\_264201 Leu TAA  
-GCTCGGGTGGTGAATTTGGTA-GACACAAGAGACTTAAATCTCTTGCTCA-----TTT---TGGGCGTGAAGGTTTCGAGTCCCTTCCTTCGCA---  
>tdbD00007098 Candidatus\_Protochlamydia\_amoebophila\_UWE25\_264201 Leu TAG  
-GCCAGATGGTGAATTTGGTA-GACACGCAGATTTAGGTTCTGGTGCC-----GTAA-----GGTGTGAGGTTTCGAGTCCCTTCCTTCGCA---  
>tdbD00006533 Caulobacter\_crescentus\_CB15\_190650 Leu CAA  
-GCGGGCGTGGTGAATTTGGTA-GACGCGCGGACTCAAAATCCGGTTCC-----GAAA-----GGAGTGTGCGGTTTCGACCCCGACCCCGCACCA  
>tdbD00006534 Caulobacter\_crescentus\_CB15\_190650 Leu CAG  
-GCCAGGTGGCGGAATTTGGTA-GACGCGCTGGCTTCAGGTGCCAGTGACC-----GAAA-----GGTCGTGGAGGTTTCGAGTCCCTTCCTGGGCACCA  
>tdbD00006536 Caulobacter\_crescentus\_CB15\_190650 Leu TAA  
-GGGGACGTGGCGGAATTTGGTA-GACGCGCGGACTTAAATCCCGTTGGA-----GCAA-----TCCGTGTGGGTTTCGAGTCCACCGTCCCTACCA  
>tdbD00006537 Caulobacter\_crescentus\_CB15\_190650 Leu TAG  
-GCGGATGTGGCGGAAATTTGGTA-GACGCACTGGATTTAGGTTCCAGCGCC-----GCGA-----GGCGTGGAGGTTTCGAGTCCCTTCATCCGCACCA  
>tdbD00006600 Chlamydia\_muridarum\_Nigg\_243161 Leu CAA  
-GCCGCGTGGCGGAATTTGGTA-GACGCGGTAGACTCAAAATCTACTCTTA-----GCAG-----TAAGGTGTTGGTTCGAGTCCAATCGCCGGCA---  
>tdbD00006603 Chlamydia\_muridarum\_Nigg\_243161 Leu CAG  
-GCAGTATGGCGGAAATTTGGTA-GACGCGCTAGATTCAGGTTCTAGTGAGC-----TTTT---GCTCATGGAAGTTCAAAGTCTCTTCCTAGCTGCA---  
>tdbD00006601 Chlamydia\_muridarum\_Nigg\_243161 Leu GAG  
-GCGGAAGTGGCGGAAATTTGGTA-TACGCGCTACTTTGAGGTTGGTAGTGA-----GCTT-----TCCTTAGGGGTTTCGAGTCCCTTCCTTCGCA---  
>tdbD00006602 Chlamydia\_muridarum\_Nigg\_243161 Leu TAA  
-GCTCAGATGGTGAATTTGGTA-GACACTAGGGACTTAAATCCCTTGGGC-----TTTG-----GCCCGTGCAGGTTTCGAGTCTTGTCTGAGCA---  
>tdbD00006599 Chlamydia\_muridarum\_Nigg\_243161 Leu TAG  
-GCCAGGTGGTGAATTTGGTA-GACACGCTGGATTTAGGATCCAGTGCT-----TTGC-----GGCATGTAGGTTCAAAGTCCCTTCCTGGGCA---  
>tdbD00006441 Chlamydia\_trachomatis\_D/UW-3/CX\_272561 Leu TAG  
-GCCAGGTGGTGAATTTGGTA-GACACGCTGGATTTAGGATCCAGTGCT-----TCGC-----GGCATGTAGGTTCAAAGTCCCTTCCTGGGCA---  
>tdbD00006427 Chlamydia\_pneumoniae\_AR39\_115711 Leu CAA  
-GCCGCTGTGGCGGAATTTGGTA-GACGCGGTAGACTCAAAATCTACTCTTA-----GCAA-----TAAGGTGTTGGTTCGAGTCCGATCACCGGCA---  
>tdbD00006428 Chlamydia\_pneumoniae\_AR39\_115711 Leu CAG  
-GCAGTATGGCGGAAATTTGGTA-GACGCGCTAGATTCAGGTTCTAGTGAGC-----TTAT-----GCTCATGGAAGTTCAAAGTCTCTTCCTAGCTGCA---  
>tdbD00006430 Chlamydia\_pneumoniae\_AR39\_115711 Leu TAA  
-GCTCAGATGGTGAATTTGGTA-GACACTAGGGACTTAAATCCCTTGGGC-----GTAG-----GCCCGTGCAGGTTTCGAGTCTTGTCTGAGCA---  
>tdbD00006431 Chlamydia\_pneumoniae\_AR39\_115711 Leu TAG  
-GCCAGGTGGTGAATTTGGTA-GACACGCTGGATTTAGGATCCAGTGCT-----TTTC-----GGCATGTAGGTTCAAAGTCCCTTCCTGGGCA---  
>tdbD00006826 Chlorobium\_tepidum\_TLS\_194439 Leu CAA  
-GCCAAGTGGCGGAAATTTGGTA-GACGCGCTGGACTCAAAATCCAGTGCC-----GCAA-----GCTCGTGTGGGTTTCGAGTCCACCTTTGGTA---  
>tdbD00006828 Chlorobium\_tepidum\_TLS\_194439 Leu CAG  
-GCCGAATGGCGGAAATTTGGTA-GACGCACTCGTTTCAGGGGCGAGCGCC-----GAGA-----GGTGTAGGAGTTTCGAATCTCTTCCTTCGGCACCA  
>tdbD00006825 Chlorobium\_tepidum\_TLS\_194439 Leu GAG  
-GCCGAGTGGTGAATTTGGTA-GACACACCATCTTGGAGGGGTGGCGCC-----GTTA-----GGTGTAGGAGTTTCGAATCTCTTCCTTCGGGCA---  
>tdbD00006823 Chlorobium\_tepidum\_TLS\_194439 Leu TAA  
-GCCGAAGTGGCGGAAATTTGGTA-AACGCCCCGAGACTTAAATCCCGTGTTC---GCAA---TGGACGTGCAGGTTTCGATTCCCTGCCTTCGGCACCA  
>tdbD00006824 Chlorobium\_tepidum\_TLS\_194439 Leu TAA  
-GCCGAAGTGGCGGAAATTTGGTA-GACGCCCCGGACTTAAATCCCGTGTTC---GCAA---TGGACGTGCAGGTTTCGATTCCCGCCTTCGGGCA---  
>tdbD00006827 Chlorobium\_tepidum\_TLS\_194439 Leu TAG  
-GCGAGATGGTGAATTTGGTA-TACACGCTAGTCTTAGGAACTAGTGCC-----GTGA-----GGCGTAAGGGTTTCGAGTCCCTTCCTTCGCA---  
>tdbD00006614 Clostridium\_acetobutylicum\_ATCC\_824\_272562 Leu CAA  
-GCCGAAGTGGTGAATTTGGTA-GACGCAACGGACTCAAAATCCCGTCCGTA---GCAA---TACCATGCGGGTTTCGACTCCCGCCTCCGGCACCA  
>tdbD00006612 Clostridium\_acetobutylicum\_ATCC\_824\_272562 Leu CAG  
-GCGGATATGGCGGAAATTTGGTA-TACGCGCTAGTTTCAGGTTACTAGTGA-----GAAA-----TCATGCAGGTTTCGAATCCCTGTATCCGCACCA  
>tdbD00006613 Clostridium\_acetobutylicum\_ATCC\_824\_272562 Leu GAG  
-GCGAGATGGTGAATTTGGTA-GACAGGCACGTTTGGAGGGCGTGTGC-----ATT-----GACGTACGGGTTCAAAGTCCCGTCTCTCGCACCA

>tdbD00006616 Clostridium acetobutylicum ATCC\_824\_272562\_Leu\_TAA  
-GCCGAAGTGGCGGAACT-GGCA-GACGCACAGGACTTAAAATCCTGCGATGCT---AAT---CACATCGTACCGGTTTCGATTCCGGTCTTCGGCACCA  
>tdbD00006615 Clostridium acetobutylicum ATCC\_824\_272562\_Leu\_TAG  
-GCAGTGTGGCGGAACT-GGCA-GACGCACAGGACTTAGGATCTAGCGCC-----TAC-----GGCGTGGGGGTTTCGACTCCCTTACCTGCACCA  
>tdbD00006594 Clostridium perfringens\_str.\_13\_195102\_Leu\_CAA  
-GCCGAAGTGGCGGAACT-GGCA-GACGCACAGGACTTAAAATCCTGCGGGCT---AAT---ACTCG-TACGGGTTTCGAGTCCCGTCTTCGGCACCA  
>tdbD00006595 Clostridium perfringens\_str.\_13\_195102\_Leu\_GAG  
-GCAGATATGGTGGAAT--GGCA-GACACGATATCTTGAGGGGGTATTACTT-----TTAG----GAGTGTGGGGTTCAAGTCCCGTATCTGCACCA  
>tdbD00006593 Clostridium perfringens\_str.\_13\_195102\_Leu\_TAA  
-GCCGAAGTGGCGGAACT-GGCA-GACGCACAGGACTTAAAATCCTGCGGTGTC---TAAC---ACACCGTACCGGTTTCGATTCCGGTCTTCGGCACCA  
>tdbD00006598 Clostridium perfringens\_str.\_13\_195102\_Leu\_TAA  
-GCCGAAGTGGCGGAACT-GGCA-GACGCACAGGACTTAAAATCCTGCGATGC---TAAC---ACATCGTACCGGTTTCGATTCCGGTCTTCGGCACCA  
>tdbD00006596 Clostridium perfringens\_str.\_13\_195102\_Leu\_TAG  
-GCAGATGTGGCGGAACT-GGCA-GACGCACAGGACTTAGGATCTAGCGCC-----TAC-----GGCGTGGGGGTTTCGACTCCCTTATCTGCACCA  
>tdbD00006968 Clostridium tetani\_E88\_212717\_Leu\_CAA  
-GCCGAAGTGGTGGAAT--GGCA-GACGCGCTGGATTCAAATCCAGTGGGGCT---TAA---ACCTCG-TGCGGGTTTCGATTCCCGCTTCGGCACCA  
>tdbD00006967 Clostridium tetani\_E88\_212717\_Leu\_GAG  
-GCCAGTGTGGCGGAACT-GGCA-GACGCACAGGACTTAAAATCCTGCGGTGTC-----AAC-----GAACGTATGGGTTTCAGTCCCTTACCTGCACCA  
>tdbD00006966 Clostridium tetani\_E88\_212717\_Leu\_TAA  
-GCCGAAGTGGCGGAACT-GGCA-GACGCACAGGACTTAAAATCCTGCGGTGTT---TTGA--AGCACCGTACCGGTTTCGATTCCGGTCTTCGGCACCA  
>tdbD00006969 Clostridium tetani\_E88\_212717\_Leu\_TAG  
-GCAGTGTGGCGGAACT-GGCA-GACGCACAGGACTTAAAATCCTGCGGTGTC-----TTT-----GGCGTGGGGGTTTCGACTCCCTTACCTGCACCA  
>tdbD00007082 Corynebacterium diphtheriae\_NCTC\_13129\_257309\_Leu\_CAA  
-GCCCTGTATCCCAATT-GGCA-GAGGAAACGGATTCAAACCCCGTGC-----AGTGTGAGTTTCGAGTCTCACCAGGGGCACCA  
>tdbD00007080 Corynebacterium diphtheriae\_NCTC\_13129\_257309\_Leu\_CAG  
-GCCCAGTGGCGGAACT-GGCA-GACGCGCTGCTTCAGGTGCCAGTGTTC-----GCAA---GGACGTGGGGGTTTCAGTCCCCCCTGGGCA---  
>tdbD00007083 Corynebacterium diphtheriae\_NCTC\_13129\_257309\_Leu\_GAG  
-GCCCGGGTGGCGGAACT--GGCA-GACGCGCTAGCTTGAGGTGCTAGTGTCTTA---CTA---ACGGACGTGGGGGTTTCAGTCCCCCCTCGGCA---  
>tdbD00007081 Corynebacterium diphtheriae\_NCTC\_13129\_257309\_Leu\_TAA  
-GCCCCATAGCCCAATC-GGCA-GAGGCAATCGACTTAAAATCGATC-----AGTGTGGGTTTCGAGTCCCACTGGGGGCACCA  
>tdbD00007084 Corynebacterium diphtheriae\_NCTC\_13129\_257309\_Leu\_TAG  
-GCGCCGTGGCGGAACT-GGCA-GACGCGCTGGATTAGGTTCCAGTGTTC-----TTAG----GACGTGAGAGTTTCAGTCTCTCCGGGCGCA---  
>tdbD00006914 Corynebacterium efficiens\_YS-314\_196164\_Leu\_CAA  
-GCCCTAGTAGCCCAATC-GGCA-GAGGCAACCGGATTCAAACCCCGTGC-----AGTGTGGGTTTCGAGTCCCACTGGGGGCACCA  
>tdbD00006912 Corynebacterium efficiens\_YS-314\_196164\_Leu\_CAG  
-GCCCGGGTGGCGGAACT--GGCA-GACGCGCTGGCTTCAGGTGCCAGTGTTC-----GCAA---GGCGTGGGGGTTTCAGTCCCCCCTGGGCA---  
>tdbD00006916 Corynebacterium efficiens\_YS-314\_196164\_Leu\_GAG  
-GCCCGGGTGGCGGAACT--GGCA-GACGCGCTGCTTGAGGTGCTAGTGTCTTA---TTA---ACGGACGTGGGGGTTTCAGTCCCCCCTCGGCA---  
>tdbD00006917 Corynebacterium efficiens\_YS-314\_196164\_Leu\_GAG  
-GCCCAGTGGCGGAACT--GGCA-GACGCGCTAGCTTGAGGTGCTAGTGTCTTA---TTA---ACGGACGTGGGGGTTTCAGTCCCCCCTCGGCA---  
>tdbD00006913 Corynebacterium efficiens\_YS-314\_196164\_Leu\_TAA  
-GCCCCATAGCCCAATC-GGCA-GAGGCGGTTGACTTAAAATCAATC-----AGTGTGGGTTTCGAGTCCCACTGGGGGCACCA  
>tdbD00006915 Corynebacterium efficiens\_YS-314\_196164\_Leu\_TAG  
-GCGCTGTGGCGGAACT-GGCA-GACGCGCTGGATTAGGTTCCAGTGTTC-----CCAG----GACGTGAGAGTTTCAGTCTCTCCAGGCGCA---  
>tdbD00006846 Corynebacterium glutamicum\_ATCC\_13032\_196627\_Leu\_CAA  
-GCCCTGTAGCCCAATC-GGCA-GAGGCAACCGGATTCAAACCCCGTGC-----AGTGTGAGTTTCGAGTCTCACCAGGGGCACCA  
>tdbD00006844 Corynebacterium glutamicum\_ATCC\_13032\_196627\_Leu\_CAG  
-GCCCGGGTGGCGGAACT-GGCA-GACGCGCTGGCTTCAGGTGCCAGTGTTC-----GCAA---GGACGTGGGGGTTTCAGTCCCCCCTGGGCA---  
>tdbD00006847 Corynebacterium glutamicum\_ATCC\_13032\_196627\_Leu\_GAG  
-GCCCGGGTGGCGGAACT--GGCA-GACGCGCTAGCTTGAGGTGCTAGTGTCTTA---TTA---ACGGACGTGGGGGTTTCAGTCCCCCCTGGGCA---  
>tdbD00006845 Corynebacterium glutamicum\_ATCC\_13032\_196627\_Leu\_TAA  
-GCCCCATAGCCCAATC-GGCA-GAGGCGGTTGACTTAAAATCAATC-----AGTGTGGGTTTCGAGTCCCACTGGGGGCACCA  
>tdbD00006849 Corynebacterium glutamicum\_ATCC\_13032\_196627\_Leu\_TAG  
-GCGCTGTGGCGGAACT-GGCA-GACGCGCTGGATTAGGTTCCAGTGTTC-----CTAG----GACGTGAGAGTTTCAGTCTCTCCAGGCGCA---  
>tdbD00007011 Coxiella burnetii\_RSA\_493\_227377\_Leu\_CAA  
-GCCGAGTGGCGGAACT-GGTA-GACGCGCGGACTCAAATCCGGTGGTG-----GCAA---CACCGTGGGGTTTCGAGTCCCTCCCTCGGTACCA  
>tdbD00007012 Coxiella burnetii\_RSA\_493\_227377\_Leu\_CAG  
-GCCGAGTGGTGGAAT--GGTA-GACACGCAAGTTTCAGGTACTTGTGGGGG---AAA---CCCG-TGGAGTTTCAGTCTCTCCCTCGGCA---  
>tdbD00007014 Coxiella burnetii\_RSA\_493\_227377\_Leu\_GAG  
-GCCGAAGTGGTGGAAT--GGTA-GACACGCTGTCTTGAGGGGGCAGTGGG---AAA---CCCG-TGCCGGTTTCGAGTCCGGCTTCGGCA---  
>tdbD00007013 Coxiella burnetii\_RSA\_493\_227377\_Leu\_TAA  
-GCCCGGGTGGCGGAACT-GGTA-GACGCAAGGACTTAAAATCCCTCGGGTG---AAT---AACCCGTGCCGGTTTCGAGTCCGGCCCCGGGCACCA  
>tdbD00007010 Coxiella burnetii\_RSA\_493\_227377\_Leu\_TAG  
-GCGAGAGTGGCGGAACT-GGTA-GACGCGCTGGATTAGGTTCCAGTAGG-----TTAG----CCTGTGAGAGTTTCGAGTCTCTCTCTCGCACCA  
>tdbD00006538 Deinococcus radiodurans\_R1\_243230\_Leu\_CAA  
-GCCGATATGGCGGAACT-GGTA-GACGCACCTCGACTCAAATCGAGCGGG-----AAA-----CCG-TAAGGGTTTCGAGTCCCTTTATCGGCACCA  
>tdbD00006539 Deinococcus radiodurans\_R1\_243230\_Leu\_CAG  
-GCCGAGTGGCGGAACT-GGTA-GACGCACCTAGTTTCAGGACTAGCGCC-----GCGA-----GGTGTGTGGGTTCAAATCCCATCTCGGCACCA  
>tdbD00006540 Deinococcus radiodurans\_R1\_243230\_Leu\_GAG  
-GCTCGGGTGGCGGAACT-GGTA-GACGCGCACGTTTGAGGGGGCTGTGGG-----TAA-----CCG-TGTGGGTTTCAGTCCCATCTCGAGCACCA  
>tdbD00006541 Deinococcus radiodurans\_R1\_243230\_Leu\_TAA  
-GTCGGGATGGCGGAACT-GGTA-GACGCATTCGACTTAAAATCGACCAG-----GCAA-----CTCGTGGGGTTTCAGTCCCGTTCGGGCACCA  
>tdbD00006542 Deinococcus radiodurans\_R1\_243230\_Leu\_TAG  
-GCCGAGTGGCGGAACT-GGTA-GACGCACCTAGACTTAGGATCTAGTATCC-----GTA-----GGATGTGAGGGTTTCAGTCCCTTCTCTCGCACCA  
>tdbD00007180 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Leu\_CAA

-GCCGGAATGGTGAATT-GGTA-GACGCAGCGGACTCAAAATCCGCCGGTG----GCAA----CACCTGTGAGTTCGAGTCTGACTTCCGGTACCA  
>tdbD00007177 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Leu\_CAG  
-GCCGAAGTGGTGAATT-GGTA-GACACGCTAGGTTGAGGGTCTAGTTGGG----GTTT----CCAGTGGGAGTTCGAGTCTCCCTTCCGGCACCA  
>tdbD00007179 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Leu\_GAG  
-GCCGAGGTGGTGAATT-GGTA-GACACGCTATCTTGAGGGGGTAGTGGGA----GAAA----TCCCGTGAGGGTTCGAGTCCCTCCTTCCGGCACCA  
>tdbD00007181 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Leu\_GAG  
-GCCGAGGTGGTGAATT-GGTA-GACACGCTATCTTGAGGGGGTAGTGGGA----GAAA----TCCCGTGAGGGTTCGAGTCCCTCCTTCCGGCACCA  
>tdbD00007176 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Leu\_TAA  
-GCCCGGATGGCGGAACT-GGCA-GACGCAAGGGACTTAAAATCCCTCGGCC----TTCG----GGCTGTACGAGTTCATCCTCGTTCGGGTACCA  
>tdbD00007178 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Leu\_TAG  
-GCGAGAGTGGCGGAATA-GGTA-GACGCACTGGACTTAGAATCCAGCGCC----TTTG----TGCGTGGGAGTTCGAGTCTCCCTTCCGGCACCA  
>tdbD00006972 Enterococcus\_faecalis\_V583\_226185\_Leu\_CAA  
-GCCCGCGTGGCGGAAAT-GGCA-GACGCGCTGGACTCAAAATCCAGTTCCT----TCAC----GGGAGTGCCGGTTCGACCCCGCCCGCGTA---  
>tdbD00006973 Enterococcus\_faecalis\_V583\_226185\_Leu\_GAG  
-GCAGATGTGTGGAATT-GGCA-GACAAGCATGATTGAGGGTTCATGTGGAC----AGAT----GTCCTGTGGGTTTCGAGTCCCATCATCTGCA---  
>tdbD00006971 Enterococcus\_faecalis\_V583\_226185\_Leu\_TAA  
-GCCCGGGTGGCGGAACT-GGCA-GACGCACAGGACTTAAAATCCTGCGGTGA----GTGA----TCACCGTACCGGTTTCGATTCGGTCCCTCGGCA---  
>tdbD00006970 Enterococcus\_faecalis\_V583\_226185\_Leu\_TAG  
-GCGGGTGTGGCGGAAAT-GGCA-GACGCACTAGATTAGGATCTAGCGCC----GCAA----GGCGTGGGGTTCAAGTCCCTTCAACCCGCA---  
>tdbD00001535 Escherichia\_coli\_562\_Leu\_CAA  
-GCCGAAGTGGCGAAATC-GGTA-GACGCAGTTGATTCAAAATCAACCGTA-----GAAA-----TACGTGCCGGTTCGAGTCCGGCCTTCCGGCACCA  
>tdbD00001533 Escherichia\_coli\_562\_Leu\_CAG  
-GCGAAGTGGCGGAAAT-GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC----TTAC----GGACGTGGGGTTCAAGTCCCCCCCCCTCGCACCA  
>tdbD00001536 Escherichia\_coli\_562\_Leu\_GAG  
-GCCGAGGTGGTGAATT-GGTA-GACACGCTACCTTGAGGTGGTAGTGTCC----AATA----GGGCTTACGGGTTCAAGTCCCGTCCCTCGGTACCA  
>tdbD00001537 Escherichia\_coli\_562\_Leu\_TAA  
-GCCCGGATGGTGAATC-GGTA-GACACAAGGGATTAAAATCCCTCGGCG----TTCG----CGTGTGCGGGTTCAAGTCCCGTCCGGGTACCA  
>tdbD00001534 Escherichia\_coli\_562\_Leu\_TAG  
-GCGGGAGTGGCGAAAT-GGTA-GACGCACAGGACTTAAAGTTCAGGTTCTGGCGCC----GCAA----GGTGTGCGAGTTCAGTCTCGCTCCCGCACCA  
>tdbD00007028 Escherichia\_coli\_CFT073\_199310\_Leu\_CAG  
-GCGAAGTGGCGGAAAT-GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTTC----TTAC----GGACGTGGGGTTCAAGTCCCCCCCCCTCGCACCA  
>tdbD00006831 Fusobacterium\_nucleatum\_subsp.\_nucleatum\_ATCC\_25586\_190304\_Leu\_CAA  
-GCCTGAGTGGTGAATT-GGTA-GACGCACAGGACTCAAAATCTGGAATTC----TTCG----GAATGTGCGGGTTCAAGTCCCGCCTCAGGCACCA  
>tdbD00006829 Fusobacterium\_nucleatum\_subsp.\_nucleatum\_ATCC\_25586\_190304\_Leu\_TAA  
-GCCTGGATGGCGGAATA-GGTA-GACGCACAGGACTTAAAATCCTGTGGTAC----TTA----GTACCGTGGCGGTTTCGATTCGGCTCTAGGCACCA  
>tdbD00006830 Fusobacterium\_nucleatum\_subsp.\_nucleatum\_ATCC\_25586\_190304\_Leu\_TAG  
-GCGGGATGGCGGAAAT-GGCA-GACGCGCTAGACTTAGGATCTAGTGTG----CCA----GACGTGAGAGTTCAGTCTCTCTCCTCCGCACCA  
>tdbD00007126 Geobacter\_sulfurreducens\_PCA\_243231\_Leu\_CAA  
-GCCCGAGTGGTGAATC-GGTA-GACGCAGCGGACTCAAAATCCGCCGGGG----CAA----CCCCG-TGTCGGTTTCGATTCGACCTCCGGCACCA  
>tdbD00007125 Geobacter\_sulfurreducens\_PCA\_243231\_Leu\_CAG  
-GCCGAAGTGGTGAATT-GGTA-GACACGCAAGATTCAGGATCTTGTGCGG----GCAA----CCGTGTGCTGGTTCGAGTCCAGTCTTCCGGCACCA  
>tdbD00007127 Geobacter\_sulfurreducens\_PCA\_243231\_Leu\_GAG  
-GCGGTAGTGGCGGAAAT-GGTA-GACGCACAGGACTTAAAGTTCAGGTTGCGGGGG----TTA----CCCCG-TGATGGTTTCGAGTCCATTCTACCGCACCA  
>tdbD00007129 Geobacter\_sulfurreducens\_PCA\_243231\_Leu\_TAA  
-GCCCGGATGGTGAATC-GGTA-GACACAAGGGATTAAAATCCCTCGGCA----GCAA----TGCTGTGCGGGTTTCGAGCCCGGCTCCGGGCACCA  
>tdbD00007128 Geobacter\_sulfurreducens\_PCA\_243231\_Leu\_TAG  
-GCGAGAGTGGCGGAAAT-GGCA-GACGCACTGGACTTAGGATCCAGCGGG----CAA----CCG-TAGGGGTTTCGACTCCCTCTCTCGCACCA  
>tdbD00001548 Haemophilus\_influenzae\_727\_Leu\_CAA  
-GCCTGGTGGCGAAAT-GGTA-GACGCAGCGGATTCAAAATCCGCCGGT----AAT----AAACGTGTGCGGTTTCGAGTCCGACCTTAGGCACCA  
>tdbD00001547 Haemophilus\_influenzae\_727\_Leu\_GAG  
--CTCTGGTGGTGAATT-GGTA-GACACGCTATCTTGAGGGGGTAGTGACC----ACA----GGTCGTGCGAGTTCAGTCTCGCCAGAGCACCA  
>tdbD00001545 Haemophilus\_influenzae\_727\_Leu\_TAA  
-GCCCGAGTGGTGAATC-GGTA-GACACAAGGGATTAAAATCCCTCGCCT----TTCG----ACGCGTGCAGGTTCAAGTCTGGCTTCCGGCACCA  
>tdbD00001546 Haemophilus\_influenzae\_727\_Leu\_TAA  
-GCCCGAGTGGTGAATC-GGTA-GACACAAGGGATTAAAATCCCTCGCCT----TTCG----AGCGGTGCAGGTTCAAGTCTGGCTTCCGGCACCA  
>tdbD00001549 Haemophilus\_influenzae\_727\_Leu\_TAG  
-GCGGGACTGGCGAAAT-GGTA-GACGCACAGGATTTAGGTTCTGGCGCC----GGAA----GGTGTGGGGTTCAAGTCCCTCGTCCCGCACCA  
>tdbD00006522 Haemophilus\_influenzae\_Rd\_KW20\_71421\_Leu\_GAG  
-GCTCTGGTGGTGAATT-GGTA-GACACGCTATCTTGAGGGGGTAGTGACC----ACA----GGTCGTGCGAGTTCAGTCTCGCCAGAGCACCA  
>tdbD00006524 Haemophilus\_influenzae\_Rd\_KW20\_71421\_Leu\_TAG  
-GCGGGACTGGCGAAAT-GGTA-GACGCACAGGATTTAGGTTCTGGCGCC----GAGA----GGTGTGGGGTTCAAGTCCCTCGTCCCGCACCA  
>tdbD00001524 Helicobacter\_pylori\_210\_Leu\_CAA  
-GCCGAAGTGGTGAATC-GGTA-GACACGCTAGACTCAAAATCCTGGTGGGA----GCAA----TCCCGTGTGCGGTTTCGAGTCCGACCTTCCGGCACCA  
>tdbD00001525 Helicobacter\_pylori\_210\_Leu\_GAG  
-GACTGTGGTGGTGAATT-GGTA-GACACGCTATCTTGAGGGGGTGGTGGGA----GCAA----TCTCGTGCAGGTTTCGAGTCTCGCCAGTGCACCA  
>tdbD00001523 Helicobacter\_pylori\_210\_Leu\_TAA  
-GCCCAGTGGTGAATC-GGTA-GACACAAGGGACTTAAAATCCCTCGGTA----GCAA----TACCGTGCAGGTTTCAGTCCGGCTTGGGCACCA  
>tdbD00001526 Helicobacter\_pylori\_210\_Leu\_TAG  
-GCGGAAGTGGCGAAAT-GGTA-GACGCACTAGACTTAGGATCTAGCGCC----GCAA----GGCATGAAGGTTTCGATTCCTTTCTTCCGCACCA  
>tdbD00007131 Lactobacillus\_johnsonii\_NCC\_533\_257314\_Leu\_AAG  
-GCGGCGTGGCGGAAAT--GGCA-GACGCGCAAGACTAAGGATCTTGTGATCGC---TTT---TAGATCGTGAAGTTCGAGTCTTCTCGCCCGCACCA  
>tdbD00007134 Lactobacillus\_johnsonii\_NCC\_533\_257314\_Leu\_CAA  
-GGCGTGTGGCGGAAAT-GGCA-GACGCGTACAGACTCAAAATCTGGTGTCC----CCTG----GGACGTATCGGTTTCGACCCCGATCACCGCTA---  
>tdbD00007130 Lactobacillus\_johnsonii\_NCC\_533\_257314\_Leu\_CAG  
-GCCTCAATGGCGGAAAT-GGCA-GACGCGCAGCGTTCAGGTCGCTGTTAC----GCAA----GTGAGTGCAGGTTTCGACTCCTGTTGAGGCA---



>tdbD00007132 *Lactobacillus\_johnsonii*\_NCC\_533\_257314\_Leu\_TAA  
-GCCGGGGTGGCGGAACT-GGCA-GACGACGCGGACTTAAAAATCCCGCGGTG----GTGA---CAACCGTACCGGTTTCGATTCCGGTCTCGGCA---  
>tdbD00007133 *Lactobacillus\_johnsonii*\_NCC\_533\_257314\_Leu\_TAG  
-GCGGGTGTGGCGGAAATT-GGCA-GACGCGCTAGATTTAGGTCTAGTGTT-----TTCG----GACGTGTGGGTTCAAGTCCCACCACCGTACCA  
>tdbD00006974 *Lactobacillus\_plantarum*\_WCFS1\_220668\_Leu\_AAG  
-GCGGCATGGCGGAAATT-GGCA-GACGCGCAAGATTAAGGATCTTGTCTGGGG----TTA----ACCCGGTGAAGTTCAATCTTCTTGGCCGCA---  
>tdbD00006977 *Lactobacillus\_plantarum*\_WCFS1\_220668\_Leu\_CAA  
-GCCGGCTGGCGGAAATT-GGCA-GACGCGCTGGACTCAAAATCCAGTTCCCG----TTG----AGGGAGTATCGGTTTCGACCCCGATCGCCGGTA---  
>tdbD00006978 *Lactobacillus\_plantarum*\_WCFS1\_220668\_Leu\_CAG  
-GCCCAGTGGCGGAACT-GGCA-GACGCGCAGGTTTCAAGTTCAGTGTATG----GAAA----CAATGTACAGGTTCAATCCTGCCTGGGGCA---  
>tdbD00006976 *Lactobacillus\_plantarum*\_WCFS1\_220668\_Leu\_TAA  
-GCCGGGGTGGCGGAAATT-GGCA-GACGACAGGACTTAAAAATCCTGCGGTTA----GTGA---TAACCGTACCGGTTTCGATCCCGGTTCTCGGCA---  
>tdbD00006975 *Lactobacillus\_plantarum*\_WCFS1\_220668\_Leu\_TAG  
-GCGGGTGTGGCGGAAATT-GGCA-GACGCGCTAGATTTAGGTCTAGTGTC-----TTAC----GACGTGGGGTTTCGAGTCCCTTACCCGCA---  
>tdbD00007137 *Leifsonia\_xyli*\_subsp.\_*xyli*\_str.\_CTCB07\_281090\_Leu\_CAA  
-GCCGTGTGGCGGAACT-GGCA-GACGCGGAGCACTTAAAAATGCTTTGTCTCT---TCA---CGGGCGTGTGGGTTCAATCCCACCAGCGGCA---  
>tdbD00007135 *Leifsonia\_xyli*\_subsp.\_*xyli*\_str.\_CTCB07\_281090\_Leu\_CAG  
-GCCGAGTGGCGGAAATT-GGCA-GACGCGCTGGCTTCAAGTTCAGGTTCCCGC---GCAA----GGCGTGGGGTTCAAGTCCCCCTCGCGCA---  
>tdbD00007139 *Leifsonia\_xyli*\_subsp.\_*xyli*\_str.\_CTCB07\_281090\_Leu\_TAA  
-GCCCCATAGCCCAATC-GGCA-GAGGCAGCGCACTTAAAAATCGCTTC-----AGTGTGGGTTTCGATCCCCTGCGGGCA---  
>tdbD00007138 *Leifsonia\_xyli*\_subsp.\_*xyli*\_str.\_CTCB07\_281090\_Leu\_TAG  
-GCCGAGTGGCGGAAATT-GGCA-GACACGAGGATTTAGGTTCTGTGTC-----TTCG----GCGTGAGGTTTCGAGTCCCTTCTCCCGCA---  
>tdbD00006922 *Leptospira\_interrogans*\_serovar\_*Lai*\_str.\_56601\_189518\_Leu\_CAA  
-GCCGATGTGGTGAACT-GGTA-GACGCGTGGATTCAAAAATCCACCGGGGG---CAA---CTCTG-TGTCGGTTTCGAGTCCGACCATCGGCA---  
>tdbD00006921 *Leptospira\_interrogans*\_serovar\_*Lai*\_str.\_56601\_189518\_Leu\_CAG  
-CCGAAGTGGCGGAAATT-GGTA-GACGCACTGGCTTCAAGTTCAGGTTCCAGCACC---GCAA----GGTGTGGGGTTTCGAGTCCCTTCTCGGCA---  
>tdbD00006920 *Leptospira\_interrogans*\_serovar\_*Lai*\_str.\_56601\_189518\_Leu\_GAG  
-GCTCGGGTGGTGAAATT-GGTA-GACACGCAAGCTTGGAGTCTTGTGTC---TTT---AGTGTAGGGTTTCGAGTCCCCTCTCGAGCA---  
>tdbD00006918 *Leptospira\_interrogans*\_serovar\_*Lai*\_str.\_56601\_189518\_Leu\_TAA  
-GCCTGGATGGTGAAAT--GGTA-GACACCCAGGACTTAAAAATCCTGTGAGA---GCAA----TCTCGTGGAGTTTCGAGTCTCGTCCAGGTACCA  
>tdbD00006919 *Leptospira\_interrogans*\_serovar\_*Lai*\_str.\_56601\_189518\_Leu\_TAG  
-GCGAGTATGGTGAAATT-GGTA-GACACGCGAGATTTAGGTTCTGTGTC-----GAAA----TGTGTGGGGTTTCGAGTCCCTTACTCTCGCA---  
>tdbD00006588 *Listeria\_innocua*\_Cliph1262\_272626\_Leu\_CAA  
-GCCGGCTGGCGGAAATT-GGCA-GACGCGCTGGACTCAAAATCCTGTGTC---GCAA----GGCGTGGCGGTTTCGACCCCGCCCGCGGTA---  
>tdbD00006587 *Listeria\_innocua*\_Cliph1262\_272626\_Leu\_GAG  
-GCGGTCTGGCGGAAATC-GGCA-GACGCGCTAGGTTGAGGGCCTAGTGAGGT---AAA---ACTCG-TGGAGTTCAAGTCTCTCGGCCGCA---  
>tdbD00006586 *Listeria\_innocua*\_Cliph1262\_272626\_Leu\_TAA  
-GCCGGGTGGCGGAAATT-GGCA-GACGACAGGACTTAAAAATCCTGCGGATA---GTGA---TATCCGTACCGGTTTCGATCCCGTCTCGGCA---  
>tdbD00006585 *Listeria\_innocua*\_Cliph1262\_272626\_Leu\_TAG  
-GCGGGTGTGGCGGAAATT-GGCA-GACGACAGATTTAGGATCTGCGCC---GCGA----GGCGTGGGGTTTCAGTCCCTTACCCGCA---  
>tdbD00006591 *Listeria\_monocytogenes*\_EGD-a\_169963\_Leu\_GAG  
-GCGGTCTGGCGGAAATC-GGCA-GACGCGCTAGGTTGAGGGCCTAGTGGGGT---AAA---ACCG-TGGAGTTCAAGTCTCTCGGCCGCA---  
>tdbD00007187 *Mesoplasma\_florum*\_L1\_265311\_Leu\_CAA  
-GCCTCTTGGCGGAAATT-GGCA-GACGCATCAGACTCAAAATCTGACGAG-----GAAA----CTCGTATCGGTTTCGACCCCGATAGGAGGCACCA  
>tdbD00007188 *Mesoplasma\_florum*\_L1\_265311\_Leu\_TAA  
-CCCAAGTGGCGGAAATC-GGTA-GACGCGTGGACTTAAAAATCCACCGGGCT---TTAT---CTCCGTGCCAGTTCAAGTCTGCGCTTGGGGACCA  
>tdbD00007186 *Mesoplasma\_florum*\_L1\_265311\_Leu\_TAG  
-GCGGGATTGGCGGAAATT-GGCA-GACGCACTAGACTTAGGATCTAGCGTC-----TTC----GACGTAAGGTTTCGAGTCCCTTATCCCGACCA  
>tdbD00006629 *Mesorhizobium\_lotii*\_MAFF303099\_266835\_Leu\_CAA  
-GCCCTATGGCGGAAATT-GGTA-GACGCGCTGACTCAAAATCGAGTTCC---GCAA----GGAGTGTGGTTTCGATCCCGGCTAGGGCACCA  
>tdbD00006630 *Mesorhizobium\_lotii*\_MAFF303099\_266835\_Leu\_CAG  
-GCCAGATGGCGGAAATT-GGTA-GACGCGCAGGTTTCAAGTCCGTGTTCC---GCAA----GGAGTGGAGTTTCGAGTCCCTTCTTGGGCACCA  
>tdbD00006626 *Mesorhizobium\_lotii*\_MAFF303099\_266835\_Leu\_TAA  
-GCGGACGTGGCGGAAATT-GGTA-GACGCAAGGACTTAAAAATCCCTCGATC---TCT---GATCGTACGGTTTCGATCCCGTCTCGCACCA  
>tdbD00006627 *Mesorhizobium\_lotii*\_MAFF303099\_266835\_Leu\_TAG  
-GCGGATGTGGCGGAACT-GGTA-GACGCCCTGGATTTAGGTTCCAGTGCC---GAAA----GGCGTGGGGTTTCGAGTCCCTTCTATCCGCACCA  
>tdbD00007004 *Mycobacterium\_bovis*\_AF2122/97\_233413\_Leu\_CAA  
-GCCCTCGTATCCCAACT-GGCA-GAGGAAACGACTCAAAACCCGTCC-----AGTGTGGGTTTCGATCCCACCAGGGCACCA  
>tdbD00007001 *Mycobacterium\_bovis*\_AF2122/97\_233413\_Leu\_CAG  
-GGCGAGTGGCGGAAAT--GGCA-GACGCGCTGGCTTCAAGTTCAGTGTGTC---TTCG---GGAGTGGGGTTTCAGTCCCCTTTCGCCA---  
>tdbD00007005 *Mycobacterium\_bovis*\_AF2122/97\_233413\_Leu\_GAG  
-GTCCGAGTGGCGGAAAT--GGCA-GACGCGCTAGCTTCAAGTGTGCTAGTGCCCTA---CTAA---TGGGCG-TGGGGTTTCAGTCCCCTTTCGGACA---  
>tdbD00007002 *Mycobacterium\_bovis*\_AF2122/97\_233413\_Leu\_TAA  
-GCCCCATAGCCCAATT-GGCA-GAGGCAGCGACTTAAAAATCCGTCA-----AGTGTGGGTTTCGAGTCCGACTGGGGGCA---  
>tdbD00007003 *Mycobacterium\_bovis*\_AF2122/97\_233413\_Leu\_TAG  
-GCGGGCTGATGAAATT-GGCA-AACATGCCGTTTTAGGTGCGGTTGCTC---GAAA----GAGTTTGGGGTTTCGAGTCCCTTTCGCCGCA---  
>tdbD00001539 *Mycobacterium\_leprae*\_1769\_Leu\_CAG  
-GGCGAGTGGCGGAAAT--GGCA-GACGCGCTGGCTTCAAGTTCAGTGTGTC---CTCG---GGAGTGGGGTTTCAGTCCCCTTTCGCCA---  
>tdbD00006484 *Mycobacterium\_leprae*\_TN\_272631\_Leu\_CAA  
-GCCCTCGTATCCCAACT-GGCA-GAGGAAACGACTCAAAACCCGTCC-----AGTGTGGGTTTCGATCCCACCAGGGGCA---  
>tdbD00006486 *Mycobacterium\_leprae*\_TN\_272631\_Leu\_GAG  
-GTCCGAGTGGCGGAAAT--GGCA-GACGCGCTAGCTTCAAGTGTGCTAGTGCCCTA---CTAA---TGGGCG-TGGGGTTTCAGTCCCCTTTCGGACA---  
>tdbD00006488 *Mycobacterium\_leprae*\_TN\_272631\_Leu\_TAG  
-GCGGGCTGATGAAAT--GGCA-GACATGCCGTTTTAGGTGCGGTTGCTC---GAAA----GAGCGTGGGGTTTCGACTCCCTTTCGCCGCA---  
>tdbD00001499 *Mycoplasma\_capricolum*\_2095\_Leu\_TAA

-CCCCAAGTGGCGGAATA-GGTA-GACGCATTGGACTTAAAAATCCAACGGGCT----TAAT---ATCCTGTGCCGGTTCAAGTCCGGCCTTGGGGACCA  
>tdbD00001500 Mycoplasma\_capricolum 2095 Leu TAG  
--GGGGATTGGCGGAATT-GGCA-GACGCACTAGACTTAGGATCTAGCGTC-----TTT-----GACGTAAGGGTTCAAGTCCCTTATCCCCACCA  
>tdbD00007000 Mycoplasma\_gallisepticum\_R 233150 Leu CAA  
-CCTGGAGTGGCGGAAT--GGCA-AAACGCATCAGACTCAAAATGTGACGGGT---TAC-----ACCTTGTGAGTTCAAGTCTCATCTCCAGGACCA  
>tdbD00006999 Mycoplasma\_gallisepticum\_R 233150 Leu TAA  
-GCCCAAGTACGGAAT--GGTA-GACGTACAGGACTTAAAAATCCTGGGGTA----GCGA----TACCGTGCCGGTTCAAGTCCGGCTTGGGCACCA  
>tdbD00006998 Mycoplasma\_gallisepticum\_R 233150 Leu TAG  
-GACTCGTGGCGGAAT--GGCA-GACGCGCTAGACTTAGGATCTAGTATCA-----TTA-----CGATGTGGGGTTCAAGTCCCTTCGAGTGCACCA  
>tdbD00001503 Mycoplasma\_genitalium 2097 Leu GAG  
-GTCGGAGTGGTGAAT--GGTA-GACACGCAAGCTTGAGGTGCTTGTGGTCG---TTAA---AGACTGTGCCAGTTCAAGTCTGGTCTCCGACACCA  
>tdbD00001501 Mycoplasma\_genitalium 2097 Leu TAA  
-GCCCAAGTGGCGGAAT--GGTA-GACGCATGGGATTTAAGATCCCACGCCA----GTAA----TGGTGTGCCGGTTCAAGTCCGGCTTGGGCACCA  
>tdbD00001502 Mycoplasma\_genitalium 2097 Leu TAG  
-GACTCGTGGCGGAAT--GGTA-GACGCGCTAGACTTAGGATCTAGTTTCA-----TCT-----AGAAGTGGGGTTCAAGTCCCTTCGGGTGCACCA  
>tdbD00006543 Mycoplasma\_genitalium\_G37 243273 Leu CAA  
-CCTGGAGTGGCGGAAT--GGTA-GACGCGGTGGACTCAAAACCCACTAGG-----AAA-----CTG-TAGGAGTTCAAGTCTCCTCTCCAGGACCA  
>tdbD00001506 Mycoplasma\_pneumoniae 2104 Leu TAA  
-GCCCAAGTGGCGGAAT--GGTA-GACGCATGGGATTTAAGATCCCACGCTA----GCAA----TAGCGTGCCGGTTCAAGTCCGGCTTGGGCACCA  
>tdbD00001505 Mycoplasma\_pneumoniae 2104 Leu TAG  
-GACTCGTGGCGGAAT--GGTA-GACGCGCTAGACTTAGGATCTAGTTTCA-----TTG-----TGGAGTGGGGTTCAAGTCCCTTCGAGTGCACCA  
>tdbD00006548 Mycoplasma\_pneumoniae\_M129 272634 Leu GAG  
-GTCGGAGTGGTGAAT--GGTA-GACACGCAAGCTTGAGGGGCTTGTGGTC---GCAA----GACTGTGCCAGTTCAAGTCTGGTCTCCGACACCA  
>tdbD00006655 Mycoplasma\_pulmonis\_UAB\_CTIP 272635 Leu CAA  
-GCCCAGTGGTGAAT--GGCA-GACACAGTTGACTCAAAATCAACCGCT-----TCAC-----GGCGTGTGGTTCAAGTCCAGTCTCCGGCACCA  
>tdbD00006656 Mycoplasma\_pulmonis\_UAB\_CTIP 272635 Leu TAA  
-GCCCAGTGGCGGAATA-GGTA-GACGCAGGGGACTTAAAAATCCCCCGGCA----GTAG----TGCCGTGTGGTTCAATTCAGTTCGGGTACCA  
>tdbD00006657 Mycoplasma\_pulmonis\_UAB\_CTIP 272635 Leu TAG  
-GCGGAGTGGTGAAT--GGCA-GACACGCTAGATTAGGCTCTAGTGCT-----TTAC-----AGTGTGAGGGTTCAAGTCCCTCCTCGTGCACCA  
>tdbD00001506 Mycoplasma\_sp\_PG50 2126 Leu TAG  
-GGGGATTGGCGGAATT-GGCA-GACGCACTAGACTTAGGATCTAGCGTC-----TTT-----GACGTAAGGGTTCAAGTCCCTTATCCCCACCA  
>tdbD00006462 Neisseria\_meningitidis\_MC58 122586 Leu CAA  
-GCCCAGTGGCGAAAT--GGTA-GACGCAGGGGACTCAAAATCCCCCGCC-----GCAA----GGTGTGTCGGTTTCGAGTCCGACCCCTGGGCACCA  
>tdbD00006463 Neisseria\_meningitidis\_MC58 122586 Leu CAG  
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>tdbD00006464 Neisseria\_meningitidis\_MC58 122586 Leu CAG  
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>tdbD00006465 Neisseria\_meningitidis\_MC58 122586 Leu TAA  
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>tdbD00006466 Neisseria\_meningitidis\_MC58 122586 Leu TAG  
-GCGGAGTGGCGAAAT--GGTA-GACGCACAGATTAGGTTCTGGCGCC-----GAGA----GGTGTGAGAGTTTCGAGTCTCTCCGTCCGCACCA  
>tdbD00006468 Neisseria\_meningitidis\_Z2491 122587 Leu CAG  
-GCCCAGTGGCGGAATT-GGTA-GACGCGCCAGCTTCAGGTGCTGATATCC-----TCAC-----GGGTGTGGAAGTTTCGAGTCTTCTCCCGGCACCA  
>tdbD00006469 Neisseria\_meningitidis\_Z2491 122587 Leu GAG  
-GCCGACATGGTGAAT--GGTA-GACACGCTATCTTGAGGGGGTAGTGGCC-----GTA-----GGCTGTGCGAGTTCAAATCTCGCTGTCCGCACCA  
>tdbD00007053 Nitrosomonas\_europaea\_ATCC\_19718 228410 Leu CAA  
-GCGGGATGGCGGAAT--GGTA-GACGCACGGGACTCAAAATCCCCGATG---GTGA----CATCATGGGGTTTCGATTCCCCCTCCCGGCACCA  
>tdbD00007052 Nitrosomonas\_europaea\_ATCC\_19718 228410 Leu CAG  
-GCCGAGATGGCGGAAT--GGTA-GACGCGCATGGTTTCAGGTCCATGTGCC-----TTCC-----GGTGTGAGAGTTTCGAGTCCCTTCTTGGGCACCA  
>tdbD00007054 Nitrosomonas\_europaea\_ATCC\_19718 228410 Leu GAG  
-GCGGACGTGGTGAAT--GGTA-GACACGCGTCTTGAGGGGGCGGTGGC-----GAAA----GCTGTGCGAGTTTCGATTCTCGCGTCCGCACCA  
>tdbD00007050 Nitrosomonas\_europaea\_ATCC\_19718 228410 Leu TAA  
-GCCCAGTGGTGAAT--GGTA-GACACAAGGGACTTAAAAATCCCTCGGACA---TTAA---CGTCCGTGCCGGTTTCGATTCCGGCCCCGGGCACCA  
>tdbD00007051 Nitrosomonas\_europaea\_ATCC\_19718 228410 Leu TAG  
-GCGAAAGTGGCGGAAT--GGTA-GACGCACAGATTAGGTTCTGGCGCC---ATG----AGGTGTGGGGTTTCGAGTCCCCCTTTCGCACCA  
>tdbD00006649 Nostoc\_sp.\_PCC\_7120 103690 Leu CAA  
-ACTCCTGTAGCCCAATT-GGCA-GAGGCGGCTGTTTCAAAAACAGTCT-----G-----TGTATGGGTTCAAATCCCATCAGGAGTACCA  
>tdbD00006650 Nostoc\_sp.\_PCC\_7120 103690 Leu CAA  
-GGGCGGTGGCGGAAT--GGTA-GACGCACACACTCAAAATGTGGCGACC-----TTGC-----GGTCATAGGAGTTTCGATTCTCCTCTGCCCA---  
>tdbD00006651 Nostoc\_sp.\_PCC\_7120 103690 Leu CAG  
-GCGGAACTGGCGGAAT--GGCA-GACGCGCTAGATTTCAGGTCTAGTGCC-----GCAA----GGCTTCCGGGTTCAAGTCCCGGGTTCCGCA---  
>tdbD00006652 Nostoc\_sp.\_PCC\_7120 103690 Leu GAG  
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>tdbD00006646 Nostoc\_sp.\_PCC\_7120 103690 Leu TAA  
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>tdbD00006654 Nostoc\_sp.\_PCC\_7120 103690 Leu TAA  
-GGGGTGTGGCGGAAT--GGTA-GACGCTACGGACTTAAAAATCCGTTGACCT---TAAA---CGGTCTGTGGGTTCAAGTCCCTCCACCCCCA---  
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-GCCCTGTGACGCAATT-GGCA-GACGTAGCCGCTTAGACCGGGTTT-----GTTGCAGGTTCAACTCCTGTCAAGGTA---  
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-GCGGATGTGGCGGAAT--GGCA-GACGCGCTAGATTAGGTTCTAGTTCC-----GAGA----GGAGTGAAGTTTCAGTCCCTTTCATCCGCA---  
>tdbD00006925 Oceanobacillus\_ihayensis\_HTE831 221109 Leu GAG  
-GCGGTCTGGCGGAAT--GGCA-GACGCGCTAGGTGAGGGCCTAGTGGGCG---TAT---AGCCCGTGTGGGTTCAAATCCCCTGACCGCA---  
>tdbD00006924 Oceanobacillus\_ihayensis\_HTE831 221109 Leu TAA  
-GCCCAGTGGCGGAAT--GGCA-GACGCACAGACTTAAAAATCCTGCGGTAG---GTGA---CTACCGTACCGGTTTCGATTCCGGTCTCCGCACCA

>tdbD00006923 *Oceanobacillus\_iheyensii\_HTE831\_221109\_Leu\_TAG*  
-GCGGTGTGGCGGAATT-GGCA-GACGCGCTAGACTTAGGATCTAGTGTC-----TTCG-----GACGTGGGGGTTCAAGTCCCTTACCCGCACCA  
>tdbD00007086 *Onion\_yellows\_phytoplasma\_OY-M\_262768\_Leu\_CAA*  
-GCTGATGTGGCGGAATT--GGTA-GACGCACTTGACTCAAAATCAACGCGAGC-----AAT-----ACTCATGTGCGTTTCGAGTCCGACCATCAGTACCA  
>tdbD00007088 *Onion\_yellows\_phytoplasma\_OY-M\_262768\_Leu\_GAG*  
-GCGGATATGACGGAAC--GGTA-GACGTGCATGCTTGAGGGGCGATGTAAGA-----AATA-----TCTTGTGTGAGTTCAAATCTCACTATCCGCACCA  
>tdbD00007087 *Onion\_yellows\_phytoplasma\_OY-M\_262768\_Leu\_TAA*  
-GCCTGGATGGTGAATC-GGTA-GACACGTGGGACTTAAAATCCCATGGTT-----TAT-----AGCCGTGTCGTTCAAGTCCGACTCCAGGTACCA  
>tdbD00007085 *Onion\_yellows\_phytoplasma\_OY-M\_262768\_Leu\_TAG*  
-GCGGTGTGGCGGAATT--GGAA-GACGCACTAGACTTAGGATCTAGCGC-----TTAG-----GCGTGCAGGTTCAAATCCTGTACCCCGTACCA  
>tdbD00006551 *Pasteurella\_multocida\_subsp.\_multocida\_str.\_Pm70\_272843\_Leu\_CAA*  
-GCCTGGGTGGCGAAATT--GGTA-GACGCACTTGACTCAAAATCAACCGCC-----TTCG-----GGTGTGCGGTTTCGAGTCCGGCCCTAGGCACCA  
>tdbD00006552 *Pasteurella\_multocida\_subsp.\_multocida\_str.\_Pm70\_272843\_Leu\_TAA*  
-GCCGAGGTGGCGAAATC-GGTA-GACACAAGGGATTAAAATCCCTGCTT-----TTCG-----AAGCGTGCAGTTCAAGTCTGGCCTCGGCACCA  
>tdbD00006553 *Pasteurella\_multocida\_subsp.\_multocida\_str.\_Pm70\_272843\_Leu\_TAG*  
-GCGGACTGGCGAAATT--GGTA-GACGCACTAGACTTAGGATCTAGCGC-----GCGA-----GGTGTGTTGGGTTCAAGTCCCTCGTCCGCACCA  
>tdbD00001540 *Photobacterium\_leiognathi\_658\_Leu\_TAG*  
-GCGAAGTGGCGGAATT--GGTA-GACGCACTAGACTTAGGATCTAGCGC-----GTA-----AGGTGTGAGAGTTCAAGTCTCTCTCTCCGCACCA  
>tdbD00007103 *Photobacterium\_luminescens\_subsp.\_laumondii\_TTO1\_243265\_Leu\_CAA*  
-GCCGAGTGGCGAAATC-GGTA-GACGCACTTGACTCAAAATCAACCGCC-----TTCG-----GGTGTGCGGTTTCGAGTCCGGCCCTCGGCACCA  
>tdbD00007101 *Photobacterium\_luminescens\_subsp.\_laumondii\_TTO1\_243265\_Leu\_CAG*  
-GCGAGGTGGCGGAATT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC-----TTAC-----TGACGTGGGGTTCAAGTCCCCCCTTCGCACCA  
>tdbD00007102 *Photobacterium\_luminescens\_subsp.\_laumondii\_TTO1\_243265\_Leu\_CAG*  
-GCGAGGTGGCGGAATT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC-----TTAC-----GGAGGTGAGGTTCAAGTCCCTCTCTTCGCACCA  
>tdbD00007105 *Photobacterium\_luminescens\_subsp.\_laumondii\_TTO1\_243265\_Leu\_CAG*  
-GCGAGGTGGCGGAATT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC-----TTAC-----GGAGGTGAGGTTCAAGTCCCCCCTTCGCACCA  
>tdbD00007104 *Photobacterium\_luminescens\_subsp.\_laumondii\_TTO1\_243265\_Leu\_GAG*  
-GCCGAGTGGTGAATC-GGTA-GACACGCTACTTTCAGGTGTTAGTGTCC-----CACT-----AGGGTTCAGGGTTCAAGTCCCGTCTCGGTACCA  
>tdbD00007100 *Photobacterium\_luminescens\_subsp.\_laumondii\_TTO1\_243265\_Leu\_TAA*  
-GCCGAGTGGTGAATC-GGTA-GACACAAGGGATTAAAATCCCTGCTT-----GTAA-----GGTGTGCGGGTTCAAGTCCCGCCTCGGCACCA  
>tdbD00007141 *Porphyromonas\_gingivalis\_W83\_242619\_Leu\_CAA*  
-GCCCGATGGCGGAATT--GGTA-GACGCGTGGTCTCAAACACCAATGAAT-----GCAA-----ATTCGTGCCGTTTCGATCCCGCTCCGGCA---  
>tdbD00007144 *Porphyromonas\_gingivalis\_W83\_242619\_Leu\_CAG*  
-GCCCGATGGCGGAATT--GGTA-GACGCGTGGTCTCAAACACCAATGAAT-----AAA-----AGAGTGCAGGTTTCGATCCTGTCCCGGCA---  
>tdbD00007143 *Porphyromonas\_gingivalis\_W83\_242619\_Leu\_GAG*  
-GCGCGGTGGTGAATC-GGTA-GACACGCTACTTTCAGGTGTTAGTGTCC-----GTTA-----CGGTGTGAGTTCAAATCTCATCTCGCGTA---  
>tdbD00007140 *Porphyromonas\_gingivalis\_W83\_242619\_Leu\_TAA*  
-GCCCGATGGTGAATC-GGTA-GACACAAGGGATTAAAATCCCTGCTT-----TTAT-----CGGTGTGCGGGTTCAAGTCCCGCTCCGGTA---  
>tdbD00007142 *Porphyromonas\_gingivalis\_W83\_242619\_Leu\_TAG*  
-GCGGTGTGGTGAATC-GGTA-GCCACGCTAGACTTAGGATCTGGTGTCT-----TCAC-----GGCGTGCAGTTTCGAGTCTCGCCAGCCGCA---  
>tdbD00007190 *Propionibacterium\_acnes\_KP171202\_267747\_Leu\_CAA*  
-GCCGAGTGGCGGAAT--GGTA-GACGCGGCGCACTCAAAATCCGCTGTCC-----TTGC-----GGCGTAGGGTTTCGACTCCCTCTCGGGCA---  
>tdbD00007193 *Propionibacterium\_acnes\_KP171202\_267747\_Leu\_CAG*  
-GCGGAGTGGCGGAAT--GGCA-GACGCGTGGCTTCAGGTGCCAGTGTCC-----CTTG-----GGAGTGGAGTTCAACTCCTCTCTCGCGCA---  
>tdbD00007191 *Propionibacterium\_acnes\_KP171202\_267747\_Leu\_GAG*  
-GTCCGGTGGCGGAAT--GGTA-GACGCGCTAGCTTCAGGTGCTAGTGGCCG-----ATTA-----AGGCTGTGAGGTTCAAGTCTCTCTCGGACA---  
>tdbD00007189 *Propionibacterium\_acnes\_KP171202\_267747\_Leu\_TAA*  
-GCCCGTAGCCCAACC-GGCA-GAGGCAGACGGCTTAAACCCGTCCC-----AGTGGGGTTTCGAATCCCGTCCGGGGTA---  
>tdbD00007192 *Propionibacterium\_acnes\_KP171202\_267747\_Leu\_TAG*  
-GCCGAGTGGTGAATC-GGTA-GACACGCAAGGATTAAAATCCCTGCTT-----TTGT-----GGTGTGAGGTTTCGAGTCCCTCTCGGCA---  
>tdbD00006559 *Pseudomonas\_aeruginosa\_PA01\_208964\_Leu\_CAA*  
-GCCTGGTGGCGGAATC-GGTA-GACGCGGCGGATTCAAAATCCGTTTCTG-----GCGA-----CAGAGTGCAGTTTCGAGTCTCTCCGAGGCACCA  
>tdbD00006560 *Pseudomonas\_aeruginosa\_PA01\_208964\_Leu\_CAG*  
-GCCGAGTGGCGGAAT--GGTA-GACGCACTAGGTTTCAGGTCTAGCGGTG-----GCAA-----CACCGTGAAGTTTCGAGTCTCTCTCGGCACCA  
>tdbD00006561 *Pseudomonas\_aeruginosa\_PA01\_208964\_Leu\_GAG*  
-GCCGAGTGGTGAATC-GGTA-GACACGCTACTTTCAGGTGTTAGTGTCC-----ATA-----GGTGTAGGGTTTCGAGTCCCTCTCGGTACCA  
>tdbD00006562 *Pseudomonas\_aeruginosa\_PA01\_208964\_Leu\_TAA*  
-GCCCGATGGCGAAATC-GGTA-GACGCAAGGGACTTAAAATCCCTCGGGG-----TAA-----CCCCG-TGCCGTTTCGACCCCGCTCCGGGCACCA  
>tdbD00006563 *Pseudomonas\_aeruginosa\_PA01\_208964\_Leu\_TAG*  
-GCGGAGTGGTGAATC-GGTA-GACACACTGGATTTAGGTTCCAGCGCC-----GCAA-----GGCGTGCAGTTTCGAGTCTCTCCGTCGCGACCA  
>tdbD00007060 *Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283\_Leu\_CAA*  
-GCCCTGATGGCGGAAT--GGTA-GACGCGGCGGATTCAAAATCCGTTTTC-----GAAA-----GAAGTGGGAGTTTCGATCCTCTCTCGGGCACCA  
>tdbD00007064 *Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283\_Leu\_CAG*  
-GCCAGATGGTGAATC-GGTA-GACACGCGAGTTTCAGGTGCTGGTGACC-----GCAA-----GGTGTGAGGTTTCGAGTCTCTCTCGGCACCA  
>tdbD00007063 *Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283\_Leu\_GAG*  
-GCCGAGTGGTGAATC-GGTA-GACACGCAACCTTCAGGTGTTAGTGTCC-----AAT-----GGTGTAGGGTTTCGAGTCCCTCTCTCGGTACCA  
>tdbD00007061 *Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283\_Leu\_TAA*  
-GCCCGATGGCGAAAT--GGTA-GACGCAAGGGACTTAAAATCCCTGCTT-----TTT-----GGAGTGCAGTTTCGAGTCCCGCTCCGGGCACCA  
>tdbD00007062 *Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283\_Leu\_TAG*  
-GCGGATGGTGAATC-GGTA-GACACACTGGATTTAGGTTCCAGCGCC-----GCAA-----GGTGTGAGGTTTCGAGTCTCTCCGTCGCGACCA  
>tdbD00006645 *Ralstonia\_solanacearum\_GMI1000\_267608\_Leu\_CAA*  
-GCCCGGTGGTGAACA-GGTA-GACGCAAGGGACTCAAAATCCCGCC-----GCAA-----GGCGTGCAGTTTCGAGTCCGACCCCGGCACCA  
>tdbD00006642 *Ralstonia\_solanacearum\_GMI1000\_267608\_Leu\_CAG*  
-GCCGAGTGGCGGAAT--GGTA-GACGCACTAGTTTCAGGTACTAGCGGG-----TAAC-----TCCGTGAGGTTTCGAGTCTCTCTCGGCACCA  
>tdbD00006644 *Ralstonia\_solanacearum\_GMI1000\_267608\_Leu\_GAG*

-GCCGACGTGGTGA AATT-GGTA-GACACGCTATCTTGAGGGGGTAGTGGC-----GAAA-----GCTGTGCGAGTTCGAGTCTCGCCGTCGGCACCA  
>tdbD00006641 Ralstonia\_solanacearum\_GMI1000\_267608\_Leu\_TAA  
-GCCCGAGTGGTGA AATT-GGTA-GACACCGCGGACTTAAATCCGCTGCGCCC---TCAC---CGGCGGTGCGGGTTCGACCCCGCCTCGGGCACCA  
>tdbD00006643 Ralstonia\_solanacearum\_GMI1000\_267608\_Leu\_TAG  
-GCGAGGGTGGCGAA AATT-GGTA-GACGCACCAGGTTTAGGTCTGACGCCA-----GCAA----TGGTGTAGGGGTTTCGAGTCCCCTCCCTCGCACCA  
>tdbD00007041 Rhodopirellula\_baltica\_SH\_1\_243090\_Leu\_CAA  
-GCCGAAGTGGCGGA AATT-GGCA-GACGCGCTGGATTCAAATCCAGTTGGA-----GCAA----TCCAGTGAGGGTTCGAGTCCCCTCCCTCGGTA---  
>tdbD00007048 Rhodopirellula\_baltica\_SH\_1\_243090\_Leu\_CAA  
-GCTGTGTTACGCAA ACC-GGCA-AAGCGGGCAATTCAAACGTTCTGTG-----TTTGAAGGGTTCGACTCCCCTCCCGCAGTA---  
>tdbD00007042 Rhodopirellula\_baltica\_SH\_1\_243090\_Leu\_CAG  
-GCGGATGTGGCGGA AATT-GGCA-GACGCGCTAGACTCAGGATCTAGTGCCCG---ATA---AGGGCGTGGAGGTTCAATCCTCTCATCCGTA---  
>tdbD00007047 Rhodopirellula\_baltica\_SH\_1\_243090\_Leu\_CAG  
-AGCCAAGTGGTGA AACT-GGTA-GACACGCGACACTCAGAATGTCGTGCC---ACAG---CGGCGTGCAGGTTCAACTCTCGCTTGGCTA---  
>tdbD00007044 Rhodopirellula\_baltica\_SH\_1\_243090\_Leu\_GAG  
-GCGGCGTGGCGGA AACT-GGCA-GACGCGCTAGGTTGAGGGCCTAGTGGGAG---TTA---ATCCCGTGGAGGTTTCGAGTCCCTCTCGGCCA---  
>tdbD00007046 Rhodopirellula\_baltica\_SH\_1\_243090\_Leu\_GAG  
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>tdbD00007043 Rhodopirellula\_baltica\_SH\_1\_243090\_Leu\_TAA  
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>tdbD00007049 Rhodopirellula\_baltica\_SH\_1\_243090\_Leu\_TAA  
-GCTTAGATACGCAA ACC-GGCC-GAGCGGCTCGACTTAAACCCGAGTG-----TTTCGAGGTTTCGACTCCTGTCTGGGCA---  
>tdbD00007040 Rhodopirellula\_baltica\_SH\_1\_243090\_Leu\_TAG  
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>tdbD00007045 Rhodopirellula\_baltica\_SH\_1\_243090\_Leu\_TAG  
-GGGGTGTGGCGGA AACT-GGCA-GACGCGCTAGATTAGGATCTAGTTCC-----TTCG---GGAGTGCAGGTTTCGATTCTCTGTCAGCCCTA---  
>tdbD00007107 Rhodopseudomonas\_palustris\_CGA009\_258594\_Leu\_CAA  
-GCCCTGTGGCGGA AACT-GGTA-GACGCGCTCGACTCAAATTCGAGTTCC-----GCAA----GGAGTGTGGTTCGATCCCCTCCCGCAGGGCACCA  
>tdbD00007106 Rhodopseudomonas\_palustris\_CGA009\_258594\_Leu\_CAG  
-GCCAGGTGGCGGA AATT-GGTA-GACGCGCTGGTTTCAGGTACCAGTGGGT---AAC---ACCG-TGGAGGTTTCGAGTCCCTCTCCCTGGGCACCA  
>tdbD00007109 Rhodopseudomonas\_palustris\_CGA009\_258594\_Leu\_GAG  
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>tdbD00007110 Rhodopseudomonas\_palustris\_CGA009\_258594\_Leu\_TAA  
-GCGGGCGTGGCGAA AATT-GGTA-GACGCAAGGGACTTAAATCCCTCGGCTC---GAAA---GAGCTGTGCCGTTTCGACCCCGCCCGCCCGCACCA  
>tdbD00007108 Rhodopseudomonas\_palustris\_CGA009\_258594\_Leu\_TAG  
-GCGGGCGTGGCGGA AATT-GGTA-GACGCGCTGGATTAGGTTCCAGTGAC---GAAA---GTGTGGGGTTCGAGTCCCCTCCCGCCCGCACCA  
>tdbD00006617 Rickettsia\_conorii\_str\_Malish\_7\_272944\_Leu\_GAG  
-GCGGTCTGTGGCGAA AATT-GGTA-GACGCGCAGCATGAGGGTGTCTGTCTG---TAAA---AAGATTGGAAGTTCAAGTCTTCTCGACCGCACCA  
>tdbD00006618 Rickettsia\_conorii\_str\_Malish\_7\_272944\_Leu\_TAA  
-GCCCGCGTGA TGGAAT--GGTA-GACATAACGGACTTAAATCCCGTGGAGC---GTAA---GCTCTTCCCGGTTCAAGTCCCGCCCGGGTACCA  
>tdbD00006619 Rickettsia\_conorii\_str\_Malish\_7\_272944\_Leu\_TAG  
-GCGGATGTGA TGGAAT--GGTA-GACATGAAGATTAGGTTCTTGTGCC---GTGA---GGCGTGGGGTTCAGTCCCTTCATCCGTACCA  
>tdbD00006841 Rickettsia\_prowazekii\_str\_Madrid\_E\_272947\_Leu\_GAG  
-GCGGTCTGTGGCGAA AATT-GGTA-GACGCGCAGCATGAGGGTGTCTGTCTG---TAAA---AGGATTGGAAGTTCAATCTTCTCGACCGCACCA  
>tdbD00006843 Rickettsia\_prowazekii\_str\_Madrid\_E\_272947\_Leu\_TAG  
-GCGGATGTGA TGGAAT--GGTA-GACATGAAGATTAGGTTCTTGTGCT---GTGA---GGCGTGGGGTTCAGTCCCTTCATCCGTACCA  
>tdbD00007146 Rickettsia\_typhi\_str\_Wilmington\_257363\_Leu\_TAA  
-GCCCGCGTGA TGGAAT--GGTA-GACATAACGGACTTAAATCCCGTGGAGT---GTAA---ACTCTTCCCGGTTCAAGTCCCGCCGTGGTACCA  
>tdbD00006665 Salmonella\_enterica\_subsp\_enterica\_serovar\_Typhi\_str\_CT18\_220341\_Leu\_GAG  
-GCCGAGGTGGTGA AATT-GGTA-GACACGCTACCTTGAGGTGGTAGTGCC---AATA---GGGCTTACGGGTTCAAGTCCCCTCCCTCGGTACCA  
>tdbD00006937 Shewanella\_oneidensis\_MR-1\_211586\_Leu\_CAA  
-GCCAGAGTGGTGA AATC--GGTA-GACACAGTGGATTCAAATCCACCGCCCT---TAA---AAGCG-TGACGTTTCGAGTCCGCTCTGTTACCA  
>tdbD00006934 Shewanella\_oneidensis\_MR-1\_211586\_Leu\_CAG  
-GCAGGTGTGGTGA AATT-GGTA-GACACGCCAGCTTCAGGTGCTGGTGCC---TTGC---GGGCGTGGAGGTTCAAGTCCCTCTCATCTGTACCA  
>tdbD00006935 Shewanella\_oneidensis\_MR-1\_211586\_Leu\_GAG  
-GCAGATGTGGTGA AATC--GGTA-GACACGCCAGCTTCAGGTGCTGGTGCC---TTGC---GGGCGTGGAGGTTCAAGTCCCTCTCATCTGTACCA  
>tdbD00006933 Shewanella\_oneidensis\_MR-1\_211586\_Leu\_GAG  
-GCCGAGGTGGTGA AATT-GGTA-GACGCGCAGCCTTGAGGTGGCTGTGTCC---TAAC---GGACGTGCGGGTTCAGTCCCCTCTCGGCACCA  
>tdbD00006936 Shewanella\_oneidensis\_MR-1\_211586\_Leu\_TAA  
-GCCCGAGTGGTGA AATC--GGTA-GACACAAGGGATTAAATCCCTCGCTG---GTAA---CAGCGTGCAGGTTCAAGTCTGGCTCGGGTACCA  
>tdbD00006938 Shewanella\_oneidensis\_MR-1\_211586\_Leu\_TAG  
-GCGGGAATGGTGA AATT-GGTA-GACACGCCAGATTAGGTTCTGGTGCC---GCAA---GGTGTGAGAGTTCAAGTCTCTCTTCCCGTACCA  
>tdbD00006939 Shewanella\_oneidensis\_MR-1\_211586\_Leu\_TAG  
-GCGGGAATGGTGA AATC--GGTA-GACACGCCAGATTAGGTTCTGGTGCC---GCGA---GGTGTGAGAGTTCAAGTCTCTCTTCCCGTACCA  
>tdbD00006673 Sinorhizobium\_meliloti\_1021\_266834\_Leu\_CAA  
-GCCCATTTGGCGGA AATT-GGTA-GACGCGCTCGACTCAAATTCGAGTTCC---GAAA---GGAGTGTGGTTCGACTCCGGCATGGGCACCA  
>tdbD00006672 Sinorhizobium\_meliloti\_1021\_266834\_Leu\_TAA  
-GCGGAGTGGCGAA AACT-GGTA-GACGCAAGGGACTTAAATCCCTCGGG---AAA---CCG-TACGGGTTTCGATTCCCCTCGTCCGCACCA  
>tdbD00006671 Sinorhizobium\_meliloti\_1021\_266834\_Leu\_TAG  
-GCGGTATGGTGA AATT-GGTA-GACACGCCAGATTAGGTTCTGGTGCC---GCAA---GGCGTGGGAGTTCAAGTCTCTCTACCCGCACCA  
>tdbD00001522 Staphylococcus\_aureus\_1280\_Leu\_CAA  
-GCCGAGTGGCGGA AATT-GGCA-GACGCGCGGACTCAAATCCCGTTCCA---CTTG---TGTAAGTGTGGTTCGACCCCGACCCGGTA---  
>tdbD00001521 Staphylococcus\_aureus\_1280\_Leu\_TAA  
-GCCGGGTGGCGGA AACT-GGCA-GACGCAAGGGACTTAAATCCCTCGGTGA---GTGA---TCACCGTACCGGTTTCGATTCCGGTCCCTCGGCACCA  
>tdbD00001520 Staphylococcus\_aureus\_1280\_Leu\_TAG  
-GCGGTGTGGCGGA AATT-GGCA-GACGCACTAGACTTAGGATCTAGCGCCT---TTA---CGGCGTGGGGTTCGACTCCCTTACCCGCA---

>tdbD00007112 Staphylococcus\_aureus\_subsp.\_aureus\_MRSA252\_282458\_Leu\_CAA  
-GCCGTGTGGCGGAATT-GGCA-GACGCGCGGGACTCAAAATCCCGTTCCA-----CTTG----TGGAGTGTGGTTTCGACCCCGACCACCGGTA---  
>tdbD00007115 Staphylococcus\_aureus\_subsp.\_aureus\_MRSA252\_282458\_Leu\_GAG  
-GCGGTCTGGCGGAATT--GGCA-GATGCGCTAGGTTGAGGGCCTAGTGGGA-----GAAG----TCCCGTGGAGGTTCAAGTCTCTCGGCCGCA---  
>tdbD00007111 Staphylococcus\_aureus\_subsp.\_aureus\_MRSA252\_282458\_Leu\_TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGGACTTAAAAATCCCGTGGGA-----GAGA---TCACCGTACCGGTTTCGATTCCGGTCTCGGCACCA  
>tdbD00007114 Staphylococcus\_aureus\_subsp.\_aureus\_MRSA252\_282458\_Leu\_TAG  
-GCGGGTGTGGCGGAATT-GGCA-GACGCACTAGACTTAGGATCTAGCGCC-----TTAC----GGCGTGGGGGTTTCGACTCCCTTACCCGCA---  
>tdbD00006854 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620\_Leu\_GAG  
-GCGGTCTGGCGGAATT--GGCA-GACGCGCTAGGTTGAGGGCCTAGTGGGA-----GAAA----TCCCGTGGAGGTTCAAGTCTCTCGGCCGCA---  
>tdbD00006979 Staphylococcus\_epidermidis\_ATCC\_12228\_176280\_Leu\_CAA  
-GCCGTGTGGCGGAATT-GGCA-GACGCGCGGGACTCAAAATCCCGTTCCCT-----TTAT----TGGAGTGTGGTTTCGATCCCGACCACCGGTA---  
>tdbD00006982 Staphylococcus\_epidermidis\_ATCC\_12228\_176280\_Leu\_GAG  
-GCGGTCTGGCGGAATT--GGCA-GACGCGCTAGGTTGAGGGCCTAGTGGGA-----TTA---ATCCCGTGGAGGTTCAAGTCTCTCGGCCGACCA  
>tdbD00006948 Streptococcus\_agalactiae\_2603V/R\_208435\_Leu\_AAG  
-GCGGGATGGCGGAATT-GGCA-GACGCGCAGACTAAGGATCTTGTGACCG-----CTTT---TGTCGTGAGGGTTCAAGTCCCTCTCTCGCA---  
>tdbD00006947 Streptococcus\_agalactiae\_2603V/R\_208435\_Leu\_CAA  
-GCCGGCTGGCGGAATT-GGCA-GACGCGCTGACTCAAAATCCCGTTC-----TCAC----GGAGTGGCGGTTTCGACCCCGCCCGCGGTA---  
>tdbD00006946 Streptococcus\_agalactiae\_2603V/R\_208435\_Leu\_TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGGACTTAAAAATCCCGTATG-----TAA---ACATCGTACCGGTTTCGATTCCGGTCTCTCGCA---  
>tdbD00006945 Streptococcus\_agalactiae\_2603V/R\_208435\_Leu\_TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCACAGACTTAGGATCTGCGCT-----TAAC----GGCGTGGGGGTTTCGATTCCCTTACCCGCA---  
>tdbD00006954 Streptococcus\_mutans\_UA159\_210007\_Leu\_CAA  
-GCCGGCTGGCGGAATT-GGCA-GACGCGCTGACTCAAAATCCAGTGTCC-----GCAA----GGAGTGGCGGTTTCGACCCCGCCCGCGGTA---  
>tdbD00006950 Streptococcus\_mutans\_UA159\_210007\_Leu\_CAG  
-GCGGATGGTGAAC--GGCA-GACACGATGCTTCAGGCGCATGTGCTC-----GTAT----GAGCGTGGGGTTCAAAATCCCTTCTCTCGCA---  
>tdbD00006951 Streptococcus\_mutans\_UA159\_210007\_Leu\_TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGGACTTAAAAATCCCGCAAG-----GGAA---CCTTCGTACCGGTTTCGATTCCGGTCTCTCGCA---  
>tdbD00006953 Streptococcus\_mutans\_UA159\_210007\_Leu\_TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGGACTTAAAAATCCCGCAAG-----GGAA---CCTTCGTACCGGTTTCGATTCCGGTCTCTCGCA---  
>tdbD00006952 Streptococcus\_mutans\_UA159\_210007\_Leu\_TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCACAGATTTAGGATCTGCGCT-----TAAG----GGCGTGGGGGTTTCGATTCCCTTACCCGCA---  
>tdbD00006608 Streptococcus\_pneumoniae\_TIGR4\_170187\_Leu\_AAG  
-GCCGGATGGCGGAATT-GGCA-GACGCGCAGGACTAAGGATCCTGTGACCG-----CTTT---AGTCTGTGGGGTTTCGATTCCCTCTCTCGCA---  
>tdbD00006609 Streptococcus\_pneumoniae\_TIGR4\_170187\_Leu\_TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGGACTTAAAAATCCCGGATG-----GTAA---CGATCGTACCGGTTTCGATTCCGGTCTCTCGCA---  
>tdbD00006610 Streptococcus\_pneumoniae\_TIGR4\_170187\_Leu\_TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCACAGATTTAGGATCTGCGCT-----TAAC----GGCGTGGGGGTTTCGATTCCCTTACCCGCA---  
>tdbD00006607 Streptococcus\_pyogenes\_M1\_GAS\_160490\_Leu\_AAG  
-GCCGGATGGCGGAATT-GGCA-GACGCGCAGGACTAAGGATCCTGTGACCG-----CTTT---AGTCTGTGGGGTTTCGATTCCCTCTCTCGCA---  
>tdbD00006605 Streptococcus\_pyogenes\_M1\_GAS\_160490\_Leu\_TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGGACTTAAAAATCCCGATG-----TTT---ACATCGTACCGGTTTCGATTCCGGTCTCTCGCA---  
>tdbD00007033 Streptomyces\_avermitilis\_MA-4680\_227882\_Leu\_CAA  
-GCCCCGTAGTCCAGC--GGTA-GAGACACGGTGTCAAACCACCGAC-----AGCGTGGGTTTCGATTCCCGACTCGGGGCA---  
>tdbD00007031 Streptomyces\_avermitilis\_MA-4680\_227882\_Leu\_CAG  
-GCGGGGTGGCGGAATT-GGCA-GACGCGCTGATTCCAGTTCAGTGCCC-----GCAA----GGCGTGGGGGTTCAACTCCCCCTCGCGCA---  
>tdbD00007029 Streptomyces\_avermitilis\_MA-4680\_227882\_Leu\_GAG  
-GTCCGGGTGGCGGAAT--GGCA-GACGCGCTAGCTTGAGGTGCTAGTGCCCT----TTAT---CGGGCGTGGGGGTTTCGATTCCCGCTCGGACACCA  
>tdbD00007032 Streptomyces\_avermitilis\_MA-4680\_227882\_Leu\_TAG  
-GCGGCCGTTGCTGAAT--GGTA-TAAGCGGAGGTTTATAGTGCCTCTGGCT-----TTA---CGCCATGTGGGTTTCGATTCCCGCTCGGCGCA---  
>tdbD00006931 Streptomyces\_coelicolor\_A3(2)\_100226\_Leu\_CAA  
-GCCTCGTGTAGTCCAGC--GGTA-GAGACACGGTGTCAAACCACCGAC-----AGCGTGGGTTTCGATTCCCGCTCGGGGCA---  
>tdbD00006928 Streptomyces\_coelicolor\_A3(2)\_100226\_Leu\_CAG  
-GCGGGGTGGCGGAATT-GGCA-GACGCGCTGATTCCAGTTCAGTGCCC-----GCAA----GGCGTGGGGGTTCAACTCCCCCTCGCGACCA  
>tdbD00006929 Streptomyces\_coelicolor\_A3(2)\_100226\_Leu\_GAG  
-GTCCGGGTGGCGGAAT--GGCA-GACGCGCTAGCTTGAGGTGCTAGTGCCCT----TTAT---CGGGCGTGGGGGTTTCGATTCCCGCTCGGACACCA  
>tdbD00006932 Streptomyces\_coelicolor\_A3(2)\_100226\_Leu\_TAG  
-GCGGCCGTTGTTGAATT-GGCA-GTACGCTGGGTTTAGTCCCAGTGGGG-----TAAC----TCCCGTGGAGGTTTCGAGTCCCTCCGGCCGACCA  
>tdbD00007150 Symbiobacterium\_thermophilum\_IAM\_14863\_292459\_Leu\_CAA  
-GCCAAGTGGTGAAT--GGCA-GACGCGCCGACTCAAAATCCGGTGGGGT-----AAC---CCCCGTGGGGTTTCGAGTCCCGCTTCGGCACCA  
>tdbD00007148 Symbiobacterium\_thermophilum\_IAM\_14863\_292459\_Leu\_CAG  
-GCAGATGTGGCGGAATT-GGCA-GACGCGCAGGCTCAGGACCGTGTCCGGTA---ACCA---CTCCCGTGGGAGTTTCGAGTCTCCCATCTGCACCA  
>tdbD00007151 Symbiobacterium\_thermophilum\_IAM\_14863\_292459\_Leu\_GAG  
-GTCGAGTGGCGGAATT-GGCA-GACGCGTACGTTTGGAGGCGTATGGG-----CAA-----CCG-TGCGGGTTTCGATTCCCGCTTCGGCACCA  
>tdbD00007152 Symbiobacterium\_thermophilum\_IAM\_14863\_292459\_Leu\_GAG  
-GTCGAGTGGCGGAATT-GGCA-GACGCGTACGTTTGGAGGCGTATGGG-----TTT-----CCCGTGGGGTTTCGATTCCCGCTTCGGCACCA  
>tdbD00007153 Symbiobacterium\_thermophilum\_IAM\_14863\_292459\_Leu\_TAA  
-GCCGAGTGGCGGAAT--GGCA-GACGCACAGACTTAAAAATCTGGGGCCG---CAG---AGGCGTGGGGTTTCGAGTCCCGCTTCGGCACCA  
>tdbD00007149 Symbiobacterium\_thermophilum\_IAM\_14863\_292459\_Leu\_TAG  
-GCGAGTGGCGGAATT-GGCA-GACGCGCAGACTTAGGATCTCGTGCC-----GCAA----GGCGTGGGGGTTTCGATTCCCTCTCTCGCACCA  
>tdbD00001555 Synechococcus\_sp.\_1131\_Leu\_TAA  
-GGGGCGTGGCGGAAC--GGTA-GACGCAGCGGACTTAAAAATCCGCTGACTG----TAA---AGTCTGTGGGGTTTCGAGTCCCTCCGCCCA---  
>tdbD00001552 Synechocystis\_sp.\_1143\_Leu\_CAA  
-GGGCGGTGGCGGAATT-GGTA-GACGCACCACTCAAAATGTGGCGAC-----TTCG----GTCGTGAGGTTTCGAGTCTCTCGCTGCCCA---  
>tdbD00001554 Synechocystis\_sp.\_1143\_Leu\_CAG

-GCGGAACTGGCGGAATT-GGTA-GACGCGCTAGATTACAGTTCTAGTGTTCC-----GTAA-----GGACTTCCGGGTTCAAGTCCCGGGTTCGCA---  
>tdbD00001551 Synechocystis\_sp. 1143 Leu GAG  
-GCGGATGTGGCGGAATT-GGTA-TACGCGCACGTTTGGAGGGCGTGTGGC-----TTT-----GCCTTGCAGAGTTCGAGTCTCGCCATCCGCA---  
>tdbD00001553 Synechocystis\_sp. 1143 Leu TAA  
-GGGGGTGTGGCGGAAT--GGTA-GACGCTGCGGATTTAAAATCCGTTGAGCCC--TTAT--AAGCTCGTGAGAGTTCGAGTCTCTCCACCCCCA---  
>tdbD00001550 Synechocystis\_sp. 1143 Leu TAG  
-GCGGACGTGGCGGAATT-GGTA-GACGCGCTAGATTTAGGTTCTAGTGTC-----TTT-----GGCGTGGGAGTTCGAGTCTCCCGTCCGCA---  
>tdbD00006568 Synechocystis\_sp. PCC\_6803 1148 Leu TAA  
-GGGGGTGTGGCGGAAT--GGTA-GACGCTGCGGATTTAAAATCCGTTGAGCCT--TAT--AAGCTCGTGAGAGTTCGAGTCTCTCCACCCCCA---  
>tdbD00006875 Thermoanaerobacter\_tengcongensis MB4 273068 Leu CAA  
-GCCGAAGTGGTGGAACT-GGCA-GACGCGCTGGACTCAAAAATCCAGTGGGGCT--CAC--ACCCCG-TGCGGGTTCGACTCCCGCCTTCGGCACCA  
>tdbD00006872 Thermoanaerobacter\_tengcongensis MB4 273068 Leu CAG  
-GCGGGAGTGGCGGAATT-GGCA-GACGCGCTAGATTCAGGTTCTAGTGCCC-----GAAA-----GGGCTTATGGGTTCAAGTCCCGTCTCCCGCACCA  
>tdbD00006874 Thermoanaerobacter\_tengcongensis MB4 273068 Leu GAG  
-GCGGCGGTGGCGGAAT--GGCA-GACGCGTACGTTTGGAGGGCGTATGGGC-----TAA-----TCCCGTGTGGGTTCAAGTCCACCCCGCCGACCA  
>tdbD00006876 Thermoanaerobacter\_tengcongensis MB4 273068 Leu TAA  
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>tdbD00006873 Thermoanaerobacter\_tengcongensis MB4 273068 Leu TAG  
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>tdbD00006863 Thermosynechococcus\_elongatus\_BP-1 197221 Leu CAA  
-GGGCGAGTGGCGAAAT--GGTA-GACGCACTACACTCAAAAATGTAGCGGGG-----TTT-----CCCATGTTCAGTTCGAGTCTGACCTCGCCCA---  
>tdbD00006867 Thermosynechococcus\_elongatus\_BP-1 197221 Leu CAG  
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>tdbD00006866 Thermosynechococcus\_elongatus\_BP-1 197221 Leu TAA  
-GGGGCGTGGCGGAAT--GGTA-GACGCTGCGGACTTAAGAAAATCCGTTGACC--TTAA--ACAAGTCGTGAGGGTTCAAGTCCCTCCGCCCA---  
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-GCGGACGTGGCGGAAT--GGCA-GACGCGCTAGATTTAGGTTCTAGTACC-----GCAA-----GGTGTGTGGGTTCAAGTCCCTCCGTCGCA---  
>tdbD00006570 Thermotoga\_maritima\_MSB8 243274 Leu CAA  
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>tdbD00006574 Thermotoga\_maritima\_MSB8 243274 Leu TAG  
-GCGAGAGTGGCGGAAT--GGCA-GACGCGCTGGACTTAGAATCCAGTGGGC-----TGAA-----GCCCGTGTGGGTTCAAGTCCACCTCTCGCACCA  
>tdbD00007194 Thermus\_thermophilus\_HB27 262724 Leu CAA  
-GCCGGGTGGCGGAACC--GGTA-GACGCGGACACTCAAAAATCTGTGTCC-----GCAA-----GGAGTGCGGGTTTCGAGTCCCGCCCCGGCACCA  
>tdbD00007197 Thermus\_thermophilus\_HB27 262724 Leu CAG  
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>tdbD00007198 Thermus\_thermophilus\_HB27 262724 Leu GAG  
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>tdbD00007195 Thermus\_thermophilus\_HB27 262724 Leu TAG  
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>tdbD00007203 Treponema\_denticola\_ATCC\_35405 243275 Leu CAA  
-GCCGGCTGGTGAAT--GGTA-TACACGATAGACTCAAAAATCTATTTGGGG-----CGA-----CTCCG-TAAGGTTTCAGTCCCTTCGCCGTA---  
>tdbD00007199 Treponema\_denticola\_ATCC\_35405 243275 Leu CAG  
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>tdbD00007201 Treponema\_denticola\_ATCC\_35405 243275 Leu GAG  
-GCGGCGTGGTGGAAAT--GGTA-GACACGCTCAGCTGAGGTGCTGATGCCT-----TAAC-----GGGTGTGTGGTTCAGTCCAGTTCGCCGCA---  
>tdbD00007202 Treponema\_denticola\_ATCC\_35405 243275 Leu TAA  
-GCTGAAGTGGTGGAAATA--GGTA-GACACTAGGGACTTAAAATCCCTGGCA-----GTAA-----TGCCGTACGGGTTCAATTCCCGTCTCAGCA---  
>tdbD00007200 Treponema\_denticola\_ATCC\_35405 243275 Leu TAG  
-GCGAGAGTGGTGGAAAT--GGCA-GACACGCTAGACTTAGGATCTAGTGC-----TTTCG-----GCGTGAAGGTTTCAGTCCCTCTCTCGCA---  
>tdbD00001512 Treponema\_pallidum 160 Leu CAA  
-GCCGACGTGGTGAAT--GGTA-GACACGACAGACTCAAAAATCTGTGGGG-----TAA-----CCCGTAAGGTTTCAGTCCCTCTCGCGCA---  
>tdbD00001514 Treponema\_pallidum 160 Leu CAG  
-GCCTCGATGGTGGAAAT--GGCA-GACACGCTAGCTCAGGTGCTAGTGCC-----TCAC-----CGGCGTGGGAGTTTCAGTCTCCCTCGAGGCA---  
>tdbD00001511 Treponema\_pallidum 160 Leu GAG  
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>tdbD00001510 Treponema\_pallidum 160 Leu TAA  
-GCTGGAGTGGTGGAAAT--GGTA-GACATCAGGGACTTAAAATCCCTTGACCG--GCAG--CGGTCGTACGAGTTTCAGTCTCGTCTCAGCA---  
>tdbD00001513 Treponema\_pallidum 160 Leu TAG  
-GCGAGAGTGGTGGAAAT--GGCA-GACACGCTAGACTTAGGATCTAGTGCC-----TCT-----GGCATGAGGTTTCAGTCCCTCTCTCGCA---  
>tdbD00006983 Tropheryma\_whipplei\_str. Twist 203267 Leu CAA  
-GCCGGCTGGCGGAAC--GGCA-GACGCGGAGCACTCAAAAATGCTTTGCC-----TCAT-----GGGCGTGTGGGTTCAAATCCCTCCCGCGCA---  
>tdbD00006986 Tropheryma\_whipplei\_str. Twist 203267 Leu CAG  
-GCGGAGTGGCGGAAT--GGTA-GACGCGCACGGTTCAGGTCCGTTGTCT-----GCGA-----AGACATGGGGTTTCAGTCCCGCTCGCGCA---  
>tdbD00006984 Tropheryma\_whipplei\_str. Twist 203267 Leu GAG  
-GCGGGGTGGCGGAAT--GGTA-GACGCGCTAGCTGAGGTGCTAGTGCCAAT--TTG--AAAGCGTAGGGTTTCAGTCCCGTCTCGCGCA---  
>tdbD00006987 Tropheryma\_whipplei\_str. Twist 203267 Leu TAA  
-GCCCTCGTAGCCCAAT--GGCA-GAGGCGAGACTTAAAATCGTCCC-----AGTGTGGGTTTCAGTCCCGAGGGCA---

>tdbD00006985 Tropheryma whipplei\_str.\_Twist 203267 Leu TAG  
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>tdbD00006489 Ureaplasma parvum serovar\_3 38504 Leu CAA  
-GCTCAAGTGGCGAAAT--GGCA-GACGACGTTGACTCAAAATCAACCGA-----GAAA-----TCATAAGGGTTTCAGTCCCTTCTTGAGCACCA  
>tdbD00006490 Ureaplasma parvum serovar\_3 38504 Leu TAA  
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>tdbD00006491 Ureaplasma parvum serovar\_3 38504 Leu TAG  
-GCGCTGTGGCGAAAT--GGCA-GACGCGCTAGACTTAGGATCTAGTACT-----TTGC-----GGTGTAGAGTTCAAGTCTCTTCAAGCGCACCA  
>tdbD00006472 Vibrio cholerae\_O1 biovar\_El Tor str. N16961 243277 Leu CAA  
-GCCGATGTGGTGAAT--GGTA-GACACGACGATTCAAAATCCGTTTCC-----TTCG-----GGAGTGACGGTTCAAGTCCGTCATCGGTACCA  
>tdbD00006473 Vibrio cholerae\_O1 biovar\_El Tor str. N16961 243277 Leu CAG  
-GCGGTGGTGGCGAAAT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC-----TTC-----GGACGTGAGGGTTCAAGTCCCTCTTCCGCACCA  
>tdbD00006474 Vibrio cholerae\_O1 biovar\_El Tor str. N16961 243277 Leu CAG  
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>tdbD00006475 Vibrio cholerae\_O1 biovar\_El Tor str. N16961 243277 Leu GAG  
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>tdbD00006476 Vibrio cholerae\_O1 biovar\_El Tor str. N16961 243277 Leu TAA  
-GCCGATGTGGTGAAT--GGTA-GACACAAGGGATTTAAATCCCTCGACT-----TTCG-----AGTCGTGACGGTTCAAGTCCGGCCCGGGCACCA  
>tdbD00006477 Vibrio cholerae\_O1 biovar\_El Tor str. N16961 243277 Leu TAG  
-GCGGAAGTGGCGAAAT--GGTA-GACGCACAGATTTAGGTCTGTGGCC-----GCGA-----GGCGTAAGAGTTCAAGTCTCTTCTTCCGCACCA  
>tdbD00006478 Vibrio cholerae\_O1 biovar\_El Tor str. N16961 243277 Leu TAG  
-GCGGATGTGGCGAAAT--GGTA-GACGCACAGATTTAGGTCTGTGGCC-----GCGA-----GGCGTAAGAGTTCAAGTCTCTTCTTCCGCACCA  
>tdbD00007206 Wolbachia\_endosymbiont\_of Drosophila melanogaster 163164 Leu CAA  
-GCCCTGTGGTGAAT--GGTA-GACACGCGAGACTCAAAATCTGTGTCTT-----GCAA-----AAGCATGTGGTTCAAGTCCGGCCAGGGGCA---  
>tdbD00007208 Wolbachia\_endosymbiont\_of Drosophila melanogaster 163164 Leu CAG  
-GCCGATGTGGCGAAAT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTAACTT-----TTT-----AAGTGTGGAAGTTCAAGTCTTCTCTCGGGCA---  
>tdbD00007204 Wolbachia\_endosymbiont\_of Drosophila melanogaster 163164 Leu GAG  
-GCGGCGGTGGTGAAT--GGTA-GACACGCGAGCTTGAGGTGCTGTGGCTC-----ATA-----AGGCCTTGAAGTTCAAGTCTTCTCGGCCGACCA  
>tdbD00007207 Wolbachia\_endosymbiont\_of Drosophila melanogaster 163164 Leu TAA  
-GCCGATGTGGCGAAAT--GGTA-GACGCAGCGACTTAAATCCGTTGCTT-----TTGC-----GACCTTGGGAGTTCAAGTCTCCCATGGGCACCA  
>tdbD00007205 Wolbachia\_endosymbiont\_of Drosophila melanogaster 163164 Leu TAG  
-GCGGATATGGCGAAAT--GGTA-GACGTGCCAGGTTTAGGTCTGTGTAG-----CTTG-----CTCGTGGGGTTCAAGTCCCTCTATCCGCA---  
>tdbD00006886 Xanthomonas axonopodis pv. citri str. 306 190486 Leu CAA  
-GCCGAAGTGGCGAAAT--GGTA-GACGCAAGGACTCAAAATCCGCGCCCT-----TAA-----AAGCG-TGTGGTTTCAGTCCACCTTCCGCACCA  
>tdbD00006884 Xanthomonas axonopodis pv. citri str. 306 190486 Leu CAG  
-GCCAGGTGGCGAAAT--GGTA-GACGCACTAGCTTCAGGTGCTAGCGGGGG-----CAA-----CTTCG-TGGAGTTTCAGTCCCTCTTCCGCACCA  
>tdbD00006885 Xanthomonas axonopodis pv. citri str. 306 190486 Leu CAG  
-GCCAGGTGGCGAAAT--GGTA-GACGCACTAGCTTCAGGTGCTAGCGGGGG-----CAA-----CTTCG-TGGAGTTTCAGTCCCTCTTCCGCACCA  
>tdbD00006888 Xanthomonas axonopodis pv. citri str. 306 190486 Leu GAG  
-GCCAGGTGGCGAAAT--GGTA-GACGCACTACCTTGAGGTGGTAGCGAC-----TTAG-----GTCGTAGGGTTTCAGTCCCTCTTCCGCACCA  
>tdbD00006887 Xanthomonas axonopodis pv. citri str. 306 190486 Leu TAA  
-GCCCGGTGGCGAAAT--GGTA-GACGCAAGGACTTAAATCCCTCAGCT-----GTGA-----GGCTATGCGGGTTTCAGTCCCGCCCGGGCACCA  
>tdbD00006883 Xanthomonas axonopodis pv. citri str. 306 190486 Leu TAG  
-GCGAAAGTGGCGAAAT--GGTA-GACGCACAGATTTAGGTCTGTAGCC-----GCAA-----GGCGTGGGGTTTCAGTCCCGCCCTTCCGCACCA  
>tdbD00006880 Xanthomonas campestris pv. campestris str. ATCC 33913 190485 Leu TAA  
-GCCCGGTGGCGAAAT--GGTA-GACGCAAGGACTTAAATCCCTCAGCC-----GCAA-----GGCTATGCGGGTTTCAGTCCCGCCCGGGCACCA  
>tdbD00006575 Xylella fastidiosa 9a5c 160492 Leu CAA  
-GCCGAAGTGGCGAAAT--GGTA-GACGCAAGGACTTAAATCCCGCCACCT-----TAA-----AAGTG-TGTGGTTTCAGTCCACCTTCCGCACCA  
>tdbD00006576 Xylella fastidiosa 9a5c 160492 Leu CAG  
-GCCAGGTGGCGAAAT--GGTA-GACGCACTAGTTTCAGGTACTAGCGGGT-----AAA-----ACCG-TGGAGTTTCAGTCCCTCTTCCGCACCA  
>tdbD00006577 Xylella fastidiosa 9a5c 160492 Leu GAG  
-GCCAGGTGGCGAAAT--GGTA-GACGCACTACCTTGAGGTGGTAGCGAC-----GTAA-----GTCGTAGGGTTTCAGTCCCGCCCTTCCGCACCA  
>tdbD00006578 Xylella fastidiosa 9a5c 160492 Leu TAA  
-GCCCGGTGGCGAAAT--GGTA-GACGCAAGGACTTAAATCCCTCAGCC-----TTTA-----GGTTATGCGGGTTTCAGTCCCGCCCGGGCACCA  
>tdbD00006579 Xylella fastidiosa 9a5c 160492 Leu TAG  
-GCCGATGTGGCGAAAT--GGTA-GACGCAAGGACTTAAATCCCTCAGCC-----TTT-----AGCGTGCAGTTTCAGTCCCTGTACCGGTACCA  
>tdbD00007155 Yersinia pestis biovar\_Microtus str. 91001 229193 Leu CAA  
-GCCGAAGTGGCGAAAT--GGTA-GACGCACTAGCTTCAAAATCAACCGCC-----GCGA-----GGCATGCCGGTTTCAGTCCCGCCCTCCGCACCA  
>tdbD00007158 Yersinia pestis biovar\_Microtus str. 91001 229193 Leu CAG  
-GCGATGGTGGCGAAAT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC-----TTAC-----GGACGTGAGGGTTCAAGTCCCTCCCTTCCGCACCA  
>tdbD00007159 Yersinia pestis biovar\_Microtus str. 91001 229193 Leu CAG  
-GCGATGGTGGCGAAAT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC-----TTAC-----GGACGTGAGGGTTCAAGTCCCTCCCTTCCGCACCA  
>tdbD00007154 Yersinia pestis biovar\_Microtus str. 91001 229193 Leu GAG  
-GCCCGGTGGTGAAT--GGTA-GACACGCTACCTTGAGGTGGTAGTCCC-----GATT-----GGGCTTACGGTTTCAGTCCCGTCCCTCCGTACCA  
>tdbD00007157 Yersinia pestis biovar\_Microtus str. 91001 229193 Leu TAA  
-GCCCGGTGGTGAAT--GGTA-GACACAAGGGATTTAAATCCCTCAGCC-----TAT-----GGCTGTGCGGGTTTCAGTCCCGCCCGGGCACCA  
>tdbD00007156 Yersinia pestis biovar\_Microtus str. 91001 229193 Leu TAG  
-GCGGAGTGGCGAAAT--GGTA-GACGCACAGATTTAGGTCTGTAGCC-----GCAA-----GGTGTGCGAGTTTCAGTCTCGCTCCCGCACCA  
>tdbD00007740 Acinetobacter sp. ADP1 62977 Met CAT  
-GGCTATGTAGCTCAGTT--GGTT-AGAGCACCGCACTATAATGCGGGG-----GTCACAGTTTCAGTCCCGTTCATAGCCACCA  
>tdbD00007301 Buchnera aphidicola str. APS (Acyrtosiphon pisum) 107806 Met CAT  
-GGCTACGTAGCTCAGTC--GGTT-AGAGCACAGCACTATAACGCTGGG-----GTCATGGTTTCAGTCCCGTTCATAGCTACCA  
>tdbD00007617 Buchnera aphidicola str. Bp (Baizongia pistaciae) 224915 Met CAT  
-GGCTACGTAGCTCAGTT--GGTT-AGAGCACAGCACTATAACGCTGAG-----GTCACAGTTTCAGTCCCGTTCATAGCTACCA  
>tdbD00007493 Buchnera aphidicola str. Sg (Schizaphis graminum) 198804 Met CAT

-GGCTACGTAGCTCAGTT-GGTT-AGAGCACAGCACTCATAACCGTGGG-----GTCATGGGTTCAATTCCTCGTAGCCA---  
>tdbD00007751 Candidatus\_Blochmannia\_floridanus\_203907 Met CAT  
-GGCTACGTAGCTCAGAT-GGTT-AGAGCGCAGCACTCATAATGCTGAG-----GGCACAGGTTCAAATCCTGCTGCTAGCTA---  
>tdbD00007611 Coxiella\_burnetii\_RSA\_493\_227377 Met CAT  
-GGCTATGTAGCTCAGTT-GGTT-AGAGCACGGCATTCATAATGCCGGT-----GTCGGTGGTTCAAGTCCACCCATAGCCA---  
>tdbD00001807 Escherichia\_coli\_562 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACATCACTCATAATGATGGG-----GTCACAGGTTCAATCCCGTCTAGCCACCA  
>tdbD00007489 Fusobacterium\_nucleatum\_subsp.\_nucleatum\_ATCC\_25586\_190304 Met CAT  
-GCCTAGGTAGCTCAGTT-GGCT-AGAGCATACGGTTCATACCCGTACG-----GTCGATGGTTCAATCCATTCCTAGGCACCA  
>tdbD00001811 Haemophilus\_influenzae\_727 Met CAT  
-GGCTACATAGCTCAGTT-GGTT-AGAGCACAACTCATAATGTTGGG-----GTCGCAAGTTCGAATCTCGTGTAGCCACCA  
>tdbD00007356 Pasteurella\_multocida\_subsp.\_multocida\_str.\_Pm70\_272843 Met CAT  
-GGCTATGTAGCTCAGTT-GGTT-AGAGCACAACTCATAATGTTGGG-----GTCACAGGTTCAATCCCGTCTAGCCACCA  
>tdbD00007673 Photorhabdus\_luminescens\_subsp.\_laumondii\_TTO1\_243265 Met CAT  
-GGCTACGTAGCTCAGCT-GGTT-AGAGCACAGCACTCATAATGCTGGG-----GTCACAGGTTCAATCCCGTCTAGCCACCA  
>tdbD00007359 Pseudomonas\_aeruginosa\_PAO1\_208964 Met CAT  
-GGCTACATAGCTCAGTC-GGTT-AGAGCGCAGCATTCATAATGCTGAT-----GTCCAGGTTCAAGTCCCGGTGTAGCCACCA  
>tdbD00007642 Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283 Met CAT  
-GGCTACATAGCTCAGTT-GGTT-AGAGCATAGCATTCATAATGCTGGG-----GTCCGGGTTCAAGTCCCTGTGTAGCCACCA  
>tdbD00007308 Vibrio\_cholerae\_O1\_biovar\_El\_Tor\_str.\_N16961\_243277 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACATCACTCATAATGATGGG-----GTCACAGGTTCAAATCCCGTCTAGCCACCA  
>tdbD00007523 Xanthomonas\_axonopodis\_pv.\_citri\_str.\_306\_190486 Met CAT  
-GGCTATGTAGCTCAGCC-GGTT-AGAGCACAGCACTCATAATGCTGGG-----GTCGGTGGTTCGAGTCCACCCATAGCCACCA  
>tdbD00007365 Xylella\_fastidiosa\_9a5c\_160492 Met CAT  
-GGCTATGTAGCTCAGCA-GGTT-AGAGCACAGCACTCATAATGCTGGG-----GTCGGTGGTTCGAGTCCACCCATAGCCACCA  
>tdbD00004341 Bacillus\_anthraxis\_str.\_A2012\_191218 Cys GCA  
-GGCGGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTCGCGCCT---  
>tdbD00004283 Bacillus\_halodurans\_C-125\_272558 Cys GCA  
-GGCGGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----T-CCCCGGTTCGAATCCGGGTGCGCGCCT---  
>tdbD00000257 Bacillus\_subtilis\_1423 Cys GCA  
-GGCGGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----T-CCCCGGTTCGAATCCGGGTGTCGCTCCA  
>tdbD00004149 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308 Cys GCA  
-GGCGGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----T-CCCCGGTTCGAATCCGGGTGTCGCGCCT---  
>tdbD00004343 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27\_281309 Cys GCA  
-GGCGATATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----T-CGCGGTTCAAATCCGGTATCGCGCCT---  
>tdbD00004166 Borrelia\_burgdorferi\_B31\_224326 Cys GCA  
-GGCGTGTACCCAAGT--GGCT--AAGGGAGAAGTCTGCAAAACTTTGA-----TTCGCCGGTTCGATTCGGTTCAGCGCCT---  
>tdbD00004167 Campylobacter\_jejuni\_subsp.\_jejuni\_NCTC\_11168\_192222 Cys GCA  
-GGCGACATAGCCAAGC--GGT--AAGGCATGGGCTGCAAAACCTTTA-----T-CTCCGGTTCGAATCCGGATGTGCGCTCCA  
>tdbD00004346 Candidatus\_Blochmannia\_floridanus\_203907 Cys GCA  
-GGCGGTTAAACAAAGT--GGT--AATGTAGCGGACTGCAAAATCCGTAT-----A-GCTCGGTTCAATCCCGAGACGCGCCT---  
>tdbD00004185 Clostridium\_acetobutylicum\_ATCC\_824\_272562 Cys GCA  
-GGCGTATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----T-CCCCAGTTCAAATCTGGGTGGCGCTCCA  
>tdbD00004181 Clostridium\_perfringens\_str.\_13\_195102 Cys GCA  
-GGCGTATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----TTCCCCGGTTCAAATCCGGGTGGCGCTCCA  
>tdbD00004285 Clostridium\_tetani\_E88\_212717 Cys GCA  
-GGCGTATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----TTCCCCGGTTCAAATCCGGGTGGCGCTCCA  
>tdbD00004286 Clostridium\_tetani\_E88\_212717 Cys GCA  
-GGCACTATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----TTCCCCAGTTCAAATCTGGGTGGTGCCTCCA  
>tdbD00004169 Deinococcus\_radiodurans\_R1\_243230 Cys GCA  
-GGCGTGTAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----C-CACCGGTTTCGAGTCCGGTTCAGCGCTCCA  
>tdbD00004333 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882 Cys GCA  
-GGCGCGTAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----TTCTCCGGTTCAAATCCGGACGCGCTCCA  
>tdbD00004287 Enterococcus\_faecalis\_V583\_226185 Cys GCA  
-GGCGTATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTACCGCCT---  
>tdbD00000258 Escherichia\_coli\_562 Cys GCA  
-GGCGGTTAAACAAAGC--GGT--TATGTAGCGGATGCAAAATCCGTCT-----A-GTCCGGTTCGACTCCGGAACGCGCTCCA  
>tdbD00004255 Fusobacterium\_nucleatum\_subsp.\_nucleatum\_ATCC\_25586\_190304 Cys GCA  
-GGCGACGTCCGCAAGC--GGT--AAGGCAGAGGTCTGCAAAATCTCCA-----T-CACAGTTCAATCTGGTTCGCTCGCTCCA  
>tdbD00004322 Geobacter\_sulfurreducens\_PCA\_243231 Cys GCA  
-GGCGCGTCCGCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----TTCACCGGTTCAAATCCGGTTCGCGCTCCA  
>tdbD00004165 Haemophilus\_influenzae\_Rd\_KW20\_71421 Cys GCA  
-GGCGTGTAGCCAAGC--GGT--TATGCACTGGATGCAAAATCCATGT-----A-GCTCGGTTTCGACTCCGGGACACGCTCCA  
>tdbD00000256 Helicobacter\_pylori\_210 Cys GCA  
-GGCGACATAGCCAAGT--GGT--AAGGCATGGGTCTGCAAAACCTTTGA-----TTCCCCGGTTCGAATCCGGGTGTCGCTCCA  
>tdbD00004164 Helicobacter\_pylori\_J99\_85963 Cys GCA  
-GGCGACATAGCCAAGT--GGT--AAGGCATGAGTCTGCAAAACCTTTGA-----TCCCCGGTTCGAATCCGGGTGTCGCTCCA  
>tdbD00004323 Lactobacillus\_johnsonii\_NCC\_533\_257314 Cys GCA  
-GGCGTGTAGCCAAGT--GGT--AAGGCAGGGTCTGCAAAACCTTAA-----T-CATCGGTTCAAATCCGATCACCGCCT---  
>tdbD00004276 Leptospira\_interrogans\_serovar\_Lai\_str.\_56601\_189518 Cys GCA  
-GGCGTGTGGCCAAGT--GGT--AAGGCATGGCTGCAAAAGCTTTGA-----T-CCCCGGTTCGAATCCGGGACGCGCCT---  
>tdbD00004179 Listeria\_innocua\_Clip11262\_272626 Cys GCA  
-GGCGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTCGCGCTCCA  
>tdbD00004335 Mesoplasma\_florum\_L1\_265311 Cys GCA  
-GGCGGCATAGCCAAGT--GGCT--AAGGCATGGGTCTGCAACACCCTGA-----T-CATCGGTTCAATCCGATTCGCGCTCCA



>tdbD00000248 Mycoplasma\_capricolum 2095 Cys GCA  
-GGCAACATGGCCAAGC--GGCT--AAGGCATGGGTCTGCAAAACCCCTGA-----T-CATCGGTTTCAATCCGATGTTGCTCCCA  
>tdbD00004194 Mycoplasma\_pulmonis\_UAB\_CTIP 272635 Cys GCA  
-GGCACCATAGCCAAAT--GGGC--AAGGCATGGGTCTGCAAAACCCCTGA-----T-TACCGGTTTCGAGTCCGGTGGTGCCTCCA  
>tdbD00004152 Neisseria\_meningitidis\_MC58 122586 Cys GCA  
-GGCGAGATAGCAAAGT--GGT--TATGCAGCGGATTGCAAATCCGCT-----A-CGCCGGTTTCGATTCGACTCTCGCTCCA  
>tdbD00004193 Nostoc\_sp.\_PCC\_7120 103690 Cys GCA  
-GGCGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCCCTCA-----TCCCCCGGTTCAAATCCGGGTGCCGCT---  
>tdbD00004277 Oceanobacillus\_heyensis\_HTE831 221109 Cys GCA  
-GGCGGTATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCCCTTA-----T-CACCGGTTCAAATCCGGTTACCGCTCCA  
>tdbD00004314 Onion\_yellows\_phytoplasma\_OY-M 262768 Cys GCA  
-GGCCCTGTAGCCAAGT--GGT--AAGGCATGGCTCTGCAAAAGCTTGA-----T-CAACGGTTCAAATCCGGTTACGGGCTCCA  
>tdbD00004309 Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000 223283 Cys GCA  
-GGCGAGTAGCAAAT--GGT--TATGCAGCGGATTGCAAATCCGCT-----A-CGCCGGTTTCGATTCGACTCTCGCTCCA  
>tdbD00004306 Rhodopirellula\_baltica\_SH\_1 243090 Cys GCA  
-GGCGACGTAGCCAAGT--GGT--AAGGCAGAGGATTGCAAATCCCTTA-----TTCGTGGGTTTCAATCCACCGTCCGCT---  
>tdbD00004186 Rickettsia\_conorii\_str.\_Malish\_7 272944 Cys GCA  
-GGCTGGTAGCAAAT--GGT--AATGCGTGGACTGCAAAACCCCTTA-----TTCGTGGGTTTCGATTCGACTCTCGCTCCA  
>tdbD00000252 Spiroplasma\_melliferum 2134 Cys GCA  
-GGCACTATAGCCAAGT--GGT--AAGGCATGGGACTGCAACTCCCGA-----T-CGTGGGTTTCAATCCGACTAGTGCCTCCA  
>tdbD00000255 Staphylococcus\_aureus 1280 Cys GCA  
-GGCGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCCCTTA-----T-CACCGGTTCAAATCCGGTTGCCGCTCCA  
>tdbD00004281 Streptococcus\_agalactiae\_2603V/R 208435 Cys GCA  
-GGCGGTATAGCCAAGT--GGT--AAGGCAGGCTCTGCAAAAGCTTGA-----T-CGTGGGTTCAAATCCGCTTACCGCT---  
>tdbD00000260 Synechocystis\_sp.\_1143 Cys GCA  
-GGCGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAATCTTTA-----C-CCCCAGTTTCAATCTGGGTGCCGCT---  
>tdbD00004267 Thermoanaerobacter\_tengcongensis\_MB4 273068 Cys GCA  
-GGCGACATAGCCAAGC--GGT--AAGGCAGGGGTCTGCAAAACCCCGA-----TTCCCCGGTTTCAATCCGGGTGTCGCTCCA  
>tdbD00004265 Thermosynechococcus\_elongatus\_BP-1 197221 Cys GCA  
-GGCGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCCCTTA-----TTCCCCGGTTTCAATCCGGGTGCCGCT---  
>tdbD00004176 Thermotoga\_maritima\_MSB8 243274 Cys GCA  
-GGCGCGTAGCCAAGC--GGTCAAAGCGGGGGTCTGCAAAATCCCTA-----TTCGTGGGTTTCAATCCACCGCCGCTCCA  
>tdbD00004337 Thermus\_thermophilus\_HB27 262724 Cys GCA  
-GGCGCGTAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCCCTCA-----TTCGCGGTTTCAATCCGGCCGCGCTCCA  
>tdbD00004338 Treponema\_denticola\_ATCC\_35405 243275 Cys GCA  
-GGCGCGTAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCCCTCA-----TTCATCAGTTTCGATTCGATCGGCGCT---  
>tdbD00000253 Treponema\_pallidum 160 Cys GCA  
-GGCGCGTAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAACCCCTTA-----TGCATCAGTTTCGATTCGATCGGCGCT---  
>tdbD00011780 Acinetobacter\_sp.\_ADP1 62977 Tyr GTA  
-GGTGAGATCCCCGAGC--GGTCAAAGGGGGGCGACTGTAATCCGCTACG-----AAAG-----TTT-CGAAGTTTCAATCCTTCTCACCACCA  
>tdbD00011620 Agrobacterium\_tumefaciens\_str.\_C58 176299 Tyr GTA  
-GGAGGGATGCCCGAGT--GGTTAAAGGGGACGACTGTAATCCGTTGGC-----TACG-----CCTACGTTGGTTCAAATCCAATCCTCCACCA  
>tdbD00011600 Aquifex\_aeolicus\_VF5 224324 Tyr GTA  
-GGAGGGGTGCCCGAGC--GGCAAAGGCAGGGGACTGTAATCCCCCGGGCG-----TCCG---CCCTG-CGCAGTTTCAATCCTGCCCTCCA---  
>tdbD00011781 Bacillus\_anthraxis\_str.\_A2012 191218 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACCGCGGACTGTAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTCAATCTGCCCTCCACCA  
>tdbD00011723 Bacillus\_halodurans\_C-125 272558 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACCGCGGACTGTAATCCGCTCCT-----TCAG-----GGTTCGGCGGTTTCAATCCGCTCCCTCCACCA  
>tdbD00003522 Bacillus\_subtilis 1423 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACCGCGGACTGTAATCCGCTCCT-----TCAG-----GGTTCGGCAGTTTCAATCTGCCCTCCACCA  
>tdbD00011745 Bacteroides\_thetaiotaomicron\_VPI-5482 226186 Tyr GTA  
-GGGCAAATACCAGAGT--GGCAAATGGGGCAGACTGTAATCTGCTGTCT-----TTC-----GACTTCGGTGGTTTCAATCCATCTTTGCCA---  
>tdbD00011746 Bacteroides\_thetaiotaomicron\_VPI-5482 226186 Tyr GTA  
-GGGCAAATACCAGAGT--GGCAAATGGGGCAGACTGTAATCTGCTGGCT-----TAC-----GCCTTCGGTGGTTTCAATCCATCTTTGCCA---  
>tdbD00011749 Bartonella\_henselae\_str.\_Houston-1 283166 Tyr GTA  
-GGAGGGGTGCCCGAGT--GGTTAAAGGGGGCGACTGTAATCCGTTGGC-----TATG-----CTA-CGTTGGTTTCAATCCACCCCTCCACCA  
>tdbD00011750 Bdellovibrio\_bacteriovorus\_HD100 264462 Tyr GTA  
-GGTAGGTGCCCGAGT--GGCTAAAGGGGACGACTGTAATCCGTTGGCT-----TAT-----GTCTACGAAGTTTCAATCCTTCCCTGCCACCA  
>tdbD00011710 Bifidobacterium\_longum\_NCC2705 206672 Tyr GTA  
-GGCGGATTTCCCAAGC--GGTCAAAGGGAGCTGACTGTAATCAGCCGCT-----TCGT-----GCTTCAGTGGTTTCAATCCACTATCCGCCA---  
>tdbD00003518 Borrelia\_burgdorferi 139 Tyr GTA  
-GGGGCGGTACCGAAGT--GGTTAACCGGGGCGACTGTAATCTGTTGGC-----TTTG-----CCTACGTTGGTTTCAATCCACCCCTCCCA---  
>tdbD00011611 Brucella\_melitensis\_16M 224914 Tyr GTA  
-GGAGGGATGCCCGAGT--GGTTAAAGGGGACGACTGTAATCCGTTGGC-----TATG-----CCTACGTTGGTTTCAATCCAATCCTCCACCA  
>tdbD00011566 Buchnera\_aphidicola\_str.\_APS\_(Acyrtosiphon\_pisum) 107806 Tyr GTA  
-GGTGGGTTCCCGAGC--GGCAAAGGGGAGCAGACTGTAATCTGCGCTC-----ATAG-----ACTTCGAAGTTTCAATCCTTCTCCACCA  
>tdbD00011737 Buchnera\_aphidicola\_str.\_Bp\_(Baizongia\_pistaciae) 224915 Tyr GTA  
-GGTGGGATTTCCCGAGT--GGCTAAAGGGGAGCAGACTGTAATCTGCGCTC-----AAAG-----ACTTCGAAGTTTCAATCCTTCTCCACCA---  
>tdbD00011694 Buchnera\_aphidicola\_str.\_Sg\_(Schizaphis\_graminum) 198804 Tyr GTA  
-GGTGGGATTTCCCGAGC--GGCAAAGGGGAGCAGACTGTAATCTGCGCTC-----AAG-----ACTT-CGAAGTTTCAATCCTTCTCCACCA---  
>tdbD00003529 Campylobacter\_jejuni 197 Tyr GTA  
-GGTGAGTTACTCAAGT--GGCCAACGAGGGGAGACTGTAATCTGCTGGCT-----TTC-----GCCTTCGTTGGTTTCAATCCACGACTCACCACCA  
>tdbD00011785 Candidatus\_Blochmannia\_floridanus 203907 Tyr GTA  
-GATGGGTTGCCCGAGT--GGTTAAAGGGGAGCAGACTGTAATCTGCGCTC-----GTAG-----ACTTCGAAGTTTCAATCCTTCCCTCCATCA---  
>tdbD00011754 Candidatus\_Proteochlamydia\_amoebophila\_UWE25 264201 Tyr GTA

-GGGGGTGTCGCATAGT--GGCA-ATTGCAAGGGACTGTAATCCCTCGACT-----TCG-----GTCTCCGTTGGTTCGAGTCCAACCGCCCCA---  
>tdbD00011604 Chlamydia\_muridarum\_Nigg 243161 Tyr GTA  
-GGGGGTGTCGCATAGC--GGTCAATTGCATCGGACTGTAAATCCGACTCCT-----TAC-----GGATACGTTGGTTCAAATCCAGCCACCCCCA---  
>tdbD00011560 Chlamydomydia\_pneumoniae\_AR39 115711 Tyr GTA  
-GGGGGTGTCGCATAGT--GGTCAATTGCATCGGACTGTAAATCCGCTCCT-----TAC-----GGATACGTTGGTTCAAATCCAGCCACCCCCA---  
>tdbD00011691 Chlorobium\_tepidum\_TLS 194439 Tyr GTA  
-GGGTAGGTAGCGAAGC--GGTCAAACGCAACAGACTGTAAATCTGTCGACA-----TATG-----TCTT-CGGAGGTTCGAATCCTCCCTACCCA---  
>tdbD00011608 Clostridium\_acetobutylicum\_ATCC\_824 272562 Tyr GTA  
-GGAGGAATCCCGAGT--GGCCAAAGGGGGCAGACTGTAAATCTGTTAGC-----TCAG-----CTTCCATGGTTCGAATCCATGTTCTCCACCA  
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>tdbD00011603 Clostridium\_perfringens\_str\_13 195102 Tyr GTA  
-GGTGAATCCCGAGT--GGCCAAAGGGGGCAGACTGTAAATCTGTTGTCG-----GAC-----GACTTCGAAGGTTCGAATCCTTCTCCACCACCA  
>tdbD00011725 Clostridium\_tetani\_E88 212717 Tyr GTA  
-GGAGGAGTCCCGAGT--GGCCAAAGGGGGCAGACTGTAAATCTGTTGGCT-----TTC-----GCCTTCGATGGTTCGAATCCGCTCCTCCACCA  
>tdbD00011751 Corynebacterium\_diphtheriae\_NCTC\_13129 257309 Tyr GTA  
-GCCAGGTTGCCCGAGC--GGCCAAAGGGAGCGGACTGTAAATCCGTCGGC-----ATTG-----CCTACAGAAGTTCGAATCCTTCTACCTGGCA---  
>tdbD00011712 Corynebacterium\_efficiens\_Y8-314 196164 Tyr GTA  
-GCCAGATTGCCCGAGC--GGCCAAAGGGAGCGGACTGTAAATCCGTCGGC-----TGC-----GCCTACGTTAGGTTTCGAATCCTTACATCTGGCA---  
>tdbD00011735 Coxiella\_burnetii\_RSA\_493 227377 Tyr GTA  
-GGAGGGGTTCCCGAGT--GGCCAAAGGGGATCAGACTGTAAATCTGACGGC-----TCAG-----CCTTCGTTAGGTTTCGAATCCTACCCCTCCA---  
>tdbD00011589 Deinococcus\_radiodurans\_R1 243230 Tyr GTA  
-GGGTAGGTGGCCGAGT--GGTTAAAGGGCGACAGACTGTAAATCTGTTACG-----TAAG-----TGTA-CGGCGGTTTCGAATCCGCCCTGCCACCA  
>tdbD00011773 Desulfovibrio\_vulgaris\_subsp\_vulgaris\_str\_Hildenborough\_882 Tyr GTA  
-GGTGGGGTCCCGAGT--GGCCAAAGGGGAACAGACTGTAAATCTGTCGTCG-----TAA-----GACTTCGGTGGTTCAAATCCACCCCAACCACCA  
>tdbD00011726 Enterococcus\_faecalis\_V583 226185 Tyr GTA  
-GGAGGAATAGCGAAGT--GGCTAAACGCGACGGACTGTAAATCCGTTCTC-----TAG-----GGTTCAGTGGTTCGAATCCACTTCTCCACCA---  
>tdbD00003526 Escherichia\_coli\_562 Tyr GTA  
-GGTGGGGTCCCGAGC--GGCCAAAGGGGAGCAGACTGTAAATCTGCCGTC-----ACAG-----ACTTCGAAGGTTTCGAATCCTTCCCCACCACCA  
>tdbD00003527 Escherichia\_coli\_562 Tyr GTA  
-GGTGGGGTCCCGAGC--GGCCAAAGGGGAGCAGACTGTAAATCTGCCGTC-----ATCG-----ACTTCGAAGGTTTCGAATCCTTCCCCACCACCA  
>tdbD00011692 Fusobacterium\_nucleatum\_subsp\_nucleatum\_ATCC\_25586 190304 Tyr GTA  
-GGTTGGGTTCCCGAGC--GGTCAAAGGGATCAGACTGTAAATCTGACGGC-----TCAG-----CCTTCGAAGGTTTCGAATCCTTCCCCAACCACCA  
>tdbD00011760 Geobacter\_sulfurreducens\_PCA\_243231 Tyr GTA  
-GGAGGGATTCCCGAGC--GGCCAAAGGGGAACAGACTGTAAATCTGTCGTCG-----AAC-----GACTTCGGAGGTTTCGAATCCTCCTCCCTCCACCA  
>tdbD00003531 Haemophilus\_influenzae\_727 Tyr GTA  
-TGAGGGGTTCCCGAGC--GGCCAAAGGGGGCAGACTGTAAATCTGTTGGC-----TCAG-----CCTTCGAAGGTTTCGAATCCTTCTCCCTCCACCA  
>tdbD00011584 Haemophilus\_influenzae\_Rd\_KW20\_71421 Tyr GTA  
-GGAGGGGTTCCCGAGC--GGCCAAAGGGGGCAGACTGTAAATCTGTTGGC-----TCAG-----CCTTCGAAGGTTTCGAATCCTTCTCCCTCCACCA  
>tdbD00003521 Helicobacter\_pylori\_210 Tyr GTA  
-GGTGAGATATCAAGT--GGCCAACGAGGGCAGACTGTAAATCTGTCG-----TC-----TTCCGTGGTTCGAATCCACGTTCTACCA---  
>tdbD00011582 Helicobacter\_pylori\_26695 85962 Tyr GTA  
-GGGTAGGTACTCAAGT--GGCCAACGAGGGCAGACTGTAAATCTGCTGACT-----ATG-----TCTT-CGAAGGTTTCGAATCCTTCCCTGCCACC-  
>tdbD00011583 Helicobacter\_pylori\_J99 85963 Tyr GTA  
-GGTGAGATATCAAGT--GGCCAACGAGGGCAGACTGTAAATCTGCTGACT-----ATG-----TCTT-CGTTGGTTCGAATCCACGTTCTACCACCA  
>tdbD00011762 Lactobacillus\_johnsonii\_NCC\_533 257314 Tyr GTA  
-GGAGCCCTAGCGAAGT--GGCTAAACGCGCGGCTGTAAAACCGCTCTCT-----CTG-----AGTT-CGGTGGTTCGAATCCACTGGCCTCCA---  
>tdbD00011727 Lactobacillus\_plantarum\_WCFS1 220668 Tyr GTA  
-GGAGGGTAGCGAAGTCTGGCTAAACGCGGGCAGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGTGGTTCGAATCCACTCCCTCCACCA---  
>tdbD00011763 Leifsonia\_xyli\_subsp\_xyli\_str\_CTCB07\_28109 Tyr GTA  
-GGCGAGTTACCCAAGC--GGCCAAAGGGATCTGACTGTAAATCAGCTGTCT-----ACG-----ACTT-CGGGGGTTTCGAATCCCTCACTCGCCA---  
>tdbD00011713 Leptospira\_interrogans\_serovar\_Lai\_str\_56601 189518 Tyr GTA  
-GGGTAGGTACTCAAGT--GGCCAACGAGGGCAGACTGTAAATCTGCTGACT-----ATG-----TCTT-CGAAGGTTTCGAATCCTTCCCTGCCACCA  
>tdbD00011601 Listeria\_innocua\_Clip11262 272626 Tyr GTA  
-GGAGGGTAGCGAAGT--GGCTAAACGCGGGCAGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGTGGTTCGAATCCACTCCCTCCACCA  
>tdbD00011775 Mesoplasma\_florum\_L1 265311 Tyr GTA  
-GGAGGGTAGCGAAGC--GGTCAAACGCGGGTGGCTGTAAACCACTTCTC-----TTC-----GGTTCGGGGGTTTCGAATCCCTCCCTCCACCA  
>tdbD00011612 Mesorhizobium\_loti\_MAFF303099 266835 Tyr GTA  
-GGAGAGGTGCCCGAGT--GGTTAAAGGGGACGGACTGTAAATCCGTTGGC-----TTAG-----CCTACGTTGGTTCGAATCCAACCTTCTCCACCA  
>tdbD00011733 Mycobacterium\_bovis\_AF2122/97 233413 Tyr GTA  
-GGCAGGTTGCCCGAGC--GGCCAAAGGGGAGCGGACTGTAAATCCGTCGCG-----AAAG-----CTA-CGACAGGTTTCGAATCCTGCACCTGCCACCA  
>tdbD00011573 Mycobacterium\_leprae\_TN 272631 Tyr GTA  
-GGCAGGTTGCCCGAGC--GGCCAAAGGGGAGCGGACTGTAAATCCGTCGCG-----AAAG-----CTA-CACAGGTTTCGAATCCTGTACTGCCACCA  
>tdbD00003514 Mycoplasma\_capricolum\_2095 Tyr GTA  
-GGAGGGTAGCGAAGT--GGCTAAACGCGGGTGGCTGTAAACCACTTCTC-----TAC-----GGTTCGGGGGTTTCGAATCCCTCCCTCCACCA  
>tdbD00011732 Mycoplasma\_gallisepticum\_R\_233150 Tyr GTA  
-GGGTAGGTAGCGAAGT--GGCTAAACGCTTCTGACTGTAAATCAGACACT-----TTT-----GGTTTCGGCGGTTTCGAATCCGTCCTGCCACCA  
>tdbD00003515 Mycoplasma\_genitalium\_2097 Tyr GTA  
-GGACAGGTAGCGAAGT--GGCTAAACGCTTCTGACTGTAGATCAGACACT-----TAT-----GGTTTCGGGAGTTTCGAATCCTCCTGTCCACCA  
>tdbD00011590 Mycoplasma\_genitalium\_G37 243273 Tyr GTA  
-GGACAGGTAGCGAAGT--GGCTAAACGCTTCTGACTGTAGATCAGACACT-----TTAT-----GGTTTCGGGAGTTTCGAATCCTCCTGTCCACCA  
>tdbD00003516 Mycoplasma\_pneumoniae\_2104 Tyr GTA  
-GGACAGGTAGCGAAGT--GGCTAAACGCTTCTGACTGTAGATCAGACACT-----TCAT-----GGTTTCGGGAGTTTCGAATCCTCCTGTCCACCA  
>tdbD00011619 Mycoplasma\_pulmonis\_UAB\_CTIP 272635 Tyr GTA  
-GGGGGGTAGCGAAGC--GGCCAAACGCGGGTGGCTGTAAACCACTTCT-----TCG-----GATTTCGGGGGTTTCGAATCCCTCCCTCCACCA

>tdbD00011568 *Neisseria meningitidis* MC58 122586 Tyr GTA  
-GGAGGGATTCCCAGC--GGTCAAAGGGGGCAGACTGTAAATCTGTGCG-----AAAG-----CTT-CGAAGGTTTGAATCCTTCTCCCTCCACCA  
>tdbD00011569 *Neisseria meningitidis* Z2491 122587 Tyr GTA  
-GGAGGGTTCCCAGC--GGTCAAAGGGGGCAGACTGTAAATCTGTGCG-----AAAG-----CTT-CGAAGGTTTGAATCCTTCTCCCTCCACCA  
>tdbD00011744 *Nitrosomonas europaea* ATCC 19718 228410 Tyr GTA  
-GGAGGGTTCCCAGC--GGTCAAAGGGGATCAGACTGTAAATCTGACGGC-----TCTG-----CCTTCGAAGGTTTGAATCCTTCCCCCTCCACCA  
>tdbD00011617 *Nostoc* sp. PCC 7120 103690 Tyr GTA  
-GGTTCGGTATCCAAGTCCGTTGAAGGAAGCCGTCTGTAAACCGGATGCCT-----CTG-----TGCTTCGTAGGTTCAAATCCTACTCGGCCA---  
>tdbD00011618 *Nostoc* sp. PCC 7120 103690 Tyr GTA  
-GGTTCGGTATCCAAGTCCGTTGAAGGAAGCCGTCTGTAAACCGGATGCCT-----TAC-----ACCTACGCTGGTTCAAATCCAGCCCGGCCA---  
>tdbD00011714 *Oceanobacillus iheyensis* HTE831 221109 Tyr GTA  
-GGAGGGTAGCGAAGT--GGCTAAACGCGCGGACTGTAAATCCGCTCCC-----TCG-----GGTTCGGCAGTTTGAATCTGCCCCCTCCACCA  
>tdbD00011752 *Onion yellows phytoplasma* OY-M 262768 Tyr GTA  
-GGAGGGATAGCGAAGT--GGCTAAACGCGCGGACTGTAAATCCGCTCCC-----TAA-----GGTACGTTGGTTTGAATCCACCTCCCTCCACCA  
>tdbD00011592 *Pasteurella multocida* subsp. *multocida* str. Pm70 272843 Tyr GTA  
-GGAGGGATTCCCAGC--GGCCAAAGGGGAGCAGACTGTAAATCTGCGCGC-----TCAG-----CCTTCGAAGGTTTGAATCCTTCTCCCTCCACCA  
>tdbD00011764 *Porphyromonas gingivalis* W83 242619 Tyr GTA  
-GGCAGTTTACCAGT--GGCTAAATGGGCTGACTGTAAATCCGCTGCG-----TAC-----GCCTTCGGTGGTTTGAATCCATCACTGCCA---  
>tdbD00011776 *Propionibacterium acnes* KPA171202 267747 Tyr GTA  
-GGCAGTTTACCAGT--GGCCAAAGGGGAGCGGTCTGTAAACCGCTCGGT-----TTCG-----CCTACGTTGGTTTGAATCCAACACCTGCCA---  
>tdbD00003528 *Pseudomonas aeruginosa* 287 Tyr GTA  
-GGAGGGATCCCTTAGT--GGCC-AAAGGATCAGACTGTAAATCTGACGTC-----ATAG-----ACTTCGAAGGTTTGAATCCTTCTCCCTCCACCA  
>tdbD00011594 *Pseudomonas aeruginosa* PA01 208964 Tyr GTA  
-GGAGGGATTCCCAGT--GGCCAAAGGGATCAGACTGTAAATCTGACGTC-----ATAG-----ACTTCGAAGGTTTGAATCCTTCTCCCTCCACCA  
>tdbD00011747 *Pseudomonas syringae* pv. *tomato* str. DC3000 223283 Tyr GTA  
-GGAGGGTTCCCAGC--GGCCAAAGGGATCAGACTGTAAATCTGACGTC-----ACG-----ACTT-CGAAGGTTTGAATCCTTCCCCCTCCACCA  
>tdbD00011616 *Ralstonia solanacearum* GMI1000 267608 Tyr GTA  
-GGAGAGTTGCCCGAGT--GGCTAAAGGGGGCAGACTGTAAATCTGTGGCT-----TAC-----GCCTACGTTGGTTTGAATCCAACCTCTCCACCA  
>tdbD00011743 *Rhodopirellula baltica* SH 1 243090 Tyr GTA  
-GGGGGTTTGGCCGAGT--GGTTAAAGGGGGCGGACTGTAAATCCGCTGCG-----TATG-----CCTACACAGGTTTGAATCCTGTAGCCCCCA---  
>tdbD00011610 *Rickettsia conorii* str. Malish 7 272944 Tyr GTA  
-GGAGGGTTGCCCGAGT--GGTCAATGGCAGCAGACTGTAAATCTGCCCGCG-----TAAG-----CGTT-CGAAGGTTTCAAATCCTTCTCCCTCCACCA  
>tdbD00003530 *Rickettsia prowazekii* 782 Tyr GTA  
-GGAGGGTTGCCCGAGT--GGTCAATGGCAGCAGACTGTAAATCTGCCCGCG-----GTAA-----GTTT-CGAAGGTTTGAATCCTTCTCCCTCCACCA  
>tdbD00011695 *Rickettsia prowazekii* str. Madrid E 272947 Tyr GTA  
-GGAGGGTTGCCCGAGT--GGTCAATGGCAGCAGACTGTAAATCTGCCCGCG-----TAAG-----CGTT-CGAAGGTTTGAATCCTTCTCCCTCCACCA  
>tdbD00011717 *Shewanella oneidensis* MR-1 211586 Tyr GTA  
-GGAGGGTTTCCCAGT--GGCCAAAGGGATCAGACTGTAAATCTGACGCG-----TCCG-----CCTTCGAAGGTTTGAATCCTTCTCCCTCCACCA  
>tdbD00011719 *Shigella flexneri* 2a str. 301 198214 Tyr GTA  
-GGTGGGTTCCCAGC--GGCCAAAGGGAGCTTACTGTAAATCTGTGCTC-----ACAG-----ACTTCGAAGGTTTGAATCCTTCCCCACCACCA  
>tdbD00011622 *Sinorhizobium meliloti* 1021 266834 Tyr GTA  
-GGAGGGATGCCCGAGT--GGTTAAAGGGGACGACTGTAAATCCGTTGCG-----TCAG-----CCTACGTTGGTTTCAAATCCAACCTCCCTCCACCA  
>tdbD00003520 *Staphylococcus aureus* 1280 Tyr GTA  
-GGAGGGTAGCGAAGT--GGCTAAACGCGGCGACTGTAAATCCGCTCCT-----TCGG-----GGTTCGGCAGTTTGAATCTGCCCCCTCCA---  
>tdbD00011757 *Staphylococcus aureus* subsp. *aureus* MRSA252 282458 Tyr GTA  
-GGAGGGTAGCGAAGT--GGCTAAACGCGGCGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTGAATCTGCCCCCTCCA---  
>tdbD00003525 *Stigmatella aurantiaca* 41 Tyr GTA  
-GGAGGGATACCCAAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCCCGCT-----CTAC-----GCCTTCGATGGTTTGAATCCATCTCCCTCCA---  
>tdbD00011720 *Streptococcus agalactiae* 2603V/R 208435 Tyr GTA  
-GGAGAGATAGCGAAGA--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGGGGTTTGAATCCCTCTCTCTCCA---  
>tdbD00011721 *Streptococcus agalactiae* 2603V/R 208435 Tyr GTA  
-GGAAAGATAGCGAAGA--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGGGGTTTGAATCCCTCTCTTTCCA---  
>tdbD00011722 *Streptococcus mutans* UA159 210007 Tyr GTA  
-GGAAGGTAGCGAAGA--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGGGGTTTGAATCCCTCCCTTCCA---  
>tdbD00011741 *Streptomyces avermitilis* MA-4680 227882 Tyr GTA  
-GGCGGTGTGCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCCCGC-----TCAG-----CCTTCCCAGGTTTGAATCCTGGCGCGGCCA---  
>tdbD00011767 *Symbiobacterium thermophilum* IAM 14863 292459 Tyr GTA  
-GGGAGATACCCAAGT--GGTCAAAGGGGGCTGACTGTAAATCAGTTGCGT-----AAC-----GCTT-CGGAGGTTTGAATCCTCCTCTCCCCACCA  
>tdbD00011768 *Symbiobacterium thermophilum* IAM 14863 292459 Tyr GTA  
-GGGAGATACCCAAGT--GGCCAAAGGGGGCTGACTGTAAATCAGTTGCGC-----AAC-----GCTT-CGGTGGTTTGAATCCACCTCTCCCCACCA  
>tdbD00003532 *Synechocystis* sp. 1143 Tyr GTA  
-GGTTCGATGCCCGAGT--GGTTAATGGGGGCGGACTGTAAATCCGCTGCG-----TATG-----CCTACGCTGGTTTCAAATCCAGCTCGGCCA---  
>tdbD00011704 *Thermoanaerobacter tengcongensis* MB4 273068 Tyr GTA  
-GGAGGGATACCCAAGC--GGCCAAAGGGGGCAGACTGTAAATCTGCTGGCG-----TATG-----CCTT-CGATGGTTTCAAATCCATCTCCCTCCACCA  
>tdbD00011702 *Thermosynechococcus elongatus* BP-1 197221 Tyr GTA  
-GGTTCGGTGCCTGAGT--GGTTAATGGGGGCGGACTGTAAATCCGTTGCG-----TACG-----CCTACGCTGGTTTGAATCCAGCCCGGCCA---  
>tdbD00003513 *Thermotoga maritima* 2336 Tyr GTA  
-GGTGGGTTGCCCGAGT--GGCCAAAGGGGGCGGATTGTAAATCCGCAGA-----ATC-----TT-CGGAGGTTTCAAATCCTCCCCCACCACCA  
>tdbD00011596 *Thermotoga maritima* MSB8 243274 Tyr GTA  
-GGTGGGTTGCCCGAGT--GGCCAAAGGGGGCGGACTGTAAATCCGCTGGCA-----GAAT-----GCCTTCGGAGGTTTCAAATCCTCCCCCACCACCA  
>tdbD00003524 *Thermus thermophilus* 274 Tyr GTA  
-GGGCAGTTGCCCGAGC--GGCCAAAGGGGACGGTCTGTAAACCGTTGGCG-----TATG-----CCTT-CGCTGGTTTGAATCCAGCCCTGCCACCA  
>tdbD00011777 *Thermus thermophilus* HB27 262724 Tyr GTA  
-GGCAGTTGCCCGAGC--GGCCAAAGGGGACGGTCTGTAAACCGTTGGCG-----TATG-----CCTT-CGCTGGTTTGAATCCAGCCCTGCCACCA  
>tdbD00003517 *Treponema pallidum* 160 Tyr GTA

-GGGGAGTTTCCCGAGT--GGTCAAAGGGAGCAGACTGTAATCTGTGGCG-----TTG-----TCTT-CCAAGGTTTCAATCCTTGACTCCCCA---  
>tdbD00011729 Tropheryma\_whipplei\_str.\_Twist\_203267 Tyr GTA  
-GGCGAGTTACCCAAGT--GGCCAAAGGGATCTGACTGTAAATCAGCTGTCA-----TTC-----GACTTCGGGGGTTTCAATCCCTCACTCGCCA---  
>tdbD00011574 Ureaplasma\_parvum\_serovar\_3\_38504 Tyr GTA  
-GGACAGATAGCGAAGT--GGCCAAACGCATCCGGCTGTAAACCCGGCTCCG-----AGA-----GGTTCGTAGGTTTCAATCCTACTCTGTCCACCA  
>tdbD00011570 Vibrio\_cholerae\_O1\_biovar\_El\_Tor\_str.\_N16961\_243277 Tyr GTA  
-GGAGGGGTTCCCGAGT--GGCCAAAGGGAGCAGACTGTAAATCTGCCGGC-----TCCG-----CCTTCGATGGTTTCAATCCGTCCTCCCTCCACCA  
>tdbD00011779 Wolbachia\_endosymbiont\_of\_Drosophila\_melanogaster\_163164 Tyr GTA  
-GGAGGAGTGACCGAGT--GGTTAAAGGTAACAGACTGTAAATCTGTCCGCG-----TGAG-----CGTA-CGTAGGTTTCAATCCTACTCTCCCTCCA---  
>tdbD00011706 Xanthomonas\_axonopodis\_pv.\_citri\_str.\_306\_190486 Tyr GTA  
-GGAGGGATACCCAAGC--GGCCAAACGGGGCAGACTGTAAATCTGTGGCT-----TAC-----GCCTTCGGTGGTTTCAATCCACCTCCCTCCACCA  
>tdbD00011597 Xylella\_fastidiosa\_9a5c\_160492 Tyr GTA  
-GGAGGGATACCCAAGC--GGCCAAACGGGGCAGACTGTAAATCTGTGGCT-----TGC-----GCCTTCGGTGGTTTCAATCCACCTCCCTCCACCA  
>tdbD00011598 Xylella\_fastidiosa\_9a5c\_160492 Tyr GTA  
-GGTGGGGTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCCGTC-----ATCG-----ACTTCGAAGGTTTCAATCCTCCCTCCACACC-  
>tdbD00011599 Xylella\_fastidiosa\_9a5c\_160492 Tyr GTA  
-GGTGGGGTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCCGTC-----ACAG-----ACTTCGAAGGTTTCAATCCTCCCTCCACACC-  
>tdbD00011465 Acinetobacter\_sp.\_ADP1\_62977 Trp CCA  
-AGGTCAGTAGTTCAATT-GGT--AGAGCGTCCGGTCTCCAAAACCGAAT-----GTTGGGGGTTTCGAGTCCCTCCTGGCCTGCCA  
>tdbD00011427 Bacillus\_anthraxis\_str.\_Ames\_198094 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAAGTGAAGTCTCCAAAACCTCCA-----G-TGTGGGTTTCGATTCTCTACTGCCCCCTGCCA  
>tdbD00011428 Bacillus\_anthraxis\_str.\_Ames\_198094 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAAGTGAAGTCTCCAAAACCTCCA-----G-TGTGGGTTTCGATTCTCTACTGCCCCCTG---  
>tdbD00011397 Bacillus\_halodurans\_C-125\_272558 Trp CCA  
-AGGGGCATAGTTTAA--GGT--AGAACAGAGGTTCCAAAACCTCCG-----G-TGTGGGTTTCGATTCTCTACTGCCCCCTGCCA  
>tdbD00011290 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308 Trp CCA  
-AGGGGCATAGTGTAA--GGT--AGAACAGAGGTTCCAAAACCTCCG-----G-TGTGGGTTTCGATTCTCTACTGCCCCCTGCCA  
>tdbD00011429 Bartonella\_henselae\_str.\_Houston-1\_283166 Trp CCA  
-AGGGGTATAGCTCAGTT-GGT--AGAGCGCGGTCTCCAAAACCGCAG-----GTCGCGGGTTTCGAGCCCTGCTGCCCCCTGCCA  
>tdbD00011465 Bartonella\_quintana\_str.\_Toulouse\_283165 Trp CCA  
-AGGGGTATAGCTCAGTT-GGT--AGAGCGCGGTCTCCAAAACCGCAG-----GTCGCGGGTTTCAAGCCCTGCTGCCCCCTGCCA  
>tdbD00011430 Bdellovibrio\_bacteriovorus\_HD100\_264462 Trp CCA  
-AGGGGTGTAGCTCCAGC-GGT--AGAGCGAACGACTCCAAATCGTTAG-----GTCGTTGGGTTTCGAAATCCCTCCGCCCCCTGCCA  
>tdbD00011386 Bifidobacterium\_longum\_NCC2705\_206672 Trp CCA  
-AGGGAAGTGGCGCAATT-GGT--AGCGCAACGGTCTCCAAAACCGTAG-----GTTGTGGGTTTCGAGTCCCGCCTTCCCTGCCA  
>tdbD00003284 Borrelia\_burgdorferi\_139 Trp CCA  
-AGGTCAGTAGTTCCAAC-GGT--AGAACGACAGTCTCCAAAACCTGTAT-----GCTGGGGGTTTCGAAATCCCTCCTGACCTG---  
>tdbD00011398 Bradyrhizobium\_japonicum\_USDA\_110\_224911 Trp CCA  
-AGGAGTGTAGCTCAATT-GGT--AGAGCACGGTCTCCAAAACCGGGG-----GTCGCGAGTTTCGAGCCCTGCCACTCCTGCCA  
>tdbD00011329 Brucella\_melitensis\_16M\_224914 Trp CCA  
-AGGGGTATAGCTCAGTT-GGT--AGAGCGACGGTCTCCAAAACCGTAG-----GTCGCGGGTTTCGAACCCCTGCTGCCCCCTGCCA  
>tdbD00011291 Buchnera\_aphidicola\_str.\_APS\_(Acyrtosiphon\_pisum)\_107806 Trp CCA  
-AGGGGTGTAGTTCAATTTGGT--AGAGCATCGGTCTCCAAAACCGAAA-----GTTGTAGGTTTCAAATCCTTCCACCCCTG---  
>tdbD00011417 Buchnera\_aphidicola\_str.\_Bp\_(Baizongia\_pistaciae)\_224915 Trp CCA  
-AGGGATGTAGCTCAATT-GGT--AGAGTATCGGTCTCCAAAACCGAAT-----GTTGGGGGTTTCAATTCCTCCATCCCTG---  
>tdbD00011372 Buchnera\_aphidicola\_str.\_Sg\_(Schizaphis\_graminum)\_198804 Trp CCA  
-AGGGGTGTAGTTCAATTTGGT--AGAGCATCGGTCTCCAAAACCGAAA-----GTTGTAGGTTTCAAAGTCTTCCACCCCTGCCA  
>tdbD00011307 Campylobacter\_jejuni\_subsp.\_jejuni\_NCTC\_11168\_192222 Trp CCA  
-AGGGCAATAGCTCCAAC-GGT--AGAGCGCGGATTCCAAATCCGATG-----GTTGGGGGTTTCGAAATCCCTCTGCCCCCTGCCA  
>tdbD00011466 Candidatus\_Blochmannia\_floridanus\_203907 Trp CCA  
-AGGGGTGTAGTTCAAT--GGT--AGAATATCGGTCTCCAAAACCGAGG-----GTTGGGAGTTTCAAGTCTCTTCAACCCCTG---  
>tdbD00011308 Caulobacter\_crescentus\_CB15\_190650 Trp CCA  
-AGGAGTGTAGCTCAGCT-GGT--AGAGCATCGGTCTCCAAAACCGAGG-----GCCGGGGGTTTCGAGTCCCTCCACTCCTGCCA  
>tdbD00011327 Clostridium\_acetobutylicum\_ATCC\_824\_272562 Trp CCA  
-AGGGGTATAGCTCAATT-GGT--AGAGTAACGGTCTCCAAAACCGTAG-----GTTGTGGGTTTCGATTCTCTACTGCCCCCTGCCA  
>tdbD00011322 Clostridium\_perfringens\_str.\_13\_195102 Trp CCA  
-AGGGGTATGCTCAATT-GGT--AGAGTAGTGGTCTCCAAAACCATG-----GTTGTGGGTTTCAAAGTCTCTACTGCCCCCTGCCA  
>tdbD00011323 Clostridium\_perfringens\_str.\_13\_195102 Trp CCA  
-AGGGGTATGCTCAATT-GGT--AGAGTAGTGGTCTCCAAAACCATG-----GTTGTGGGTTTCGAGTCTCTACTGCCCCCTGCCA  
>tdbD00011399 Clostridium\_tetani\_E88\_212717 Trp CCA  
-AGGGGTATAGCTCAATT-GGT--AGAGTAGCGGTCTCCAAAACCGTTG-----GTTCCGGGTTTCAAAGTCTCTGCCCCCTGCCA  
>tdbD00011431 Corynebacterium\_diphtheriae\_NCTC\_13129\_257309 Trp CCA  
-AGGGCGTAGTCTCAATT-GGT--AGAGCAACGGTCTCCAAAACCGTAG-----GTTGCAGGTTTCAAAGTCTCTGCGCCCCCTG---  
>tdbD00011388 Corynebacterium\_efficiens\_YS-314\_196164 Trp CCA  
-AGGGCGTAGTCTCAATT-GGC--AGAGCAACGGTCTCCAAAACCGTAG-----GTTGCAGGTTTCAAAGTCTCTGCGCCCCCTG---  
>tdbD00011374 Corynebacterium\_glutamicum\_ATCC\_13032\_196627 Trp CCA  
-AGGGCGTAGTCTCAATT-GGC--AGAGCAACGGTCTCCAAAACCGTAG-----GTTGCAGGTTTCGATTCTCTGCGCCCCCTG---  
>tdbD00011413 Coxiella\_burnetii\_RSA\_493\_227377 Trp CCA  
-AGGCCAGTAGTCTCAATT-GGC--AGAGCAGCGGTCTCCAAAACCGCAG-----GTTGGGGGTTTCGATTCCCTCCTGGCCTGCCA  
>tdbD00011453 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882 Trp CCA  
-AGGGCAGTAGTCTCAAT--GGT--AGAGCGCGGGTCTCCAAAACCGGAT-----GTTGGGGGTTTCAAATCCTCTGCCCCCTGCCA  
>tdbD00011401 Enterococcus\_faecalis\_V583\_226185 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAACAACGGTCTCCAAAACCGTTG-----G-TGTGGGTTTCAAATCCTGCTGCCCCCTGCCA  
>tdbD00003289 Escherichia\_coli\_562 Trp CCA  
-AGGGCGTAGTCTCAATT-GGT--AGAGCACCGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCCCTGCCA

>tdbD00011370 *Fusobacterium nucleatum* subsp. *nucleatum* ATCC 25586 190304 Trp CCA  
-AGGTCAATGGCTCAATT-GGT--AGAGCATCGGTCTCCAAAACCGAGG-----GTTGGGGGTTTCGAGTCCCTCTTGACCTGCCA  
>tdbD00011441 *Geobacter sulfurreducens* PCA 243231 Trp CCA  
-AGGCCAGTAGCTCTAAC-GGCT-AGAGCGCGGTCTCCAAAACCGGAT-----GTTGGGGGTTTCGAATCCCTCTGGCCTGCCA  
>tdbD00003291 *Haemophilus influenzae* 727 Trp CCA  
-AGGGCGGTAGTTC AATT-GGT--AGAGCACCGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGCCTCTCCGCCCTGCCA  
>tdbD00003287 *Helicobacter pylori* 210 Trp CCA  
-AGGTCAAGTAGCTCCAAT-GGT--AGAGCGTGGTCTCCAAAACCGGTT-----GTTGGGGGTTTCGAGTCCCTCTGGCCTGCCA  
>tdbD00011442 *Lactobacillus johnsonii* NCC 533 257314 Trp CCA  
-AGGGATATCGTATAAAA--GGT--AGTACATCGGTCTCCAAAACCGGTA-----G-TGTGGGTTCAATTCTACTATCCCTG---  
>tdbD00011404 *Lactobacillus plantarum* WCFS1 220668 Trp CCA  
-AGGGATATAGTTTAAAT--GGT--AGAACAACGGTCTCCAAAACCGTCG-----G-TGTGGGTTCAACTCTACTATCCCTGCCA  
>tdbD00011443 *Leifsonia xyli* subsp. *xyli* str. CTCB07 281090 Trp CCA  
-AGGGCGGTAGTTC AATT-GGT--AGAGCACCGGTCTCCAAAACCGGAG-----GTTGCAGGTTTCGATTCTCTCGCCCTG---  
>tdbD00011389 *Leptospira interrogans* serovar *Lai* str. 56601 189518 Trp CCA  
-AGGCCTGTAGTTT T AGT--GGT--AGAAGTAGGATCTCCAAAGTCCTTG-----G-TGGGAGTTTCGATTCTCTCCGGCCCTG---  
>tdbD00011411 *Mycobacterium bovis* AF2122/97 233413 Trp CCA  
-AGGGCGGTAGTTC AACT-GGC--AGAGCAGCGGTCTCCAAAACCGGAG-----GTTGCAGGTTCAAGTCTCTCGCCCTG---  
>tdbD00011297 *Mycobacterium leprae* TN 272631 Trp CCA  
-AGGGCGGTAGTTC AACT-GGC--AGAGCAGCGGTCTCCAAAACCGGAG-----GTTGCAGGTTCAAACTCTCTCGCCCTG---  
>tdbD00003275 *Mycoplasma capricolum* 2095 Trp CCA  
-AGGAGAGTAGTTC AAT--GGT--AGAAGCTCGGTCTCCAAAACCGGTA-----GTTGAGGTTTCGATTCTCTCTCTCTGCCA  
>tdbD00011410 *Mycoplasma gallisepticum* R 233150 Trp CCA  
-AGGGGTGTAGTTCAAT--GGT--AGAAGTAGGTTCTCCAAAACCTTCG-----A-TGGGGTTTCGATTCTCTGACCCCTGCCA  
>tdbD00011293 *Neisseria meningitidis* MC58 122586 Trp CCA  
-AGGCCAATAGTTC AATT-GGT--AGAGTATCGGTCTCCAAAACCGGAG-----GTTGGGGGTTTCGAGACCCTCTTGCCCTGCCA  
>tdbD00011423 *Nitrosomonas europaea* ATCC 19718 228410 Trp CCA  
-AGGCCAGTAGTTC AATT-GGC--AGAGCGTGGTCTCCAAAACCGAAG-----GTTGGGGGTTTCGATGCCCTCTGGCCTGCCA  
>tdbD00011390 *Oceanobacillus iheyensis* HTE831 221109 Trp CCA  
-AGGGGTATAGTTTAAAT--GGT--AAAACGAAGGTCTCCAAAACCTTTG-----A-TGTGGGTTTCGATTCTACTACCCTGCCA  
>tdbD00011432 *Onion yellows phytoplasma* OY-M 262768 Trp CCA  
-AGGGATATGATGTCAAT--GGT--AGCATAACGGTCTCCAAAACCGGTC-----G-TTCGGGTTTCGAATCTGATATCCCTGCCA  
>tdbD00011456 *Propionibacterium acnes* KPA171202 267747 Trp CCA  
-AGGGCACTAGTTC AATT-GGC--AGAGCAGCGGTCTCCAAAACCGGAG-----GTTGGGGGTTCAAGTCCCTCTGTCCTG---  
>tdbD00011314 *Pseudomonas aeruginosa* PA01 208964 Trp CCA  
-AGGCCAGTAGTTC AATT-GGC--AGAGCGGCGGTCTCCAAAACCGGAG-----GTTGGGGGTTTCGATTCCCTCTGGCCTGCCA  
>tdbD00011426 *Pseudomonas syringae* pv. *tomato* str. DC3000 223283 Trp CCA  
-AGGTCAAGTAGTTC AATT-GGC--AGAGCAGCGGTCTCCAAAACCGTAG-----GTTGGGGGTTTCGATTCCCTCTGACCTGCCA  
>tdbD00011333 *Ralstonia solanacearum* GMI1000 267608 Trp CCA  
-AGGGGTATAGTTC AACT-GGC--AGAGCGTGGTCTCCAAAACCGAAG-----GTTGGGGGTTTCGATTCCCTCTGCCCTGCCA  
>tdbD00011421 *Rhodospirillum rubrum* SH 1 243090 Trp CCA  
-AGGGCGGTAGTTC AATT-GGC--AGAGCACTGGTTCTCCAAAACCGGAG-----GTTGTGAGTTTCGACTCTCGCCGCCCTG---  
>tdbD00011328 *Rickettsia conorii* str. Malish 7 272944 Trp CCA  
-AGGAGTGTAGTTC AATT-GGT--AGAGCGCGGTCTCCAAAACCGGAG-----GTTGCGGGTTTCGATACCTGTGCTCTGCCA  
>tdbD00003290 *Rickettsia prowazekii* 782 Trp CCA  
-AGGAGTGTAGTTC AATT-GGT--AGAGCGCGGTCTCCAAAACCGGAG-----GTTGCGGGTTTCGATTCTCTGCTCTGCCA  
>tdbD00011445 *Rickettsia typhi* str. Wilmington 257363 Trp CCA  
-AGGAGTGTAGTTC AATT-GGT--AGAGTGGCGGTCTCCAAAACCGGAG-----GTTGCGGGTTTCGATTCTCTGCTCTGCCA  
>tdbD00011392 *Shewanella oneidensis* MR-1 211586 Trp CCA  
-AGGGGTGTAGTTCCAATTGGT--AGAACAGCGGTCTCCAAAACCGATG-----GTTGCGGGTTTCGAGTCTGCCACCCTGCCA  
>tdbD00011393 *Shigella flexneri* 2a str. 301 198214 Trp CCA  
-AGGGCGGTAGTTC AATT-GGT--AGAGCACCGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTG---  
>tdbD00011338 *Sinorhizobium meliloti* 1021 266834 Trp CCA  
-AGGGGTATAGTTCAGTT--GGT--AGAGCGGCGGTCTCCAAAACCGGAG-----GTCGGGGGTTTCGAGCCCTCTGCCCTGCCA  
>tdbD00003282 *Spiroplasma citri* 2133 Trp CCA  
-AGGGGTGTAGTTTAAAT--GGT--AGAACAGCGGTCTCCAACACCGTAC-----GTTGTGGGTTCAAGTCTGTCAACCCTGCCA  
>tdbD00003286 *Staphylococcus aureus* 1280 Trp CCA  
-AGGGGCATAGTTCAAC--GGT--AGAATAGAGGTCTCCAAAACCTTTG-----G-TGTGGGTTTCGATTCTACTGCCCTGCCA  
>tdbD00011406 *Staphylococcus epidermidis* ATCC 12228 176280 Trp CCA  
-AGGGGCATAGTTCAAC--GGT--AGAATAGAGGTCTCCAAAACCTTTG-----A-TGTGGGTTTCGATTCTACTGCCCTGCCA  
>tdbD00011419 *Streptomyces avermitilis* MA-4680 227882 Trp CCA  
-AGGGTCTGTAGTTC AATT-GGT--AGAGCACTGGTCTCCAAAACCGGAG-----GTTGGGGGTTTCAGTCCCTCCGCCCTG---  
>tdbD00011446 *Symbiobacterium thermophilum* IAM 14863 292459 Trp CCA  
-AGGGGCATAGTTC AATT-GGT--AGAGCAACGGTCTCCAAAACCGTAG-----GTTGTGGGTTTCGAGTCTACTGCCCTGCCA  
>tdbD00011447 *Symbiobacterium thermophilum* IAM 14863 292459 Trp CCA  
-AGGGCGGTAGTTC AACT-GGT--AGAGCAACGGTCTCCAAAACCGTAG-----GTTGCGGGTTTCGAGTCTGCCGCCCTGCCA  
>tdbD00011380 *Thermoanaerobacter tengcongensis* MB4 273068 Trp CCA  
-AGGGGAGTAGTTC AACT-GGT--AGAGCAACGGTCTCCAAAACCGTGG-----GCTGCGGGTTCAAGTCTGTCTCCCTGCCA  
>tdbD00011316 *Thermotoga maritima* MSB8 243274 Trp CCA  
-AGGGCGGTAGTTC AACT-GGT--AGAGCGCGGTCTCCAAAACCGGAG-----GTTGCGGGTTTCGAGTCTGCCGCCCTGCCA  
>tdbD00011458 *Treponema denticola* ATCC 35405 243275 Trp CCA  
-AGGTCAAGTAGTTC AAT--GGT--AGAGCGTGGTCTCCAAAACCGAAT-----GTTGAGGTTTCGAGTCTCTCTGGCCTG---  
>tdbD00011407 *Tropheryma whippelii* str. Twist 203267 Trp CCA  
-AGGGCGGTGGTTC AATT-GGT--AGAGCAGCGGTCTCCAAAACCGGAG-----GTTGCAGGTTTCAGTCTCTCGCCCTG---  
>tdbD00011295 *Vibrio cholerae* O1 biovar *El Tor* str. N16961 243277 Trp CCA

-AGGGGTGTAGCTCCAATTGGC--AGAGCAGCGGATTCCAATCCGCGT-----GTTGGGAGTTCGAATCTCTCCACCCTGCCA  
>tdbD00011459 Wolbachia\_endosymbiont\_of\_Drosophila\_melanogaster 163164 Trp CCA  
-AGGAGTGTAGCTCAATT-GGT--AGAGCGCTGGTCTCCAAAACCAGAG-----GTTGTAGGTTCAATTCCTATCGCTCTG---  
>tdbD00004871 Acinetobacter\_sp.\_ADP1\_62977 Glu TTC  
-GTCCTATCGTCTAGA--GGCCTAGGACATCGCCCTTTCACGGCGGTA-----A-CCGGGGTTCGAATCCCCGTAGGGACGCCA  
>tdbD00004817 Bdellovibrio\_bacteriovorus\_HD100\_264462 Glu TTC  
-GTTCCCATCGTCTAGG--GGCCTAGGACACCTCCCTTTCACGGAGGAT-----A-CAGGGGTTCAAATCCCCTTGGGAACGCCA  
>tdbD00004603 Buchnera\_aphidicola\_str.\_APS\_(Acyrtosiphon\_pisum)\_107806 Glu TTC  
-GTCCCTTCGTCTAGA--GGTCTAGGACATCGCCCTTTCACGGCGGCA-----A-CAGGGGTTCAAATCCCCTAGGGGACG---  
>tdbD00004801 Buchnera\_aphidicola\_str.\_Bp\_(Baizongia\_pistaciae)\_224915 Glu TTC  
-GTCCCTTCGTCTAGA--GGACTAGGACATCGCCCTTTCACGGCGATA-----A-CAGGGGTTCAAATCCCCTAGGGGACA---  
>tdbD00004733 Buchnera\_aphidicola\_str.\_Sg\_(Schizaphis\_graminum)\_198804 Glu TTC  
-GTCCCTTCGTCTAGA--GGTT-AGGACATCGCCCTTTCACGGCGGCA-----A-CAGGGGTTCAAATCCCCTAGGGGACG---  
>tdbD00004878 Candidatus\_Blochmannia\_floridanus\_203907 Glu TTC  
-GTCCCTTCGTCTAGA--GGTT-AGGACTGCGCTTTCACGGCGGCA-----A-CAGGGGTTCGAAACCCCTAGGGGACA---  
>tdbD00004797 Coxiella\_burnetii\_RSA\_493\_227377 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACATCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTTGGGGACGCCA  
>tdbD00004859 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882 Glu TTC  
-GTTCCCATCGTCTAGCC--GGCCTAGGACAACGGCCTTTCACGGCTCG-----A-CAGGGGTTTCGAATCCCCTTGGGAACGCCA  
>tdbD00004860 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882 Glu TTC  
-GTCCATCGTCTAGCCCGCCAGGACAACGGCCTTTCACGGCTCG-----A-CAGGGGTTCAAATCCCCTTGGGGACGCCA  
>tdbD00000541 Escherichia\_coli\_562 Glu TTC  
-GTCCCTTCGTCTAGA--GGCCAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00004620 Escherichia\_coli\_O157H7\_EDL933\_155864 Glu TTC:  
-GTCCCTTCGTCTAGA--GGCCAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00004837 Geobacter\_sulfurreducens\_PCA\_243231 Glu TTC  
-GTCCCTTCGTCTAGCCCGCCAGGACACCGCCCTTTCACGGCGGCG-----A-CGGGGGTTCAAATCCCCAGGGGACGCCA  
>tdbD00000533 Haemophilus\_ducreyi\_730 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACATCGCCCTTTCACGGCGGTA-----A-CCGGGGTTCGAATCCCCGTGGGGACGCCA  
>tdbD00004809 Nitrosomonas\_europaea\_ATCC\_19718\_228410 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACACACCCTTTCACGGTGGGT-----A-CAGGGGTTTCGAATCCCCTTGGGGACGCCA  
>tdbD00004824 Photorhabdus\_luminescens\_subsp.\_laumondii\_TTO1\_243265 Glu TTC  
-GTCCCTTCGTCTAGA--GGCCTAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00000532 Plesiomonas\_shigelloides\_703 Glu TTC  
-GTCCCTTCGTCTAGA--GGCCTAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACA---  
>tdbD00004635 Pseudomonas\_aeruginosa\_PAO1\_208964 Glu TTC  
-GTCCCTTCGTCTAGT--GGCCTAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAGTCCCCTAGGGGACGCCA  
>tdbD00004661 Ralstonia\_solanacearum\_GMI1000\_267608 Glu TTC  
-GTCCCTTCGTCTAGA--GGCCTAGGACATCACCTTTCACGGTGGT-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00004751 Xanthomonas\_axonopodis\_pv.\_citri\_str.\_306\_190486 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACACACCCTTTCACGGTGGAC-----A-CCGGGGTTCGAATCCCCGTGGGGACGCCA  
>tdbD00004640 Xylella\_fastidiosa\_9a5c\_160492 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACATCACCTTTCACGGTGGCG-----A-CCGGGGTTCGAATCCCCGTGGGGACGCCA  
>tdbD00004852 Yersinia\_pestis\_biovar\_Microtus\_str.\_91001\_229193 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACTGCGCTTTCACGGCTGTA-----A-CAGGGGTTTCGAATCCCCTTGGGGACGCCA  
>tdbD00008679 Bradyrhizobium\_japonicum\_USDA\_110\_224911 Gln TTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGATTTTGATTCGGCA-----TTCGGAGGTTTCGATCCCCTCCGCCCCAGCCA  
>tdbD00008489 Buchnera\_aphidicola\_str.\_APS\_(Acyrtosiphon\_pisum)\_107806 Gln TTG  
-TGGGTATAGCCAAGT--GGTT-AAGGCACCGGTTTTTGATACCGGCA-----T-CCCTGGTTTCGAATCCAGGTACCCCAGCCA  
>tdbD00008703 Buchnera\_aphidicola\_str.\_Bp\_(Baizongia\_pistaciae)\_224915 Gln TTG  
-TGGATATAGCCAAGT--GGT--AAGGCACCGGTTTTTGATACCGGCA-----T-CCCTGGTTTCGAATCCAGGTATCCCAG---  
>tdbD00008773 Candidatus\_Blochmannia\_floridanus\_203907 Gln TTG  
-TGGGTATAGCCAAGC--GGT--AAGGCACCGGTTTTTGATCCCGCA-----CTCCCAGGTTTCGAATCCTGGTACCCCAG---  
>tdbD00008701 Coxiella\_burnetii\_RSA\_493\_227377 Gln TTG  
-TGGGTGTCGCCAAGC--GGT--AAGGCACCGGTTTTTGATCCAGCA-----TTCCCAGGTTTCGAATCCTGGCACCCCAGCCA  
>tdbD00002281 Escherichia\_coli\_562 Gln CTG  
-TGGGTATCGCCAAGC--GGT--AAGGCACCGGATTTCTGATTCGGCA-----TTCCGAGGTTTCGAATCCTCGTACCCCAGCCA  
>tdbD00002280 Escherichia\_coli\_562 Gln TTG  
-TGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATACCGGCA-----TTCCCTGGTTTCGAATCCAGGTACCCCAGCCA  
>tdbD00008735 Geobacter\_sulfurreducens\_PCA\_243231 Gln TTG  
-TGGGTGTCGCCAAGC--GGT--AAGGCACCGGATTTTGATTCGGCA-----TTCCAAGGTTTCGAATCCTTGACCCCAGCCA  
>tdbD00002282 Haemophilus\_influenzae\_727 Gln TTG  
-TGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATTCAGCA-----TTCCCTAGGTTTCGAATCCTAGTACCCCAGCCA  
>tdbD00002283 Haemophilus\_influenzae\_727 Gln TTG  
-TGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATTCAGCA-----TTCCCTAGGTTTCGAATCCTAGTACCCCAGCCA  
>tdbD00008530 Listeria\_innocua\_Clip11262\_272626 Gln TTG  
-TGGGTATAGCCAAGC--GGT--AAGGCACCGGATTTTGATTCGGTCA-----TGCGTGGTTTCGAATCCAGTAGCCCAG---  
>tdbD00008492 Neisseria\_meningitidis\_MC58\_122586 Gln TTG  
-TGGGAGTCTCAAGC--GGTT-AAGACACTGGATTTTGATTCAGCA-----TGCGAAGGTTTCGAATCCTTCCCTCCCAGCCA  
>tdbD00008713 Nitrosomonas\_europaea\_ATCC\_19718\_228410 Gln TTG  
-TGGGAGTCTCGCCAAGT--GGT--AAGGCACCGGATTTTGATTCGGCA-----TTCGTAGGTTTCGATCCCCTACCTCCCAGCCA  
>tdbD00008668 Oceanobacillus\_ihayensis\_HTE831\_221109 Gln TTG  
-TGGGCATAGCCAAGC--GGT--AAGGCATCGGGTTTTTGATCCCGTGT-----ACCCTAGGTTTCGAATCCTAGTGGCCCAGCCA  
>tdbD00008520 Pasteurella\_multocida\_subsp.\_multocida\_str.\_Pm70\_272843 Gln TTG  
-TGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATTCGGCA-----TTCCCTAGGTTTCGAATCCTAGTACCCCAGCCA

>tdbD00008727 Photorhabdus luminescens subsp. laumondii\_TT01 243265 Gln CTG  
-TGGGTATCGCCAAGC--GGT--AAGGCACCGGATTCTGATTCCGCCA-----TTCCAGGTTTGAATCCTGGTACCCAGCCA  
>tdbD00008728 Photorhabdus luminescens subsp. laumondii\_TT01 243265 Gln TTG  
-TGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTGTGATCCGCCA-----TACCAGGTTTGAATCCTGGTACCCAGCCA  
>tdbD00008729 Rhodopseudomonas palustris CGA009 258594 Gln TTG  
-TGGGCGTAGCCAAGC--GGT--AAGGCAGGGGATTTGATTCCGCCA-----TGCGGAGTTTGAATCCTCCCGCCAGCCA  
>tdbD00008672 Shewanella oneidensis MR-1 211586 Gln TTG  
-TGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTGTGATCCGCCA-----TACCTAGGTTTGAATCCTAGTACCCAGCCA  
>tdbD00008501 Ureaplasma parvum serovar\_3 38504 Gln TTG  
-TGGCCTGTAGCCAAGA--GGT--AAGGCAGAAGATTTGATTCTTCCA-----TGCGTAGGTTTGAATCCTACCAGGCCAGCCA  
>tdbD00008764 Wolbachia endosymbiont of Drosophila melanogaster 163164 Gln TTG  
-TGGGTGTAGCCAAGT--GGT--AAGGCAGCGGTTTGTGATCCGCCA-----CGCGAAGTTTGAATCCTTCCACCCAGCCA  
>tdbD00008747 Yersinia pestis biovar Microtus str. 91001 229193 Gln CTG  
-TGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTGTGATCCGCCA-----TTCCAGGTTTGAATCCTCGTACCCAGCCA  
>tdbD00008746 Yersinia pestis biovar Microtus str. 91001 229193 Gln TTG  
-TGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTGTGATCCGCCA-----TTCCAGGTTTGAATCCTGGTATCCAGCCA  
>tdbD00002430 Acholeplasma laidlawii 2148 Arg TCT  
-GTCCGAATAGCTCAGT--GGAT--AGAGCAATAGCCTTCCGAACTATCG-----GTCGGGGGTTTGAATCCTCTTCGAGCCCA  
>tdbD00009492 Acinetobacter sp. ADPl 62977 Arg ACG  
-GCGCTCATAGCTCAGT--GGAT--AGAGCACTTGGCTACGAACTAAGGG-----GTCGGGAGTTTGAATCCTCTGAGCGCACCA  
>tdbD00009493 Acinetobacter sp. ADPl 62977 Arg CCG  
-GCGCTCGTAGCTCAGT--GGAT--AGAGTACAGTTTCCGAACTGCG-----GTCGTGGGTTTGAATCCTCCGCGAGCGCACCA  
>tdbD00009494 Acinetobacter sp. ADPl 62977 Arg CCT  
-GCGCTCTTAGCTTAACT--GGAT--AGAGCAGTTGCCTCCTAAGCGACCG-----A-CGTGGGTTTGAATCCTCCGAGAGCGCA---  
>tdbD00009495 Acinetobacter sp. ADPl 62977 Arg TCT  
-GCGCTGTAGCTCAGT--GGAT--AGAGCACTCCGCTTCTAAGCGGATG-----GTCACAGGTTTGAATCCTGTGAGCGCGCCA  
>tdbD00002456 Aeromonas hydrophila 644 Arg CCG  
-GCGCCGTAGCTCAGT--GGAT--AGAGCGCTGCCCTCCGAGGCAGAG-----GTCACAGGTTTGAATCCTGTGCGGGCGCACCA  
>tdbD00002441 Agrobacterium tumefaciens 358 Arg CCT  
-GTCCAGTAGCTCAGCA--GGAT--AGAGCACAGATTCCTAATCCTGGG-----GTCGGAGGTTTGAATCCTCTCGTGACACCA  
>tdbD00009014 Agrobacterium tumefaciens str. C58 176299 Arg ACG  
-GCACCCGTAGCTCAGT--GGAT--AGAGCACCAGACTACGAATCTGGGG-----GTCAGGAGTTTGAATCCTCTCGGGTGCGCCA  
>tdbD00009016 Agrobacterium tumefaciens str. C58 176299 Arg CCG  
-GCACCCGTAGCTCAGT--GGAT--AGAGTGTGGATTCCGATTCCAAAG-----GTCACAGGTTTGAATCCTGTGCGGTGCGCCA  
>tdbD00009015 Agrobacterium tumefaciens str. C58 176299 Arg TCT  
-GGCCCTTAGCTCAACT--GGAT--AGAGCAACTGCCTTCTAAGCAGTAG-----GTCGAGGTTTGAATCCTGCAGGGGTGCGCCA  
>tdbD00008947 Aquifex aeolicus VF5 224324 Arg ACG  
-CGGGCTGTAGCTCAACT--GGAT--AGAGCGCGGACTACGGATCCCGAG-----GTTGGGGGTTTGAATCCTCCGCGCCCGGCCA  
>tdbD00008948 Aquifex aeolicus VF5 224324 Arg CCG  
-GTGCCGTAGCTCAGT--GGAT--AGAGCACGGGGCTCCGACCCCGGG-----GTCGGGGGTTTGAATCCTCCGCGGGGCACA---  
>tdbD00008949 Aquifex aeolicus VF5 224324 Arg CCT  
-GTGCCGTAGCTCAGT--GGAT--AGAGCGCGGAGATTCCTAATCTCGAG-----GTCGGGGGTTTGAATCCTCCGCGGGGCACACCA  
>tdbD00008950 Aquifex aeolicus VF5 224324 Arg TCT  
-GGCCCGTAGCTCAGT--GGAT--AGAGCAGGGGATTTCTAATCCCCAG-----GTCGGGGGTTTGAATCCTCCGCGGGCCACCA  
>tdbD00009378 Bacillus anthracis str. Ames 198094 Arg ACG  
-GCGCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAGAG-----GTTAGGGGTTTGAATCCTCTCGGGCGGCCA  
>tdbD00009379 Bacillus anthracis str. Ames 198094 Arg ACG  
-GCGCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAGAG-----GTTAGGGGTTTGAATCCTCTCGGGCGCG---  
>tdbD00009381 Bacillus anthracis str. Ames 198094 Arg CCG  
-GCGCCATAGCTCAGT--GGAT--AGAGCGGTGGTTTCCGGTACCAGT-----CT-----GCCGGGGGTTTGAATCCTCTGGGCGCG---  
>tdbD00009380 Bacillus anthracis str. Ames 198094 Arg TCT  
-GTCCAGTAGCTCAGC--GGAT--AGAGCATAAGCCTTCTAAGCGTACG-----GTCGGGAGTTTGAATCCTCTCTGGGACG---  
>tdbD00009274 Bacillus halodurans C-125 272558 Arg ACG  
-GCGCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAAAG-----GTTAGGGGTTTGAATCCTCTCGGGCGGCCA  
>tdbD00009275 Bacillus halodurans C-125 272558 Arg CCG  
-GCGCCATAGTGAAG--GGAT--ATCACACGAGATTCGGTTCTCGCG-----T-TGTGGGTTTGAATCCTGTAGGCGGCCA  
>tdbD00009276 Bacillus halodurans C-125 272558 Arg TCT  
-GTCCAGTAGCTCAGT--GGAT--AGAGCAACGGCCTTCTAAGCCGTCG-----GTCGGGAGTTTGAATCCTCTCTGGGACGCCA  
>tdbD00008818 Bacillus subtilis subsp. subtilis str. 168 224308 Arg CCG  
-GCGCTGTAGCTCAGT--GGAT--AGAGCGGTGGTTTCCGGTACCACGT-----CT-----GTCGGGGGTTTGAATCCTCCGAGCGCG---  
>tdbD00008819 Bacillus subtilis subsp. subtilis str. 168 224308 Arg CCT  
-GCTCTAGTAGCACAGC--GGAT--AGTGCAGCAGTTTCTAACTGCAG-----GTCGGGAGTTTGAATCCTCTCTAGAGCG---  
>tdbD00008820 Bacillus subtilis subsp. subtilis str. 168 224308 Arg TCT  
-GTCCAGTAGCTCAGT--GGAT--AGAGCAACGGCCTTCTAAGCCGTCG-----GTCGGGAGTTTGAATCCTCTCTGGGACG---  
>tdbD00009369 Bacteroides thetaiotaomicron VPI-5482 226186 Arg ACG  
-GGTCGCTAGCTCAACT--GAAT--AGAGTAGCTGACTACGGATCAGCCG-----GTTACAGGTTTGAATCCTGTGCGGATCACCA  
>tdbD00009370 Bacteroides thetaiotaomicron VPI-5482 226186 Arg ACG  
-GGCCCGTAGCTCAACT--GAAT--AGAGTAGCTGACTACGGATCAGCCG-----GTTACAGGTTTGAATCCTGTGCGGGTCA---  
>tdbD00009371 Bacteroides thetaiotaomicron VPI-5482 226186 Arg ACG  
-GGTCGCTAGCTCAACT--GAAT--AGAGTAGCTGACTACGGATCAGCCG-----GTTACAGGTTTGAATCCTGTGCGGATCA---  
>tdbD00009372 Bacteroides thetaiotaomicron VPI-5482 226186 Arg CCG  
-GGCCCGTAGCTTAGT--GAAT--AGAGCGTCAAGTCCGGTTCTGAAG-----GTCGTGGGTTTGAATCGACCCGGGTCA---  
>tdbD00009373 Bacteroides thetaiotaomicron VPI-5482 226186 Arg CCT  
-GGCCTGTAGTTCAAC--GGAT--AGAATAGAAGTTTCTAACTTAG-----A-TAGGGGTTTGAATCCTCCGCGGGCTA---  
>tdbD00009368 Bacteroides thetaiotaomicron VPI-5482 226186 Arg TCT

-GGTCCGTAGCTCAGCT-GGAT-AGAGCAACGCCCTTCTAAGCCGTGG-----GTCAAGCGTTTCAATCGCTTCGGAATCA---  
>tdbD00009385 Bartonella\_henselae\_str.\_Houston-1\_283166\_Arg\_CCT  
-GTCTGCGTAGCTCAGTA-GGAT-AGAGCACAGGATTCCTAATCCTGGG-----GCCGCAGGTTTCAATCCTGCCGTAGACACCA  
>tdbD00009384 Bartonella\_henselae\_str.\_Houston-1\_283166\_Arg\_TCT  
-GGTCCGTAGCTCAGCT-GGAT-AGAGCAACGCCCTTCTAAGCCGTGG-----GTCACAGGTTTCAATCCTGTCTGGGATCGCCA  
>tdbD00009386 Bdellovibrio\_bacteriovorus\_HD100\_264462\_Arg\_ACG  
-GCACTCGTAGCTCAGCT-GGAT-AGAGTACATGACTACGAATCATGTG-----GTCAGAGGTTTCAATCCTCTCGAGTGCACCA  
>tdbD00009387 Bdellovibrio\_bacteriovorus\_HD100\_264462\_Arg\_TCG  
-GCAGTCGTAGTTCAAT--GGAT-AGAGCACTTGGCTTCGAACCAAGGG-----GTTGCAGGTTTCAATCCTGCCGACTGCACCA  
>tdbD00009388 Bdellovibrio\_bacteriovorus\_HD100\_264462\_Arg\_TCT  
-GGTCCGTAGCTCAGCT-GGAT-AGAGCATCTCCCTTCTAAGGAGAGG-----GTCGTACGTTTCAATCCTGCCGACTGCACCA  
>tdbD00009227 Bifidobacterium\_longum\_NCC2705\_206672\_Arg\_ACG  
-GCGCCAGTAGCCAGC--GGATTAGAGCAGCTGACTACGGATCAGCAG-----GTCGCAGGTTTCAATCCTGTCTGGCGCA---  
>tdbD00009230 Bifidobacterium\_longum\_NCC2705\_206672\_Arg\_CCG  
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>tdbD00009229 Bifidobacterium\_longum\_NCC2705\_206672\_Arg\_CCT  
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-GTGTCATAGCTCAGTT-GGAT-AGAGCGTTAGATTGCGATTCTTAAAG-----GTCGAGGTTTCAATCCTGCCGACTGCACCA  
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-GCATTCATAGCTCAATT-GGAT-AGAGCGGCGACTTCGAATCCGAAG-----GTTGCAGGTTTCAATCCTGCCGACTGCACCA  
>tdbD00002439 Borrelia\_burgdorferi\_139\_Arg\_TCT  
-GCACCAATAGCTCAATT-GGAT-AGAGCAACAGACTTCTAATCTGTAG-----GTTTTAGGTTTCAATCCTGCCGACTGCACCA  
>tdbD00009421 Borrelia\_garinii\_PBi\_290434\_Arg\_TCG  
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>tdbD00009279 Bradyrhizobium\_japonicum\_USDA\_110\_224911\_Arg\_TCT  
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>tdbD00008901 Campylobacter\_jejuni\_subsp.\_jejuni\_NCTC\_11168\_192222\_Arg\_CCT  
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>tdbD00008902 Campylobacter\_jejuni\_subsp.\_jejuni\_NCTC\_11168\_192222\_Arg\_GCG  
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>tdbD00008903 Campylobacter\_jejuni\_subsp.\_jejuni\_NCTC\_11168\_192222\_Arg\_TCG  
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>tdbD00008904 Campylobacter\_jejuni\_subsp.\_jejuni\_NCTC\_11168\_192222\_Arg\_TCT  
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>tdbD00009505 Candidatus\_Blochmannia\_floridanus\_203907\_Arg\_ACG  
-GCACCCGTAGCTCAGTT-GGAT-AGAGCACTCGGCTACGAACCGAGAG-----GTCGGGGTTTCAATCCTGCCGACTGCACCA  
>tdbD00009506 Candidatus\_Blochmannia\_floridanus\_203907\_Arg\_CCG  
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>tdbD00009507 Candidatus\_Blochmannia\_floridanus\_203907\_Arg\_CCT  
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>tdbD00009508 Candidatus\_Blochmannia\_floridanus\_203907\_Arg\_TCT  
-GCGCTCTTAAGTCAATA-GGAT-AGAGTAAACGGCCTTCTAAGCCGTAA-----GTTATAGGTTTCGAATCCTATAGAGCGCA---  
>tdbD00009399 Candidatus\_Protochlamydia\_amoebophila\_UWE25\_264201\_Arg\_ACG  
-GCACCTGGTAGCTCAATT--GGAT-AGAGTACCCGGCTACGAACCGGGCG-----GTTAGAGGTTTCGAATCCTCTCCGGTGCA---  
>tdbD00009400 Candidatus\_Protochlamydia\_amoebophila\_UWE25\_264201\_Arg\_CCT  
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>tdbD00008907 Caulobacter\_crescentus\_CB15\_190650\_Arg\_CCT  
-GGCCCGTAGCTCAGT--GGAT-AGAGCAGCGCTTTCCTAAGCGAAG-----GTCGGGGGTTTCGAGTCCCTCCCGGGCCCA  
>tdbD00008908 Caulobacter\_crescentus\_CB15\_190650\_Arg\_TCT  
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>tdbD00008965 Chlamydia\_muridarum\_Nigg\_243161\_Arg\_ACG  
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>tdbD00008964 Chlamydia\_muridarum\_Nigg\_243161\_Arg\_TCG  
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>tdbD00008810 Chlamydia\_trachomatis\_D/UW-3/CX\_272561\_Arg\_ACG  
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>tdbD00008802 Chlamydia\_pneumoniae\_AR39\_115711\_Arg\_ACG  
-GCACCGATAGCTCAAT--GGAT-AGAGTACCTGGCTACGAACCGAGTG-----GTCAGAGGTTTCGAGTCCCTCTCTGGTGCG---  
>tdbD00008803 Chlamydia\_pneumoniae\_AR39\_115711\_Arg\_CCT  
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>tdbD00008804 Chlamydia\_pneumoniae\_AR39\_115711\_Arg\_TCG  
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>tdbD00008805 Chlamydia\_pneumoniae\_AR39\_115711\_Arg\_TCT  
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>tdbD00009159 Chlorobium\_tepidum\_TLS\_194439\_Arg\_ACG  
-GCACCGTAGCTCAACT--GGAT-AGAGCATTTCGACTACGGATCAGAAG-----GTTAGGGGTTTCGAATCCTCTCGGGTGTACCA  
>tdbD00009161 Chlorobium\_tepidum\_TLS\_194439\_Arg\_CCG  
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>tdbD00009162 Chlorobium\_tepidum\_TLS\_194439\_Arg\_CCT  
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-GCGATAGTACCTCAACT--GGAT-AGAGGACTCGGCTACGAACCGAGGC-----GCTGGGGGTTTCGACTCCTGCCTGTCCACCA  
>tdbD00008976 Clostridium\_acetobutylicum\_ATCC\_824\_272562\_Arg\_CCT  
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>tdbD00008977 Clostridium\_acetobutylicum\_ATCC\_824\_272562\_Arg\_TCG  
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>tdbD00008959 Clostridium\_perfringens\_str.\_13\_195102\_Arg\_ACG  
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>tdbD00008960 Clostridium\_perfringens\_str.\_13\_195102\_Arg\_CCT  
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>tdbD00008961 Clostridium\_perfringens\_str.\_13\_195102\_Arg\_TCG  
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>tdbD00009283 Clostridium\_tetani\_E88\_212717\_Arg\_ACG  
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>tdbD00009469 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882 Arg CCG  
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>tdbD00009467 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882 Arg CCT  
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>tdbD00009468 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882 Arg TCT  
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>tdbD00009342 Escherichia\_coli\_CFT073 199310 Arg TCT  
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-GCGCTGTAGCTCAGCT-GGAT-AGAGCAACGGACTTCTAATCCGTAG-----GTCAGAGTTTCAATCCTCTCAGGGGTGCCA  
>tdbD00002460 *Haemophilus influenzae* 727 Arg ACG  
CGCACCCTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCAAAGTTTCAATCCTTTTCGGGTGCGCCA  
>tdbD00002461 *Haemophilus influenzae* 727 Arg ACG  
-GCACCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCAGAGTTTCAATCCTCTCGGGTGCGCCA  
>tdbD00002462 *Haemophilus influenzae* 727 Arg ACG  
-GCACCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCAGAGTTTCAATCCTCTCGGGTGCGCCA  
>tdbD00002458 *Haemophilus influenzae* 727 Arg CCG  
-GCGTTCGTAGCTCAGTT-GGAT-AGAGCGTTGGCCTCCGGAGCCAAAG-----GTCGCAAGTTTCAATCTTGTTCGAGCGCGCCA  
>tdbD00002459 *Haemophilus influenzae* 727 Arg TCT  
-GCGCCCTTAGCTCAGCT-GGAT-AGAGCAACGCCCTTCTAAGCGTGG-----GTCAAAGTTTCAATCCTTTAGGGCGTGCCA  
>tdbD00008894 *Haemophilus influenzae* Rd KW20 71421 Arg ACG  
-GCACCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCAAAGTTTCAATCCTTTTCGGGTGCGCCA  
>tdbD00009317 *Helicobacter hepaticus* ATCC 51449 235279 Arg CCT  
-GTCCTCGTAGCTCAGCT-GGAT-AGAGCACACGATTCCTAATCGTGAG-----GTCATGCGTTTCAATCGCATCGGGGACACCA  
>tdbD00009318 *Helicobacter hepaticus* ATCC 51449 235279 Arg GCG  
-GTGCTCGTAGCTCAGCT-GAAT-AGAGCAACAGGTTGCGGTCTGTAG-----GTCGGGGTTTGAATCCCTCCGAGCACGCCA  
>tdbD00009315 *Helicobacter hepaticus* ATCC 51449 235279 Arg TCG  
-GCGTTCGTAGCTCAATT-GGAT-AGAGCACCAGACTTCGGATCTGGGG-----GTTAGGGTTTCAATCCTCTCGGGCGTGCCA  
>tdbD00009316 *Helicobacter hepaticus* ATCC 51449 235279 Arg TCT  
-GCGCTCATAGCTCAGCT-GGAT-AGAGCAACGGCCTTCTAAGCCGTAG-----GTCAGAGTTTCAATCCTCTTGGGCGTACCA  
>tdbD00002447 *Helicobacter pylori* 210 Arg CCT  
-GTCCTGTAGCTCAGCT-GGAT-AGAGCGTATGATTCCTAATCGTAAG-----GTCGTTGGTTTCAATCCCGCAAGGACACCA  
>tdbD00002448 *Helicobacter pylori* 210 Arg CCG  
-GTGCTCGTAGCTCAGCT-GAAT-AGAGCAACAGGTTGCGGTCTGTAG-----GTCGGGGTTTGAATCCCTCCGAGCACACCA  
>tdbD00002445 *Helicobacter pylori* 210 Arg TCG  
-GCGTTCGTAGCTCAATT-GGAT-AGAGCACCAGACTTCGGATCTGGGG-----GTTAGGGTTTCAATCCTCTCGGGCGTACCA  
>tdbD00002446 *Helicobacter pylori* 210 Arg TCT  
-GCGCTGTAGCTCAGCT-GGAT-AGAGCAACAGCCTTCTAAGCCGTAG-----GTCGAGGTTTCAATCCTCTGCAAGCGCACCA  
>tdbD00002443 *Lactobacillus delbrueckii* subsp. *bulgaricus* 1585 Arg ACG  
-GCACCCATAGCGCAACT-GGAT-AGAGTGTCTGACTACGAATCAGAAG-----GTTGTAGTTTCAAGTCTACTGGGTGCA---  
>tdbD00009429 *Lactobacillus johnsonii* NCC 533 257314 Arg ACG  
-GCACCCCTAGCGCAACT-GGAT-AGAGTGTCTGACTACGAATCAGAAG-----GTTGAAGTTTCAATCCTTTCAGGGTGCA---  
>tdbD00009427 *Lactobacillus johnsonii* NCC 533 257314 Arg CCT  
-GACCCCGTAGTTCATCT-GGAT-AGAACAATGGTCTCCTAACCCTAG-----A-GGTGAGTTTCAATCTCACCGGGGTCA---  
>tdbD00009428 *Lactobacillus johnsonii* NCC 533 257314 Arg TCT  
-GGTTTGTAGCTCAGCT-GGAT-AGAGCAACGGTCTTCTAACCCTAG-----GTCGTTGAGTTTCAATCTCACCCAAATCA---  
>tdbD00009292 *Lactobacillus plantarum* WCFS1 220668 Arg ACG  
-GCACCCATAGCGCAACT-GGAT-AGAGTGTCTGACTACGAATCAGAAG-----GTTGTAGTTTCAAGTCTACTGGGTGCA---  
>tdbD00009291 *Lactobacillus plantarum* WCFS1 220668 Arg CCG  
-GCGCCCGTGGTGAAT--GGAT-AGCAGGTAAGATTCCGGTCTTGTAG-----A-TGGGGTTTCAATCCTTCCGGGCGCA---  
>tdbD00009293 *Lactobacillus plantarum* WCFS1 220668 Arg CCT  
-GGCCTCATAGCACAAC--GGAT-AGGCGACCCGCTCCTAAGCGGTTG-----A-TCCCGTTTCAAGTCCGGGTGAGGTCA---  
>tdbD00009294 *Lactobacillus plantarum* WCFS1 220668 Arg TCT  
-GTCACGGTAGCTCAACT-GGAT-AGAGCATCCGCTTCTAAGCGGAGG-----GTTGTGAGTTTCAAGTCTCACTCGTGACA---  
>tdbD00009430 *Leifsonia xyli* subsp. *xyli* str. CTB07 281090 Arg ACG  
-GCGCCACTAGCTCAAC--GGAT-AGAGCATCTGACTACGGATCAGAAG-----GTTGGGGTTTCAATCCTCTGGGCGCA---  
>tdbD00009431 *Leifsonia xyli* subsp. *xyli* str. CTB07 281090 Arg CCG  
-GCCCCATAGCTCAGG--GGAT-AGAGCGTCTGCCTCCGGAGCAGAAG-----GCCGTAGTTTCAATCCTACTGGGGGCA---  
>tdbD00009433 *Leifsonia xyli* subsp. *xyli* str. CTB07 281090 Arg CCT  
-GCCTCTGTAGCTCAGT--GGA--AGAGCGAGTGCCTCCTAAGCACCAG-----GTCGGGGTTTCAATCCTTCCAGGGGCA---  
>tdbD00009432 *Leifsonia xyli* subsp. *xyli* str. CTB07 281090 Arg TCT  
-GCCCTATAGCTCAAT--GGAT-AGAGCAACGGCCTTCTAATCCGTAG-----GTTGCAGTTTCAAGTCTCTGGGGGCA---  
>tdbD00009240 *Leptospira interrogans* serovar *Lai* str. 56601 189518 Arg ACG  
-GCGCCATAGCTCAGCT-GGAT-AGAGCGTCTGACTACGGATCAGAAG-----GTCGGAGTTTCAAGTCTCTGGGCGGCCA  
>tdbD00009242 *Leptospira interrogans* serovar *Lai* str. 56601 189518 Arg CCG  
-GTACCTATAGCTCAAC--GGAT-AGAGTACAGGCTCCGGAGCCTGTG-----G-TCCGGTTTCAAGTCCCGGTAGGTACA---  
>tdbD00009239 *Leptospira interrogans* serovar *Lai* str. 56601 189518 Arg CCT  
-GCTCCCGTAGCTCAGGT-GGAC-AGAGCAGAAGTTTCTAACAATTTTG-----GTCGGAGTTTCAATCCTCTCGGGGCA---  
>tdbD00009241 *Leptospira interrogans* serovar *Lai* str. 56601 189518 Arg TCT  
-GACTCGGTAGCTCAGTT-GGAT-AGAGCAACTGCCTTCTAAGCAGTGG-----GTCGGGGTTTCAATCCTCTCGGGTACCA  
>tdbD00008951 *Listeria innocua* Clip11262 272626 Arg ACG  
-GCGCCATAGCTCAACT-GGAT-AGAGTACTGACTACGAATCAAGCG-----GTTAGAGTTTCAAGTCTCTTGGGCGCA---  
>tdbD00008954 *Listeria innocua* Clip11262 272626 Arg CCG  
-GCCCTCGTGGTGCAAC--GGAT-AGCAGGTAAGATTCCGGTCTTAAA-----A-TGGGGTTTCAATCCTTCCGAGGGCA---  
>tdbD00008953 *Listeria innocua* Clip11262 272626 Arg CCT

-GCCCATATAGTTAAAC--GGAT-ATAACAAGCCCCTCCTAAGGGCTAG-----T-TCGTGGTTCGATTCGCGTATGGGCG---  
>tdbD00008952 *Listeria\_innocua*\_Clip11262\_272626 Arg TCT  
-GTCCTGATAGCTCAGCT-GGAT-AGAGCAACGGCCTTCTAAGCCGTCG-----GTCGGGGGTTTCAATCCCTCTCAGGACG---  
>tdbD00009474 *Mesoplasma\_florum*\_L1\_265311 Arg ACG  
-GCGCCCGTAGATCAATT-GGAT-AGATCGTTTACTACGGATCAAAAAG-----GTTGGGGGTTTCGAGTCCCTCCGGGCGCACCA  
>tdbD00009475 *Mesoplasma\_florum*\_L1\_265311 Arg TCT  
-GCCCATGTAGCTCAGTT-GGAT-AGAGCACGCGCCTTCTAAGCGTGAG-----GTCGGAAGTTCGAGCCTTCTCGTGGGCACCA  
>tdbD00008987 *Mesorhizobium\_loti*\_MAFF303099\_266835 Arg ACG  
-GCGCCCGTAGCTCAGCT-GGAT-AGAGCACCAGACTACGAATCTGGGG-----GTCAGGAGTTCGAATCTCTTCGGGCGGCCA  
>tdbD00008988 *Mesorhizobium\_loti*\_MAFF303099\_266835 Arg CCG  
-GCACCCGTAGCTCAGCT-GGAT-AGAGCGCTGCCCTCCGAAGGCAGAG-----GTCACAGGTTTCAATCCTGTCCGGTGCGCCA  
>tdbD00008986 *Mesorhizobium\_loti*\_MAFF303099\_266835 Arg CCT  
-GGTCCCGTAGCTCAGTA-GGAT-AGAGCGGCAGATTCTAATCTGTAG-----GTCACAGGTTTCGATTCTGTCCGGATCACCA  
>tdbD00008989 *Mesorhizobium\_loti*\_MAFF303099\_266835 Arg TCT  
-GGTCCCGTAGCTCAGCT-GGAT-AGAGCACCGGCCTTCTAAGCCGATG-----GTCACAGGTTTCAATCCTGTCCGGATGCGCCA  
>tdbD00009322 *Mycobacterium\_bovis*\_AF2122/97\_233413 Arg ACG  
-GCGCCCGTAGCTCAAC--GGAT-AGAGCATCTGACTACGGATCAGAAG-----GTTGGGAGTTCGAATCTCTTCGGGCGCG---  
>tdbD00009320 *Mycobacterium\_bovis*\_AF2122/97\_233413 Arg CCG  
-GCCCCCGTAGCTCAGG--GGAT-AGAGCGTCTGCCCTCCGGAGCAGAAG-----GCCCGAGGTTTCAATCCTGCCGGGGGCA---  
>tdbD00009319 *Mycobacterium\_bovis*\_AF2122/97\_233413 Arg CCT  
-GCCCTCGTAGCTCAGG--GGAT-AGAGCAGGGCTCTCCTAAAGCCGGT-----GTCGAGGTTTCAATCCTGCCGGGGGCA---  
>tdbD00009321 *Mycobacterium\_bovis*\_AF2122/97\_233413 Arg TCT  
-GCCTCCGTAGCTCAGGT-GGAT-AGAGCAAGGGCCTTCTAATCCCTAG-----GTCGCACGTTTCGAGTCGTGCCGGGGGCA---  
>tdbD00008845 *Mycobacterium\_leprae*\_TN\_272631 Arg ACG  
-GCGCCCGTAGCTCAAC--GGAT-AGAGCATCTGACTACGGATCAGAAG-----GTTAGGGGTTTCAATCCCTTCGGGCGCG---  
>tdbD00008846 *Mycobacterium\_leprae*\_TN\_272631 Arg CCG  
-GCCCCCGTAGCTCAGG--GGAT-AGAGCATCTGCCCTCCGGAGCAGAAG-----GTCGAGGTTTCAATCCTGCCGGGGGCA---  
>tdbD00008847 *Mycobacterium\_leprae*\_TN\_272631 Arg CCT  
-GCCCTCGTAGCTCAGG--GGAT-AGAGCAGGGCTCTCCTAAAGCCGGT-----GTCACAGGTTTCAATCCTGTCCGGGGGCA---  
>tdbD00002419 *Mycoplasma\_capricolum*\_2095 Arg ACG  
-GCGCCCGTAGATCAATT-GGAT-AGATCGCTTACTACGGATCAAAAAG-----GTTGGGGGTTTCGAGTCCCTCCGGGCGCACCA  
>tdbD00002420 *Mycoplasma\_capricolum*\_2095 Arg TCT  
-GCCCATGTAGCTCAGTA-GGAT-AGAGCACGCGCCTTCTAAGCGTGAG-----GTCGGAAGTTCGAGCCTTCTCGTGGGCACCA  
>tdbD00009311 *Mycoplasma\_gallisepticum*\_R\_233150 Arg GCG  
-GTCGGCATAGCTCAACT-GGAT-AGAGAATCAGTTTTCGGAACTGAAG-----GTTACAGGTTTCAAGTCTGTGTGTCGACGCCA  
>tdbD00009312 *Mycoplasma\_gallisepticum*\_R\_233150 Arg GCG  
-GTCGGCATAGCTCAACT-GGAT-AGAGCATCAGTTTTCGGAACTGAAG-----GTTACAGGTTTCAAGTCTGTGTGTCGACGCCA  
>tdbD00009314 *Mycoplasma\_gallisepticum*\_R\_233150 Arg TCG  
-GCGCCCATAGTTCAATT-GGAT-AGAACATCTGACTTTCGGATCAGACG-----GTTATAGGTTTCAAGTCTTATGGGCGCGCCA  
>tdbD00009313 *Mycoplasma\_gallisepticum*\_R\_233150 Arg TCT  
-GCGCCCGTAGCTCAGTT-GGAT-AGAGCACATGCCTTCTAAGCCTGTT-----GTCAGGGGTTTCAATCCCTTTCGGGCGGCCA  
>tdbD00002423 *Mycoplasma\_genitalium*\_2097 Arg CCT  
-CTTCCCTTGGTGCAAT--GGAC-AGCACAACTGAGTCCCTAATCAGTAA-----A-TAGAGGTTTCAACTCCTCTAGGGAAGGCCA  
>tdbD00002422 *Mycoplasma\_genitalium*\_2097 Arg GCG  
-GTCATCATAGCTCAATA-GGAC-AGAGTATCAGCTTTCGGGAGCTGAGG-----GTTACAGGTTTCAAGTCTGTGTGTCGACGCCA  
>tdbD00002424 *Mycoplasma\_genitalium*\_2097 Arg TCG  
-GCGCCCATAGCTCAATC-GGAT-AGAGTGTCTGGCTTCGGACCAAGAA-----GTTATGGGTTTCAAGTCTTATGGGCGCGCCA  
>tdbD00002421 *Mycoplasma\_genitalium*\_2097 Arg TCT  
-TCAGTGGTAGCTCAGT--GGAT-AGAGTACAGCCTTCTAAGCGTGTT-----GTCGTGGGTTTCAATCCCTCCCATGCGGCCA  
>tdbD00008916 *Mycoplasma\_genitalium*\_G37\_243273 Arg TCT  
-GCGTCCGTAGCTCAGT--GGAT-AGAGTACAGCCTTCTAAGCGTGTT-----GTCGTGGGTTTCAATCCCTCCCATGCGGCCA  
>tdbD00002428 *Mycoplasma\_pneumoniae*\_2104 Arg TCG  
-GCGCCCATAGCTCAATT-GGAT-AGAGTGTCTGGCTTCGGACCAAGAA-----GTTATGGGTTTCAAGTCTTATGGGCGCGCCA  
>tdbD00008917 *Mycoplasma\_pneumoniae*\_M129\_272634 Arg CCT  
-CTTCCCTTGGTGTAAT--GGAT-AACACGACTGAGTCCCTAATCAGTAA-----A-TGGAGGTTTCAAGTCTCTAGGGAAGGCCA  
>tdbD00008920 *Mycoplasma\_pneumoniae*\_M129\_272634 Arg TCT  
-GCGTCCGTAGCTCAGC--GGAT-AGAGTACAGCCTTCTAAGTGTGTT-----GTCGTGGGTTTCAAGTCCCACCCGATGCGGCCA  
>tdbD00009011 *Mycoplasma\_pulmonis*\_UAB\_CTIP\_272635 Arg GCG  
-GCACTCATAGCTCAACT-GGAT-AGAGTACTAGGTTGCGGTCTTAGAG-----GTTAGGGGTTTCAAGTCTCTTAGTGCGCCA  
>tdbD00009012 *Mycoplasma\_pulmonis*\_UAB\_CTIP\_272635 Arg TCG  
-GCGTTAGTAGCTCAACT-GGAT-AGAGTACTTGGTTTCGGCCCAAGAG-----GTTAGGGGTTTCAAGTCTCTTAGCAGGCCA  
>tdbD00009013 *Mycoplasma\_pulmonis*\_UAB\_CTIP\_272635 Arg TCT  
-GGTCCGTAGCTCAGAT-GGAC-AGAGCACGAGCCTTCTAAGCTTGTG-----GTCAGAGGTTTCAATCCTCTCGTGATCGGCCA  
>tdbD00008828 *Neisseria\_meningitidis*\_MC58\_122586 Arg ACG  
-GCACCCGTAGCTCAGTT-GGAT-AGAGTATCTGGCTACGAACCAGAGG-----GTCGGGCGTTTCAATCGCTCCGGGTGCGGCCA  
>tdbD00008830 *Neisseria\_meningitidis*\_MC58\_122586 Arg CCG  
-GCACCCATAGCTCAGTT-GGA--AGAGTGTAGTTTCCGAAGCTGGAG-----GTCACAGGTTTCAATCCTGTGGGTGCGGCCA  
>tdbD00008831 *Neisseria\_meningitidis*\_MC58\_122586 Arg CCT  
-CTCGCCATAGTTCAAC--GGAT-AGAACGTATGCCCTAAGCGTAAA-----A-TACAGGTTTCAAGTCTGTGGCGAGG---  
>tdbD00008832 *Neisseria\_meningitidis*\_MC58\_122586 Arg TCT  
-GCGCCCGTAGCTCAACC-GGAT-AGAGCACCGACCTTCTAAGTCCGGG-----GTTACAGGTTTCAAGTCTGTCCGGGCGGCCA  
>tdbD00009365 *Nitrosomonas\_europaea*\_ATCC\_19718\_228410 Arg ACG  
-GCGCCCGTAGCTCAGTT-GGAT-AGAGTACTTGGCTACGAACCAAGGG-----GTCGTGGGTTTCAATCCTGCCGGGCGCGGCCA  
>tdbD00009367 *Nitrosomonas\_europaea*\_ATCC\_19718\_228410 Arg CCG  
-GCGCCCATAGCTCAGT--GGAT-AGAGTACTGCCCTCCGAAGGCAGG-----GTCACACGTTTCAATCGTGTGGGCGCGGCCA

>tdbD00009364 Nitrosomonas\_europaea\_ATCC\_19718\_228410\_Arg\_CCT  
-GCCCTGGTAGCTCAGG--GGAT-AGAGCGACCCCCCTCTAAGGGGTAG-----GTCGGACGTTTCGATTCTGCTCCAGGGCGCCA  
>tdbD00009366 Nitrosomonas\_europaea\_ATCC\_19718\_228410\_Arg\_TCT  
-GTGCCGTAGCTCAACC-GGAT-AGAGCACCAGCCTTCTAAGCTGGGG-----GTTACAGGTTTCGATTCTGTGCGGGCAGGCCA  
>tdbD00009006 Nostoc\_sp.\_PCC\_7120\_103690\_Arg\_ACG  
-GAGAACGTGGTGTAACT--GGAT-TGCATCTCAGATTACGAACCTGAAG-----GTTGGGGGTTCAAGTCCCTCCGTTCTCG---  
>tdbD00009010 Nostoc\_sp.\_PCC\_7120\_103690\_Arg\_ACG  
-GGGCGGTAGCTCAGT--GGACTAGAGCAGCTGGCTACGGACCACGGT-----GTCGGGGGTTCAAGTCCCTCCTCGCCCG---  
>tdbD00009009 Nostoc\_sp.\_PCC\_7120\_103690\_Arg\_CCG  
-GGGCGGTAGCTCAGT--GGAT-AGAGCAACAGATTCCGGTCTGTGG-----GTCGGGGGTTCAATCCCTCCGCGCTCG---  
>tdbD00009007 Nostoc\_sp.\_PCC\_7120\_103690\_Arg\_CCT  
-GGGCGGTAGCTCAGT--GGAT-AGAGCAGCGCCTTCTAAGCGCTAG-----GTCGTCGTTCAAGTCCGACCAGTCCCG---  
>tdbD00009005 Nostoc\_sp.\_PCC\_7120\_103690\_Arg\_TCT  
-GGAGTGTGCGCTAAT--GGA--TGGGCATCGATCTCTAATCGAAT-----TGTTAGGGGTTCAAGTCCCTTCACTCCTG---  
>tdbD00009008 Nostoc\_sp.\_PCC\_7120\_103690\_Arg\_TCT  
-GGGCGGTAGCTCAGT--GGAT-AGAGCCACGGATTCTAATCCGTTG-----GTCGCGAGTTTCGAACCTGCGCGCTCG---  
>tdbD00009246 Oceanobacillus\_ihayensis\_HTE831\_221109\_Arg\_ACG  
-GGCCTGTAGCTCAATT--GGAT-AGAGCGTTTACTACGATCCGATCCAGAG-----GTTAGGGGTTTCGACTCCTCTCAGGGCGGCCA  
>tdbD00009244 Oceanobacillus\_ihayensis\_HTE831\_221109\_Arg\_CCG  
-GCGCCGTAGCTCAGT--GGAT-AGAGCAGCGCCTTCTAAGCGCTAG-----TT-----GCCGGGGGTTTCGAATCCCTCCGGCGCG---  
>tdbD00009245 Oceanobacillus\_ihayensis\_HTE831\_221109\_Arg\_CCT  
-GCCCTGTAGCTCAGG--GGAT-AGAGCATCGGTTTCTAATCGAAT-----GTCGCGAGTTTCGAATCCTGCGGGGGCG---  
>tdbD00009243 Oceanobacillus\_ihayensis\_HTE831\_221109\_Arg\_TCT  
-GTCCAGTAGCTCAGT--GGAT-AGAGCAACAGCCTTCTAAGCTGTGG-----GTCGCGAGTTTCGAATCCTGCGCTGGGACG---  
>tdbD00009394 Onion\_yellow\_phytoplasma\_OY-M\_262768\_Arg\_ACG  
-GACCCATAGCTCAATT--GGAT-AGAGCATCTGACTACGGAACGAG-----GCTAGGGGTTTCGAATCCTTCTGGGTGTGCCA  
>tdbD00009393 Onion\_yellow\_phytoplasma\_OY-M\_262768\_Arg\_TCT  
-GTTTGTAGTAGCTCAGT--GGAT-AGAGCAACGGCCTTCTAAGCGCTCG-----GTCGGGGGTTTCGAATCCCTTCTCAAACGCCA  
>tdbD00008922 Pasteurella\_multocida\_subsp.\_multocida\_str.\_Pm70\_272843\_Arg\_CCG  
-GCGCTGTAGCTCAGT--GGAT-AGAGCGTTGGCCTCCGGAGCCAAAG-----GTCGCGAGTTTCGAATCCTGTCGAGCGGCCA  
>tdbD00008923 Pasteurella\_multocida\_subsp.\_multocida\_str.\_Pm70\_272843\_Arg\_TCT  
-GCGCCCTTAGCTCAGT--GGAT-AGAGCAACGGCCTTCTAAGCGCTAG-----GTCATGTTTCGAATCCCAATAGGGCGTGCCA  
>tdbD00009403 Photorhabdus\_luminescens\_subsp.\_laumondii\_TTO1\_243265\_Arg\_ACG  
-GTCCATAGCTCAGT--GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAGTTTCGAATCCTTCTGGATGCGCCA  
>tdbD00009404 Photorhabdus\_luminescens\_subsp.\_laumondii\_TTO1\_243265\_Arg\_CCT  
-GTCCCTTAGTTAAAT--GGAT-ATAACAAGCCCTCCTAAGGGCTAA-----T-TGTTGGTTTCGATTCCAGCAGGGGACGCCA  
>tdbD00009405 Photorhabdus\_luminescens\_subsp.\_laumondii\_TTO1\_243265\_Arg\_TCT  
-GCGCCCTTAGCTCAGT--GGAT-AGAGCAACGGCCTTCTAAGCGCTAG-----GTCACAGTTTCGAATCCTGTAGGGCGCA---  
>tdbD00009436 Porphyromonas\_gingivalis\_W83\_242619\_Arg\_CCT  
-GGCTCTGTAGTTCAAT--GGAT-AGAATAGTGGTTTCTAACCATAG-----A-TTCGGGTTTCGATTCCCGACGGAGCTACCA  
>tdbD00009437 Porphyromonas\_gingivalis\_W83\_242619\_Arg\_TCT  
-GGTCAGTAGCTCAGT--GGAT-AGAGCAATAGCCTTCTAAGCTATCG-----GTCCTGGGTTTCGAATCCAGCCTGATCA---  
>tdbD00009479 Propionibacterium\_acnes\_KP171202\_267747\_Arg\_ACG  
-GCGCCGTGGCTCAAC--GGAT-AGAGCATCTGACTACGGATCAGAAG-----GTTGGGGGTTTCGAATCCCTCCGGCGCG---  
>tdbD00009477 Propionibacterium\_acnes\_KP171202\_267747\_Arg\_CCG  
-GTCCTCGTAGCTCAGG--GGAT-AGAGCACCGCCTCCGGAGCGGGA-----G-CGAGGGTTTCGAATCCCTCCGGGAGCG---  
>tdbD00009476 Propionibacterium\_acnes\_KP171202\_267747\_Arg\_CCT  
-GGCCCGTAGCTCAGG--GGAT-AGAGCAGTGGTTTCTAACCATGT-----GTCGTAGTTTCGAATCCTATCGGGGCG---  
>tdbD00009478 Propionibacterium\_acnes\_KP171202\_267747\_Arg\_TCT  
-GGCCCGTAGCTCAGC--GGAT-AGAGCAGCAGCCTTCTAATCTGTGC-----CGCGTGGGTTTCGATTCCACCCGGGCCA  
>tdbD00008930 Pseudomonas\_aeruginosa\_PA01\_208964\_Arg\_ACG  
-GCACTCATAGCTCAGT--GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAGTTTCGAATCCTCCTGAGTGCGCCA  
>tdbD00008931 Pseudomonas\_aeruginosa\_PA01\_208964\_Arg\_CCG  
-GCATCCGTAGCTCAGT--GGAT-AGAGTACTGCCCTCCGAAGGCAGGG-----GTCGTGGGTTTCGAATCCCGCCGGATGCGCCA  
>tdbD00008932 Pseudomonas\_aeruginosa\_PA01\_208964\_Arg\_CCT  
-GTCCCGTAGCTCAATT--GGAT-AGAGCATCCCCCTCCTAAGGGGAAG-----GTTGGAGTTTCGACCCCTCCTCCGGGACGCCA  
>tdbD00008933 Pseudomonas\_aeruginosa\_PA01\_208964\_Arg\_TCT  
-GCGCCGTAGCTCAGT--GGAT-AGAGCATCCGCTTCTAAGCGGATG-----GTCGCGAGTTTCGAGTCTGCGGGTGCGCCA  
>tdbD00009375 Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283\_Arg\_ACG  
-GCACTCGTAGCTCAGT--GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCACAGTTTCGAATCCTGTGAGTGCACCA  
>tdbD00009374 Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283\_Arg\_CCG  
-GCACCAGTAGCTCAGT--GGAT-AGAGTACTGCCCTCCGAAGGCAGGG-----GTCGTGGGTTTCGAATCCCGCCTGGTGCACCA  
>tdbD00009376 Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283\_Arg\_CCT  
-GTCTCAGTAGCTCAATT--GGAT-AGAGCATCCCCCTCCTAAGGGGAAG-----GTTGCAGTTTCGAACCCCGCCTGGGACACCA  
>tdbD00009377 Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283\_Arg\_TCT  
-GTCCCGTAGCTCAGT--GGAT-AGAGCATCCGCTTCTAAGCGGATG-----GTCGCGAGTTTCGAGTCTGCGGGTGCGCCA  
>tdbD00009003 Ralstonia\_solanacearum\_GMI1000\_267608\_Arg\_ACG  
-GCGGCTGTAGCTCAGT--GGAT-AGAGTACTTGGCTACGAACCAAGGG-----GTCGTGGGTTTCGAATCCTGCCAGCCGCGCCA  
>tdbD00009004 Ralstonia\_solanacearum\_GMI1000\_267608\_Arg\_CCG  
-GCGCCGTAGCTCAAT--GGAT-AGAGTACTGCCCTCCGAAGGCAGGG-----GTTGCTGGTTTCGATCCAGCCGGGCGCGCCA  
>tdbD00009001 Ralstonia\_solanacearum\_GMI1000\_267608\_Arg\_CCT  
-CTCGCGTAGCACAAAT--GGAT-AGTGCACCGCCTCCTAAGCGTGAG-----A-TACAGTTTCGATTCTGTGCGGGGACCA  
>tdbD00009002 Ralstonia\_solanacearum\_GMI1000\_267608\_Arg\_TCT  
-CTGCCATAGCTCAGT--GGAT-AGAGCATCGGCTTCTAAGCGGACG-----GTCGGGGGTTTCGAATCCCTCCTGGCAGGCCA  
>tdbD00009358 Rhodopirellula\_baltica\_SH\_1\_243090\_Arg\_ACG

-GCACCCCTAGCTCAATT-GGAT-AGAGCATCGGTCTACGAAACCGAAG-----GTTACTGGTTCGAATCCAGTGGGGTGTA---  
>tdbD00009361 Rhodopirellula\_baltica\_SH\_1\_243090 Arg CCG  
-GCACCCGTGGCACAATT-GGAT-AGCGCGTCGGCCTCCGAAGCCGAAG-----GTTGTGGGTTTCGAACCCCGCCGGGTGTA---  
>tdbD00009360 Rhodopirellula\_baltica\_SH\_1\_243090 Arg CCT  
-GCCCTCGTAGCTCAGCT-GGAT-AGAGCAGCGCATTCCTAACCGCGCAG-----GTCACAGGTTTCGAATCCTGTTCGGGGGTA---  
>tdbD00009359 Rhodopirellula\_baltica\_SH\_1\_243090 Arg TCG  
-GCATCCGTAGCTCAATT-GGAT-AGAGCATCGGTCTTCGGAACCGAGG-----GTTGGGGGTTTCGAATCCCTCCGGGTGTA---  
>tdbD00009357 Rhodopirellula\_baltica\_SH\_1\_243090 Arg TCT  
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>tdbD00009363 Rhodopirellula\_baltica\_SH\_1\_243090 Arg TCT  
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>tdbD00009408 Rhodopseudomonas\_palustris\_CGA009\_258594 Arg ACG  
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>tdbD00009410 Rhodopseudomonas\_palustris\_CGA009\_258594 Arg TCT  
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>tdbD00008980 Rickettsia\_conorii\_str\_Malish\_7\_272944 Arg ACG  
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>tdbD00008979 Rickettsia\_conorii\_str\_Malish\_7\_272944 Arg CCG  
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>tdbD00008981 Rickettsia\_conorii\_str\_Malish\_7\_272944 Arg TCT  
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>tdbD00009176 Rickettsia\_prowazekii\_str\_Madrid\_E\_272947 Arg CCG  
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>tdbD00009023 Salmonella\_enterica\_subsp\_enterica\_serovar\_Typhi\_str\_CT18\_220341 Arg CCG  
-GCGCCCGTAGCTCAGCT-GGAT-AGAGCGCTGCCCTCCGGAGGCAGAG-----GTCTCAGGTTTCGAATCCTGTCCGGCGTACCA  
>tdbD00009020 Salmonella\_enterica\_subsp\_enterica\_serovar\_Typhi\_str\_CT18\_220341 Arg CCG  
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>tdbD00009017 Salmonella\_enterica\_subsp\_enterica\_serovar\_Typhi\_str\_CT18\_220341 Arg TCT  
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>tdbD00009018 Salmonella\_enterica\_subsp\_enterica\_serovar\_Typhi\_str\_CT18\_220341 Arg TCT  
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>tdbD00009356 Salmonella\_enterica\_subsp\_enterica\_serovar\_Typhi\_str\_Ty2\_209261 Arg CCG  
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>tdbD00002455 Salmonella\_typhimurium\_602 Arg ACG  
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>tdbD00008998 Salmonella\_typhimurium\_LT2\_99287 Arg TCT  
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>tdbD00009252 Shewanella\_oneidensis\_MR-1\_211586 Arg ACG  
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>tdbD00009253 Shewanella\_oneidensis\_MR-1\_211586 Arg ACG  
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>tdbD00009264 Shigella\_flexneri\_2a\_str\_301\_198214 Arg ACG  
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>tdbD00009258 Shigella\_flexneri\_2a\_str\_301\_198214 Arg TCT  
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>tdbD00009024 Sinorhizobium\_meliloti\_1021\_266834 Arg ACG  
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>tdbD00009025 Sinorhizobium\_meliloti\_1021\_266834 Arg TCT  
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>tdbD00002431 Spiroplasma\_melliferum\_2134 Arg ACG  
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>tdbD00002442 Staphylococcus\_aureus\_1280 Arg ACG  
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>tdbD00009412 Staphylococcus\_aureus\_subsp\_aureus\_MRSA252\_282458 Arg ACG  
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>tdbD00009413 Staphylococcus\_aureus\_subsp\_aureus\_MRSA252\_282458 Arg CCG  
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>tdbD00009184 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620\_Arg\_CCG  
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>tdbD00009297 Staphylococcus\_epidermidis\_ATCC\_12228\_176280\_Arg\_ACG  
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>tdbD00009266 Streptococcus\_agalactiae\_2603V/R\_208435\_Arg\_ACG  
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>tdbD00009267 Streptococcus\_agalactiae\_2603V/R\_208435\_Arg\_CCT  
-GTCCCTTAGTTCAAT--GGAT-ATAACAACCTCCCTCCTAAGGAGTAA-----T-TGCTGGTTGCGATTCCGGCAGGGGACA---  
>tdbD00009268 Streptococcus\_agalactiae\_2603V/R\_208435\_Arg\_TCT  
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>tdbD00009271 Streptococcus\_mutans\_UA159\_210007\_Arg\_ACG  
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>tdbD00009272 Streptococcus\_mutans\_UA159\_210007\_Arg\_CCG  
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>tdbD00009270 Streptococcus\_mutans\_UA159\_210007\_Arg\_CCT  
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>tdbD00009273 Streptococcus\_mutans\_UA159\_210007\_Arg\_TCT  
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>tdbD00008971 Streptococcus\_pneumoniae\_TIGR4\_170187\_Arg\_CCG  
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>tdbD00008972 Streptococcus\_pneumoniae\_TIGR4\_170187\_Arg\_CCT  
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>tdbD00008968 Streptococcus\_pyogenes\_M1\_GAS\_160490\_Arg\_CCT  
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>tdbD00009348 Streptomyces\_avermitilis\_MA-4680\_227882\_Arg\_ACG  
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>tdbD00009247 Streptomyces\_coelicolor\_A3(2)\_100226\_Arg\_CCT  
-GCCTCCGTAGCTCAGG--GGAT-AGAGCACCGCTCTCCTAAGCGGGT-----GTCGCAGGTTGCGAATCCTGCCGGGGGCA---  
>tdbD00002440 Streptomyces\_lividans\_1916\_Arg\_ACG  
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-GGGGCTGTAGCTCAGTC-GGAT-AGAGCGAGCGCCTCCTAAGCGCTAG-----GCCGTGCGTTCAAATCGCACCAGTCCCG---  
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>tdbD00008939 Thermotoga\_maritima\_MSB8 243274 Arg CCT  
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>tdbD00009481 Thermus\_thermophilus\_HB27 262724 Arg ACG  
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>tdbD00009482 Thermus\_thermophilus\_HB27 262724 Arg CCG  
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>tdbD00002435 Treponema\_pallidum\_160 Arg TCG  
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>tdbD00008849 Ureaplasma\_parvum\_serovar\_3 38504 Arg ACG  
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>tdbD00009308 Xylella fastidiosa Temeculal 183190 Arg CCT  
-GGCCTCGTGGCGCAATT-GGAT-AGCGCGACGACCTCCTAAGTCTGTAG-----GTTGTGGGTTTCAATCCCGCCGGGGCCACCA  
>tdbD00009447 Yersinia pestis biovar Microtus str. 91001 229193 Arg ACG  
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>tdbD00002627 Acholeplasma laidlawii 2148 Ser TGA  
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>tdbD00010210 Acinetobacter sp. ADP1 62977 Ser TGA  
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>tdbD00009766 Agrobacterium tumefaciens str. C58 176299 Ser CGA  
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>tdbD00009700 Aquifex aeolicus VF5 224324 Ser GCT  
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>tdbD00009701 Aquifex aeolicus VF5 224324 Ser GGA  
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>tdbD00009702 Aquifex aeolicus VF5 224324 Ser TGA  
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>tdbD00010091 Bacillus anthracis str. Ames 198094 Ser GGA  
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>tdbD00010003 Bacillus halodurans C-125 272558 Ser GCT  
-GGAGAAGTACCCAAGT--GGCTGAAGGGGCTCCCTGCTAAGGGAGTAGGTCGT--GTG---AGCGGCG-CGAGGTTTCAATCCCTCTCTCCGCCA  
>tdbD00010004 Bacillus halodurans C-125 272558 Ser GGA  
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>tdbD00010005 Bacillus halodurans C-125 272558 Ser TGA  
-GGAGGAGTACCCAAGTCTGGCTGAAGGGATCGGTCTTGAAACCCGACAGGGGG---TTA---AACCGCG-CGGGGGTTTCAATCCCTCTCTCCGCCA  
>tdbD00002651 Bacillus sp. PS3 2334 Ser GGA  
-GGAGAGCTGTCCGAGT--GGTCAAGGAGCAGGATTGAAATCGGTATAGGCGTG--AAT---AGCGCCT-CAAGGTTTCAATCCCTTGTCTCCGCCA  
>tdbD00002648 Bacillus subtilis 1423 Ser GGA  
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>tdbD00002649 Bacillus subtilis 1423 Ser TGA  
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>tdbD00009592 Bacillus subtilis subsp. subtilis str. 168 224308 Ser TGA  
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>tdbD00010083 Bacteroides thetaiotaomicron VPI-5482 226186 Ser TGA  
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>tdbD00010084 Bacteroides thetaiotaomicron VPI-5482 226186 Ser TGA  
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>tdbD00010095 Bartonella henselae str. Houston-1 283166 Ser CGA  
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>tdbD00010222 Bartonella quintana str. Toulouse 283165 Ser CGA  
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>tdbD00010224 Bartonella quintana str. Toulouse 283165 Ser GGA  
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>tdbD00010101 Bellovibrio bacteriovorus HD100 264462 Ser GGA  
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>tdbD00009968 Bifidobacterium longum NCC2705 206672 Ser GCT  
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>tdbD00002637 Borrelia burgdorferi 139 Ser GCT

-GGAGAGATGCCAGAGT--GGCCGAATGGGGCTTCCTGCTAAGAAGTTGTCCTTT--TAA--AAGGGGACCATGGGTTTCGAATCCCATTCTCTCCG---  
>tdbD00002636 *Borrelia burgdorferi* 139 Ser GGA  
-GGAGAGATGGCCAGT--GGCTTAAGGCGCACGCTTGAAAGCGTGTATACAG---TAAA--ATGTAT-CATGGGTTTCGAATCCCATTCTCTCCG---  
>tdbD00002635 *Borrelia burgdorferi* 139 Ser TGA  
-GGAGAGGTGGCAGACT--GGTTTAATGCTACGGTCTTGAAAACCGTTGTAGGT---GTAA--GCCTAC-CGTGAGTTTCGAATCTCACCCCTCTCCG---  
>tdbD00009651 *Borrelia burgdorferi* B31 224326 Ser TGA  
-GGAGAGGTGGCAGAGT--GGTTTAATGCTACGGTCTTGAAAACCGTTGTAGGT---GTAA--GCCTAC-CGTGAGTTTCGAATCTCACCCCTCTCCG---  
>tdbD00010135 *Borrelia garinii* PBi 290434 Ser GCT  
-GGAGAGATGCCAGAGT--GGCCGAATGGGGCTTCCTGCTAAGAAGTTGTCCTTT--TGA--AAGGGGACCATGGGTTTCGAATCCCATTCTCTCCG---  
>tdbD00010137 *Borrelia garinii* PBi 290434 Ser GGA  
-GGAGAGATGGCCAGT--GGCTTAAGGCGCACGCTTGAAAGCGTGTATACGG---TAAA--ATGTAT-CATGGGTTTCGAATCCCATTCTCTCCG---  
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-GGAGAGGTGGCAGAGT--GGTTGAATGCACCGCACTCGAAATGCGGCATAGGT---GCAA--GCCTAT-CGGGGGTTTCGAATCCCCTCCCTCTCCGCCA  
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>tdbD00009735 *Brucella melitensis* 16M 224914 Ser CGA  
-GGAGAGGTGGCTGAGT--GGTTGAAAGCACCGCACTCGAAATGCGGCATGGGG---GCAA--CTCCAT-CGGGGGTTTCGAATCCCCTCCCTCTCCGCCA  
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>tdbD00009738 *Brucella melitensis* 16M 224914 Ser TGA  
-GGAAGGTGGCCAGC--GGTTTAAGGCAACGCTTTGAAAACCGCGTGCGA---GAGA--TCGTAC-CGTGGGTTTCGAATCCCACCCCTCTCCGCCA  
>tdbD00009596 *Buchnera aphidicola* str. APS (*Acyrtosiphon pisum*) 107806 Ser TGA  
-GGAGAGGTGGCCAGC--GGTTTAAGGCAACGCTTTGAAAACCGCGCACGA---GAAA--TCGTAC-CGAGAGTTTCGAATCTCTCTCTCTCCG---  
>tdbD00009914 *Buchnera aphidicola* str. Sg (*Schizaphis graminum*) 198804 Ser TGA  
-GGAGAGGTGGCCAGT--GGTTTAAGGCAACGCTTTGAAAACCGCGATGA---GCAA--TCATC-CGAGAGTTTCGAATCTCTCTCTCTCTCCG---  
>tdbD00010229 *Candidatus Blochmannia floridanus* 203907 Ser TGA  
-GGAGAGGTGGCCAGC--GGATGAAGGCGCGCTTTGAAAATCGGTAATGT---AAA---AAATT-CTAGAGTTTCGAATCTCTACTCTCTCTCCG---  
>tdbD00010114 *Candidatus Protochlamydia amoebophila* UWE25 264201 Ser GCT  
-GGAAGATGGCTGAGC--GGCCGAAAGCACGCTCCCTGCTAAGGACGCATACCCC--TAA--AGGGTAT-CGAGGGTTTCAAATCCCCTCTCTTTCCG---  
>tdbD00010115 *Candidatus Protochlamydia amoebophila* UWE25 264201 Ser GGA  
-GGAGGGTGTCCGAGT--GGCTTAAGGAGCACGCTTGAAAGCGTGTGTAGCTT---AAA--CACGTAC-CGTGGGTTTCGAATCCCACCTCTCTCCG---  
>tdbD00010113 *Candidatus Protochlamydia amoebophila* UWE25 264201 Ser TGA  
-GGAAGATGGCAGAGT--GGCCGAAATGCGTCTGTCTTGAAAACAGAGTCGGGC--AGC--CCCCGAC-CGTGGGTTTCGAATCCTACCTCTTTCCG---  
>tdbD00009655 *Caulobacter crescentus* CB15 190650 Ser CGA  
-GGAGAGGTGGCAGAGT--GGTGAATGCGCCGCACTCGAAATGCGGTTTACGT---GAAA--GCGTAA-CGTGGGTTTCGAATCCCACCCCTCTCCGCCA  
>tdbD00009656 *Caulobacter crescentus* CB15 190650 Ser GCT  
-GGAGACGTGGCCAGC--GGTGAAGGCAACGCTTTGCTAAGGCGCATACCTC--AAA--AGGGTAT-CGAGGGTTTCGAATCCCCTCCCTCTCCGCCA  
>tdbD00009718 *Chlamydia muridarum* Nigg 243161 Ser CGA  
-GGAAGATGGCAGAGT--GGTGAATGCACTGATTCGAAATCAGAAGTCCCT---CAAC--GGGGAC-CGGGGGTTCAAATCCCCTCTCTCTCCG---  
>tdbD00009720 *Chlamydia muridarum* Nigg 243161 Ser GCT  
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>tdbD00009719 *Chlamydia muridarum* Nigg 243161 Ser GGA  
-GGAGAGATGTCGAGT--GGCTTAAGGAGCACGCTTGAAAGCGTGTGTGCGT---TAAC--GCGTAC-CGAGGGTTTCGAATCCCCTCTCTCTCCG---  
>tdbD00009717 *Chlamydia muridarum* Nigg 243161 Ser TGA  
-GGAAGATGGCAGAGC--GGTTTAATGCACCTGTCTTGAAAACAGGAGACCT---GAAA---GGGTC-CGGGGGTTTCGAATCCCCTCTCTTTCCG---  
>tdbD00009573 *Chlamydia pneumoniae* AR39 115711 Ser CGA  
-GGAAGATGGCAGAGT--GGTGAATGCGTCTGATTCGAAATCAGAAGTCTC---TTA---CAGGAACAGGGGTTTCGAATCCCCTCTCTTTCCG---  
>tdbD00009574 *Chlamydia pneumoniae* AR39 115711 Ser GCT  
-GGAAGATGACTGAGT--GGTGAAGTACGCTCCCTGCTAAGGACGCGTACCCCC--TAA--AGGGTAT-CGAGGGTTTCGAATCCCCTCTCTTTCCG---  
>tdbD00009575 *Chlamydia pneumoniae* AR39 115711 Ser GGA  
-GGAGAGATGTCGAGT--GGCTTAAGGAGCACGCTTGAAAGCGTGTGTGCGT---TAAC--GCGTAC-CGTGGGTTTCGAATCCCCTCTCTCTCCG---  
>tdbD00009905 *Chlorobium tepidum* TLS 194439 Ser GCT  
-GGAGAGGTGGCCAGT--GGCTGAAGGCAACGCTTTGCTAAGGACGCTAGTTGCG-ATT-AGAGCTAC-CGAGGGTTTCGAATCCCCTCCCTCTCCG---  
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-GGAGAGATGCGATAGT--GGTCTAGTGCCTCGCTTGAAAGCGGTTAGGGTG---TAA---CAGCCCTCGAGGGTTTCGAATCCCCTCTCTCCGCCA  
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-GGAGGATTAAGCCTAATT--GGT--AAGGCAAGCAGTCTTGAAAACGCTGCCC---TTGC---GCCCTTGGGGGTTTCGAGTCCCTCATCTCTCCG---  
>tdbD00009730 *Clostridium acetobutylicum* ATCC\_824 272562 Ser CGA  
-GGAGAGATGTCGAGT--GGTCTATCGTGCATGACTCGAAATCATGTGTAGCGT---TTAA--CCCCTAC-CGAGGGTTTCAAATCCCCTCTCTCCGCCA  
>tdbD00009731 *Clostridium acetobutylicum* ATCC\_824 272562 Ser GGA  
-GGAGAGATGTCGAGT--GGTTTAAGGAGCACGCTTGAAAGCGTGTGTAGGG---GAAA--CTCTAC-CGAGGGTTTCGAATCCCCTCTTTCTCCGCCA  
>tdbD00002661 *Clostridium perfringens* 1502 Ser GGA  
-GGAGAGATGTCGAGT--GGTGAAGGAGCACGCTTGAAAGCGTGTGTAGGG---GAAA--CTCTAC-CGAGGGTTTCAAATCCCCTCTCTCCGCCA  
>tdbD00010011 *Clostridium tetani* E88 212717 Ser CGA  
-GGAGAGATGTCGAGC--GGTGAAGGAGCACGCTTGAAAGCGTGTGTAGGG---GCAA--CTCTAC-CGAGGGTTTCGAATCCCCTCTCTCCGCCA  
>tdbD00010010 *Clostridium tetani* E88 212717 Ser GGA  
-GGAGAGATGTCGAGC--GGTGAAGGAGCACGCTTGAAAGCGTGTGTAGGG---GCAA--CTCTAC-CGAGGGTTTCGAATCCCCTCTCTCCGCCA  
>tdbD00010103 *Corynebacterium diphtheriae* NCTC\_13129 257309 Ser GCT  
-GGAGACGTGCCAGAGC--GGCCGAATGGGGCTCCCTGCTAAGGAGTTGACTTGT--TTGC--GCAGGTC-CGGAGGTTTCAAATCCCCTCTCTCTCCG---

>tdbD00010102 *Corynebacterium diphtheriae*\_NCTC\_13129\_257309\_Ser\_TGA  
-GGAGATGTGGCAGAGC--GGCCGAATGCACTGGTCTTGAAAACACGCGATGG---GAAA---CCATC-CCAGGGTTCAAATCCCTCGCTCCG---  
>tdbD00009976 *Corynebacterium efficiens*\_YS-314\_196164\_Ser\_GCT  
-GGAGACGTGGCAGAGC--GGCCGAATGGGGCTCAGTCTAATGAGTTGTCTCTCT--TAAC-GGAGGAC-CGAGGGTTCAAATCCCTCGTCTCCG---  
>tdbD00009975 *Corynebacterium efficiens*\_YS-314\_196164\_Ser\_TGA  
-GGAGACGTGGCAGAGC--GGCCGAATGCACTGGTCTTGAAAACACGCGATGG---GAAA---CCATC-CGAGGGTTCAAATCCCTCGTCTCCG---  
>tdbD00009921 *Corynebacterium glutamicum*\_ATCC\_13032\_196627\_Ser\_GCT  
-GGAGACGTGGCAGAGC--GGCCGAATGGGGCTCAGTCTAATGAGTTGTCTCTCT--TAAC-GGGGGAC-CGAGGGTTCAAATCCCTCGTCTCCG---  
>tdbD00010048 *Coxiella burnetii*\_RSA\_493\_227377\_Ser\_GCT  
-GGAGAGATGGCCGAGAG--GGCTGAAGGCGCTCCCTGCTAAGGGAGTATAGGGC--GAAA-GCTCCAT-CGAGGGTTCAATCCCTCTCTCCGCCA  
>tdbD00010049 *Coxiella burnetii*\_RSA\_493\_227377\_Ser\_TGA  
-GGAGAGGTGGCAGAGC--GGTTGAATGCGACGGTCTTGAAAACCGTTGAGGGG---GCAA--CTCCTC-CGAGGGTTCAATCCCTCCCTCCGCCA  
>tdbD00009661 *Deinococcus radiodurans*\_R1\_243230\_Ser\_GGA  
-GGAAGCGTGTCCGAGT--GGTTGAAGGAGCAGCTGAAAACCGTTATAGGG---GCAA--CTCTAT-CGAGGGTTCAATCCCTCTCGTTCCGCCA  
>tdbD00010186 *Desulfovibrio vulgaris*\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Ser\_GCT  
-GGAGAGGTGTCCGAGTC--GGCCGAAGGAGCTCGCCTGCTAAGCGGTATAGGGC--ATAAACCTCTAT-CGAGGGTTCAATCCCTCCCTCCGCCA  
>tdbD00010185 *Desulfovibrio vulgaris*\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Ser\_GGA  
-GGAGAGGTGTCCGAGT--GGTTGAAGGAGCAGATTGAAAACCGTTGTTGTTACCT--AAC--CCGGTAC-CGAGAGTTCAATCTCTCCCTCCGCCA  
>tdbD00010184 *Desulfovibrio vulgaris*\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Ser\_TGA  
-GGAAGGGTGGCAGAGTCCGGTTTATTGCGCGGTCTTGAAAACCGTTGTTGTTG---GAAA--CCCCAC-CGAGGGTTCAATCCCTCCCTCCGCCA  
>tdbD00010017 *Enterococcus faecalis*\_V583\_226185\_Ser\_CGA  
-GGAGGATTACCCAAGTTTGGCTGAAGGGACGGTCTGAAAACCGTTAGGGC--TAA--CATCGTG-CAAGGGTTCAATCCCTTACTCTCCG---  
>tdbD00010016 *Enterococcus faecalis*\_V583\_226185\_Ser\_GGA  
-GGAGAGTGTCCGAG--GGCCGAAGGAGCATGATTGAAAATCATGTAGGGC--AAAC-ACTGTCT-CAAGGGTTCAATCCCTTACTCTCCG---  
>tdbD00002652 *Escherichia coli*\_562\_Ser\_CGA  
-GGAGAGATGCGCGAGC--GGTGAACGGACCGGTCTGAAAACCGGAGTAGGG---GCAA--CTCTAC-CGAGGGTTCAATCCCTCCCTCCGCCA  
>tdbD00002653 *Escherichia coli*\_562\_Ser\_TGA  
-GGAAGTGTGGCCGAGC--GGTTGAAGGCACCGGTCTTGAAAACCGGCGACCC---GAAA---GGGTT-CCAGAGTTCAATCTCTCGCTCCGCCA  
>tdbD00009632 *Escherichia coli*\_O157H7\_83334\_Ser\_CGA:  
-GGAGAGATGCGCGAGC--GGTGAACGGACCGGTCTGAAAACCGGAGTAGGG---GCAA--CTCCAC-CGAGGGTTCAATCCCTCCCTCCGCCA  
>tdbD00009908 *Fusobacterium nucleatum*\_subsp.\_nucleatum\_ATCC\_25586\_190304\_Ser\_TGA  
-GGAAGGCTATCTAATT--GGT--AAGGAACCGGTCTTGAAAACCGGCGTC---GTAA-----GACTTTAGAGTTGAGTCTCTAGCCTCCGCCA  
>tdbD00010140 *Geobacter sulfurreducens*\_PCA\_243231\_Ser\_CGA  
-GGAGAGATGGCCGAGT--GGTGAAGGCGGAGACTCGAAAATCTGTTGTACCG---CTTG--CGGTAC-CTAGGGTTCAATCCCTATCTCTCCGCCA  
>tdbD00010139 *Geobacter sulfurreducens*\_PCA\_243231\_Ser\_GCT  
-GGAGAGATGGCCGAGTA--GGTGAAGGCGCTCGCCTGCTAAGCGAGTATACGGGC--AAA-ACCTGTAT-CGAGGGTTCAATCCCTCTCTCCGCCA  
>tdbD00010141 *Geobacter sulfurreducens*\_PCA\_243231\_Ser\_GGA  
-GGAGAGATGTCGAGT--GGCCGAAGGAGCAGATTGAAAATCGTGTGTACT---GCAA---GGTAC-CGAGGGTTCAATCCCTCTCTCCGCCA  
>tdbD00010138 *Geobacter sulfurreducens*\_PCA\_243231\_Ser\_TGA  
-GGAGGGATGGCCGAGT--GGTTAAGGCGGCGGTCTTGAAAACCGTTGAAC---GAAA---GTTT-CGTGGGTTCAATCCCTACTCCCTCCGCCA  
>tdbD00010143 *Lactobacillus johnsonii*\_NCC\_533\_257314\_Ser\_GGA  
-GGAGTGTGTCCGAGT--GGCTGAAGGAGCATGATTGAAAATCATGTATACGGGC--TTT-ACCTGTAT-CGAGAGTTCAATCTCTCACACTCCG---  
>tdbD00010018 *Lactobacillus plantarum*\_WCF51\_220668\_Ser\_GGA  
-GGAGAGTGTCCGAGT--GGCTGAAGGAGCAGCATTGAAAATGCTGTAACGGGT--TAT-ACCTGTTT-CAAGGGTTCAATCCCTTACTCTCCG---  
>tdbD00010147 *Leifsonia xyli*\_subsp.\_xyli\_str.\_CTCB07\_281090\_Ser\_GCT  
-GGAGACGTGCATAGTCAGGCTTAGTCACCACCTGCTAAGGTGGAGTCC---GTAA---GGGGAC-CGAGGGTTCAAATCCCTCCGCTCCG---  
>tdbD00010149 *Leifsonia xyli*\_subsp.\_xyli\_str.\_CTCB07\_281090\_Ser\_GGA  
-GGAGAATTCGCTAGT--GGCTATGGCGCAGCTTGAAAACCGTGTGGGT---GCAA---GCCCT-CGAGGGTTCAATCCCTCCCTCCG---  
>tdbD00010148 *Leifsonia xyli*\_subsp.\_xyli\_str.\_CTCB07\_281090\_Ser\_TGA  
-GGAGGGCTGTCCGAGC--GGCCGATGGAGCCAGTCTTGAAAACCGTGGGCA---GAAA---TGTT-CGTGGGTTCAATCCCTCCCTCCGCCA  
>tdbD00009979 *Leptospira interrogans*\_serovar\_Lai\_str.\_56601\_189518\_Ser\_GCT  
-GGAGACGTGCCTGAGT--GGCCGAAAGGAGCAGTTTGTCTAACTGTCGTACGG---GTAA--CTGTAC-CCAGGGTTCAATCCCTCGCTCCG---  
>tdbD00009981 *Leptospira interrogans*\_serovar\_Lai\_str.\_56601\_189518\_Ser\_GGA  
-GGAGAAGTGTGAGT--GGTCTATTGTGCATGCTTGAAAACCGTGTGGT---AAA---AGCAC-CCGCGGTTCAATCCCTCCGCTCCG---  
>tdbD00009980 *Leptospira interrogans*\_serovar\_Lai\_str.\_56601\_189518\_Ser\_TGA  
-GGAGAAGTGGCTGAGT--GGTCTAAAGCAGCGGTCTTGAAAACCGTGTGGT---AAT---CCCAC-CGTGGGTTCAATCCCTACTCTCCG---  
>tdbD00009703 *Listeria innocua*\_Clip11262\_272626\_Ser\_CGA  
-GGAGAATAACCAAGTCCGGCTGAAGGGACAGACTCGAAATCTGTTAGGCGG---TGTA--TGCCGCGCGGGGTTCAATCCCTGTTCTCCG---  
>tdbD00009707 *Listeria innocua*\_Clip11262\_272626\_Ser\_GGA  
-GGAGAGCTGTCCGAGT--GGCCGAAGGAGCAGGTTGAAAACCGTGTAGGCGGT--GTAA-GCTGTCT-CAAGGGTTCAATCCCTTGTCTCCG---  
>tdbD00009706 *Listeria innocua*\_Clip11262\_272626\_Ser\_TGA  
-GGAGAATAACCAAGTCTGGCTGAAGGGATCGGTCTTGAAAACCGACAGGCGGG--TAA--TACCGCG-CGAGGGTTCAATCCCTCTCTCCG---  
>tdbD00010194 *Mesoplasma florum*\_L1\_265311\_Ser\_TGA  
-GGAAGATTACCAAGTCCGGCTGAAGGGATCGGTCTTGAAAACCGAGAGTGGG--GAA--ACCCGAG-CGAGGGTTCAATCCCTCATCTCCGCCA  
>tdbD00009741 *Mesorhizobium loti*\_MAFF303099\_266835\_Ser\_CGA  
-GGAGAGGTGGCAGAGT--GGTGAATGCACCGCACTCGAAATGCGGCATGGGT---GCAA--GCCCAT-CGAGGGTTCAATCCCTCCCTCCGCCA  
>tdbD00009742 *Mesorhizobium loti*\_MAFF303099\_266835\_Ser\_GCT  
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>tdbD00009740 *Mesorhizobium loti*\_MAFF303099\_266835\_Ser\_GGA  
-GGAGAGGTGGCCGAGT--GGTGAAGGCGCAGCTTGAAAACCGTGTGGT---GAGA--CCGTAA-CGAGGGTTCAATCCCTCTCTCCGCCA  
>tdbD00009739 *Mesorhizobium loti*\_MAFF303099\_266835\_Ser\_TGA  
-GGAGGGATGGCCGAGC--GGTTAAGGCACCGGTCTTGAAAACCGGCGTGGG---GCAA--GTTTAC-CGTGGGTTCAATCCCTACTCCGCCA  
>tdbD00010042 *Mycobacterium bovis*\_AF2122/97\_233413\_Ser\_GCT  
-GGAGGCGTGGCAGAGC--GGCCGAATGGGGCTCAGTCTAATGAGTTGTCCCTC---TTCA-AGGGGAC-CGAGGGTTCAAATCCCTCTCCCTCCG---  
>tdbD00010040 *Mycobacterium bovis*\_AF2122/97\_233413\_Ser\_GGA

-GGAGGATTCCGCTAGT--GGCCTATGGCGCTCGCCTGGAACCGGGTTGGGTT---AAC---AGCCCT-CGCGGGTTCAAATCCCGCATCCTCCGCCA  
>tdbD00009619 Mycobacterium\_leprae\_TN\_272631 Ser GCT  
-GGAGGCGTGCAGAGC--GGCCGAATGGGGCTACTGCTAATGAGTTGTCCCCCT-TGG-AAGGGGAC-CGAGGTTCAAATCCTCTCGCCTCCG---  
>tdbD00009620 Mycobacterium\_leprae\_TN\_272631 Ser GGA  
-GGAGGATTCCGCTAGT--GGCCTATGGCGCTCGCCTGGAACCGGGTTGGGTT---AAC---AGCCCT-CGCGGGTTCAAATCCCGCATCCTCCG---  
>tdbD00002615 Mycoplasma\_capricolum\_2095 Ser TGA  
-GGAAGATTACCCAAGTCCGGCTGAAGGGATCGGTCTTGAAAACCGAGAGTCGG---GGAA--ACCGAG-CGGGGGTTCGAATCCCTCATCTCCGCCA  
>tdbD00002620 Mycoplasma\_genitalium\_2097 Ser CGA  
-GGAGATTTACCCAAGT--GGCTGAAGGGGGCGCTCTCGAAAAGCGTTAGGGGT---GGTT--ATCCACGCGTGGGTTCAAATCCCACAATCTCCGCCA  
>tdbD00002618 Mycoplasma\_genitalium\_2097 Ser TGA  
-GGAGACTTACCCAAGC--GGCTGAAGGGTTCGGTCTTGAAAACCGAGAGGTGC---TTTA--TAGCACGCGAGGGTTCGAATCCCTCAGTCTCCGCCA  
>tdbD00009663 Mycoplasma\_genitalium\_G37\_243273 Ser CGA  
-GGAGATTTACCCAAGT--GGCTGAAGGGGGCGCTCTCGAAAAGCGTTAGGTGG---TTA---TCCACG-CGTGGGTTCAAATCCCACAATCTCCGCCA  
>tdbD00009662 Mycoplasma\_genitalium\_G37\_243273 Ser TGA  
-GGAGACTTACCCAAGC--GGCTGAAGGGTTCGGTCTTGAAAACCGAGAGGTGCT--TTA--TAAGCACGCGAGGGTTCGAATCCCTCAGTCTCCGCCA  
>tdbD00002623 Mycoplasma\_pneumoniae\_2104 Ser CGA  
-GGAGACTTACCCAAGT--GGTTAAGGGGGCGCTCTCGAAAAGCGTTGTGT----TTTT---GCATG-CGTGGGTTCGAATCCCACAGTCTCCGCCA  
>tdbD00002625 Mycoplasma\_pneumoniae\_2104 Ser TGA  
-GGAGACTTACCCAAGC--GGCTGAAGGGTTCGGTCTTGAAAACCGAGGTGCT---GAAA--AGCACG-CGAGGGTTCGAATCCCTCAGTCTCCGCCA  
>tdbD00009668 Mycoplasma\_pneumoniae\_M129\_272634 Ser CGA  
-GGAGACTTACCCAAGT--GGTTAAGGGGGCGCTCTCGAAAAGCGTTAGGTG---TTTT---TGCATGCGTGGGTTCGAATCCCACAGTCTCCGCCA  
>tdbD00009671 Mycoplasma\_pneumoniae\_M129\_272634 Ser TGA  
-GGAGACTTACCCAAGC--GGCTGAAGGGTTCGGTCTTGAAAACCGAGAGGTGC---TGAA--AAGCACGCGAGGGTTCGAATCCCTCAGTCTCCGCCA  
>tdbD00009601 Neisseria\_meningitidis\_MC58\_122586 Ser CGA  
-GGAACGTGGCAGAGA--GGCTGAATGCAGCGGACTCGAAATCCCGTGGAGGT---GCAA--ATCCTC-CGTGGGTTCGAATCCCACCGTTCCGCCA  
>tdbD00009602 Neisseria\_meningitidis\_MC58\_122586 Ser GCT  
-GGAGTAATGGCTGAGA--GGCTGAAGGCACCTCCCTGCTAAGGAACATGTGGGG-TCA-ACCTGCAT-CGAGGGTTCGAATCCCTCTACTCCGCCA  
>tdbD00009604 Neisseria\_meningitidis\_MC58\_122586 Ser TGA  
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>tdbD00009608 Neisseria\_meningitidis\_Z2491\_122587 Ser TGA  
-GGAAGCGTGGCAGAGC--GGTTAATGCAACGGTCTTGAAAACCGTCGAGGGTT--GAT--AGCCCTC-CGTGAGTTCGAATCTCACCGTTCCGCCA  
>tdbD00010079 Nitrosomonas\_europaea\_ATCC\_19718\_228410 Ser GCT  
-GGAGAGATGGCCGAGT--GGTCAAGGGCGTCCCTGCTAAGGGAGTATAGGCTC-AAA-AAGCTTAT-CGAGGGTTCGAATCCCTCTCTCCGCCA  
>tdbD00010078 Nitrosomonas\_europaea\_ATCC\_19718\_228410 Ser GGA  
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-GGAAGCGTGGCCGAGC--GGTTAAGGCACCTGGTCTTGAAAACCGCAGCGATGG---GCAA---CCATC-CGTGAGTTCGAATCTCACCGTTCCGCCA  
>tdbD00009759 Nostoc\_sp.\_PCC\_7120\_103690 Ser CGA  
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>tdbD00009757 Nostoc\_sp.\_PCC\_7120\_103690 Ser GCT  
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>tdbD00009984 Oceanobacillus\_heyensis\_HTE831\_221109 Ser GGA  
-GGAGAGCTGTCGAGA--GGCCGAAGGAGCAGATGGAATCGTAAAGCCGC--TACC-GCGGCTT-CGAGGGTTCGAATCCCTCGCTCTCCGCCA  
>tdbD00010108 Onion\_yellow\_phytoplasma\_OY-M\_262768 Ser TGA  
-GGAGGAATACCCAAGTCCGGTTGAAGGGGTGAGTCTTGAAAACCTGAGAGGTCC---GAA---AGGACG-CGGGGGTTCGAATCCCTCTCTCCGCCA  
>tdbD00010117 Photorhabdus\_luminescens\_subsp.\_laumondii\_TT01\_243265 Ser TGA  
-GGAGGGTGGCCGAGC--GGCTTAAGGCAGCGGTCTTGAAAACCGCGATGG---GAAA---CCATC-CGAGAGTTCGAATCTCTCTCTCCGCCA  
>tdbD00010119 Photorhabdus\_luminescens\_subsp.\_laumondii\_TT01\_243265 Ser TGA  
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>tdbD00010153 Porphyromonas\_gingivalis\_W83\_242619 Ser TGA  
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>tdbD00010197 Propionibacterium\_acnes\_KPA171202\_267747 Ser GCT  
-GGAGGTGTCGCTAGTACAGTCTATGGCGCCGCTGCTAAGCGGGTTGGGAG--GTA--ATCCCAT-CGCGGGTTCAAATCCCGCCACCTCCG---  
>tdbD00010195 Propionibacterium\_acnes\_KPA171202\_267747 Ser GGA  
-GGAGGATTCGCTAGA--GGCCTATGGCGCTCGCTTGAAAACCGGGTTGGGT---TCAC---GCCCT-CACGAGTTCGAATCTCGTATCTCTCCG---  
>tdbD00009679 Pseudomonas\_aeruginosa\_PAO1\_208964 Ser CGA  
-GGAGAGATGCGGGAGT--GGTCAACGGGACGGATTCGAAATCCGTTGAGTCA---GCAA--TGGTTC-CTAGGGTTCAAATCCCTATCTCTCCGCCA  
>tdbD00009680 Pseudomonas\_aeruginosa\_PAO1\_208964 Ser GCT  
-GGAGAGGTGGCCGAGT--GGCCGAAGGCGCTCCCTGCTAAGGGAGTACACCTC---AAA--AGGGTGT-CGGGGGTTCGAATCCCCCTCTCCGCCA  
>tdbD00009682 Pseudomonas\_aeruginosa\_PAO1\_208964 Ser TGA  
-GGAGGTGTCGCGAGT--GGTTAAGGCAACGGTCTTGAAAACCGTCGAAGGG---GAGA--CTCTTC-CGTGAGTTCGAATCTCACCGCTCCGCCA  
>tdbD00010088 Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283 Ser CGA  
-GGAGAGATGGCCAGAGT--GGCCGAATGGGACGGATTCGAAATCCGTTGATCT---TCAC--CGGTAC-CTAGGGTTCAAATCCCTATCTCTCCGCCA  
>tdbD00010085 Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283 Ser GCT  
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>tdbD00010087 Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283 Ser TGA  
-GGAGTATGGCCGAGT--GGTTAAGGCAGCAGTCTTGAAAACCTGCGACTG---TAA----CAGGTCTAGAGTTCAAATCTCTATGCTCTCCGCCA  
>tdbD00009756 Ralstonia\_solanacearum\_GMI1000\_267608 Ser CGA  
-GGAGAGGTGGCAGAGT--GGTCAATGTACTGACTCGAAATCAGGCGTACCG---GCAA--CGGTAC-CGTGGGTTCAAATCCCACCTCTCCGCCA  
>tdbD00009753 Ralstonia\_solanacearum\_GMI1000\_267608 Ser GCT  
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>tdbD00009755 *Ralstonia\_solanacearum* GMI1000 267608 Ser TGA  
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>tdbD00010073 *Rhodopirellula\_baltica* SH\_1 243090 Ser GCT  
-GGAGCGGTGGCTGAGT--GGTFCGAAAGCGCGGTTTGCTAAATCGGTGAACCGG--GAAA-CTGGTTC-CGCAGGTTTCAATCCTGTCCGCTCCG---  
>tdbD00010122 *Rhodopseudomonas\_palustris* CGA009 258594 Ser GCT  
-GGAGACGTGGCCGAGT--GGCTGAAGGCGCGGTTTGCTAAACCGTTATAGGGT--GTAAAGCCCTAT-CGAGGGTTTCAATCCCTCCGCTCCTCCGCCA  
>tdbD00010123 *Rhodopseudomonas\_palustris* CGA009 258594 Ser GGA  
-GGAGAGGTGGCCGAGT--GGTTGAAGGCGCACGCTGGAACGCGTATACGG---GAAA---CTGTAT-CGAGGGTTTCAATCCCTCCTCTCCTCCGCCA  
>tdbD00010121 *Rhodopseudomonas\_palustris* CGA009 258594 Ser TGA  
-GGAAGGTTGGCCGAGT--GGTTTAAGGCACCGTCTTGAAAACCGCGTGGCC---GCAA---GGGTAC-CGTGGGTTTCAATCCCACCCCTTCCGCCA  
>tdbD00009734 *Rickettsia\_conorii* str. Malish\_7 272944 Ser GCT  
-GGAGAGATGGCCGAGT--GGCCGAAGGCGCGGTTTGCTAAACCGTTATACGGG--TCAT-ACCGTAT-CGAGGGTTTCAATCCCTCCTCTCCTCCGCCA  
>tdbD00009732 *Rickettsia\_conorii* str. Malish\_7 272944 Ser GGA  
-GGAGAGATGGCCGAGT--GGTTTAAGGCGCACGCTGGAAGCGTATACGG---GCAA---CGTGT-CGGGGGTTTCAATCCCCCTCCTCTCCTCCGCCA  
>tdbD00009918 *Rickettsia\_prowazekii* str. Madrid\_E 272947 Ser GGA  
-GGAGAGATGGCCGAGT--GGCTTAAGGCGCACGCTGGAAGCGTATACGG---GAAA---TGTGT-CGGGGGTTTCAATCCCCCTCCTCTCCTCCGCCA  
>tdbD00010156 *Rickettsia\_typhi* str. Wilmington 257363 Ser GCT  
-GGAGAGATGGCCGAGT--GGCCGAAGGCGCGGTTTGCTAAACCGTTATACGGG--TTAT-ACCGTAT-CGAGGGTTTCAATCCCTCCTCTCCTCCGCCA  
>tdbD00010154 *Rickettsia\_typhi* str. Wilmington 257363 Ser GGA  
-GGAGAGATGGCCGAGT--GGCTTAAGGCGCACGCTGGAAGCGTATACGG---GAAA---TGTGT-CGGGGGTTTCAATCCCCCTCCTCTCCTCCGCCA  
>tdbD00009991 *Shewanella\_oneidensis* MR-1 211586 Ser GCT  
-GGAGAGTTGGCCGAGT--GGCCGAAGGCGCTCCCTGCTAAAGCGTATGGGG--TTAT-CTCCCAT-CGAGGGTTTCAATCCCTCCTCTCCTCCGCCA  
>tdbD00009990 *Shewanella\_oneidensis* MR-1 211586 Ser TGA  
-GGAGGGTTGGCAGAGT--GGTTTAAATGCACCGTCTTGAAAACCGCGTGGGTT--TAT--AGCCAC-CCAGGGTTCAAATCCCTGCTCCTCCGCCA  
>tdbD00009774 *Sinorhizobium\_meliloti* 1021 266834 Ser CGA  
-GGAGAGTTGGCAGAGT--GGTTGAATGCACCGCTGGAAGCGTATGGGG--GCAA---GCCAT-CGGGGGTTTCAATCCCCCTCCTCCTCCGCCA  
>tdbD00009772 *Sinorhizobium\_meliloti* 1021 266834 Ser GCT  
-GGAGAGTTGGCCGAGT--GGTFCGAAAGCGCTCCCTGCTAAAGGAGTATACGG---GAAA---CGGTAT-CGAGGGTTTCAATCCCTCCTCTCCTCCGCCA  
>tdbD00002628 *Spiroplasma\_citri* 2133 Ser CGA  
-GGAAGTATACCCAAGTCGGTTGAAGGGGCGTCTCGAAAACCGTTATGGA---GTAA--TCCATG-CAAGAGTTTCAATCTCTTTACTTCCGCCA  
>tdbD00002629 *Spiroplasma\_melliferum* 2134 Ser TGA  
-GGAAGATTACCCAAGTCTGGTTGAAGGGATCGGTCTTGAAAATTGACAGGCGGT--GAA--AGCCGCG-CGGGGGTTTCAATCCCTCATCTTCCGCCA  
>tdbD00002640 *Staphylococcus\_aureus* 1280 Ser TGA  
-GGAGGAATACCCAAGTCCGGCTGAAGGGATCGGTCTTGAAAACCGACGGGCT---TAAC--GGCTCG-CGGGGGTTTCAATCCCTCCTCCTCCG---  
>tdbD00002641 *Staphylococcus\_aureus* 1280 Ser TGA  
-GGAGGAATACCCAAGTCCGGCTGAAGGGATCGGTCTTGAAAACCGACGGGCT---TAAC--GGGCG-CGGGGGTTTCAATCCCTCCTCCTCCGCCA  
>tdbD00010126 *Staphylococcus\_aureus* subsp. aureus MRSA252 282458 Ser GGA  
-GGAGAGTTGTCCGAGT--GGCCGAAGGAGCAGCCTGGAAGTGTGTAGGCGCC--ACA--AGCTCT-CGAGGGTTTCAATCCCTCACTCCTCCG---  
>tdbD00010124 *Staphylococcus\_aureus* subsp. aureus MRSA252 282458 Ser TGA  
-GGAGGAATACCCAAGTCCGGCTGAAGGGATCGGTCTTGAAAACCGACAGGGGCT--TAA--CGGCTCG-CGGGGGTTTCAATCCCTCCTCCTCCGCCA  
>tdbD00010127 *Staphylococcus\_aureus* subsp. aureus MRSA252 282458 Ser TGA  
-GGAGGAATACCCAAGTCCGGCTGAAGGGATCGGTCTTGAAAACCGACAGGGGCT--TAA--CGGCTCG-CGGGGGTTTCAATCCCTCCTCCTCCGCCA  
>tdbD00010128 *Staphylococcus\_aureus* subsp. aureus MRSA252 282458 Ser TGA  
-GGAGGAATACCCAAGTCCGGCTGAAGGGATCGGTCTTGAAAACCGACAGGGGCT--TAA--CGGCTCG-CGGGGGTTTCAATCCCTCCTCCTCCG---  
>tdbD00009926 *Staphylococcus\_aureus* subsp. aureus MW2 196620 Ser GGA  
-GGAAGTTGTCCGAGT--GGCCGAAGGAGCAGCCTGGAAGTGTGTAGGCGTC--ACA--AGCTCT-CGAGGGTTTCAATCCCTTACCTTCCG---  
>tdbD00010023 *Staphylococcus\_epidermidis* ATCC 12228 176280 Ser GGA  
-GGAGAGTTGTCCGAGT--GGCCGAAGGAGCAGCCTGGAAGTGTGTAGGCGTC--ACA--AGCTCT-CGAGGGTTTCAATCCCTCACTCCTCCG---  
>tdbD00010025 *Staphylococcus\_epidermidis* ATCC 12228 176280 Ser TGA  
-GGAGGAATACCCAAGTCCGGCTGAAGGGATCGGTCTTGAAAACCGACAGGAGCT--TAA--CGGCTCG-CGGGGGTTTCAATCCCTCCTCCTCCG---  
>tdbD00010066 *Streptomyces\_avermitilis* MA-4680 227882 Ser GCT  
-GGAGGCTCGCTTAGTCCGGTCTATGGCGCCGACTGCTAATGCGGTTTGGGAC--TTCA-ATCCAT-CGAGGGTTCAAATCCCTCCGCTCCG---  
>tdbD00010064 *Streptomyces\_avermitilis* MA-4680 227882 Ser GGA  
-GGAGGATTCGCTAGA--GGCTAGGGCGCAGCCTTGGAAGCGTGTGGGG---GCAA---CCCCT-CACGAGTTTCAATCTCGTATCCTCCGCCA  
>tdbD00009986 *Streptomyces\_coelicolor* A3(2) 100226 Ser GCT  
-GGAGGCTCGCTTAGTCCGGTCTATGGCGCCGACTGCTAATGCGGTTTGGGTC--TTAA-AGCCAT-CGAGGGTTCAAATCCCTCCGCTCCG---  
>tdbD00009988 *Streptomyces\_coelicolor* A3(2) 100226 Ser GGA  
-GGAGGATTCGCTAGT--GGCTAGGGCGCAGCCTTGGAAGCGTGTGGGG---GCAA---CCCCT-CACGAGTTTCAATCTCGTATCCTCCGCCA  
>tdbD00002638 *Streptomyces\_griseus* 1911 Ser TGA  
-GGAGGTTGCCCGAGC--GGCTAAGGGAACGGTCTTGAAAACCGTCTGGTG---GCGA---CATCAC-CGTGGGTTCAAATCCCACACCCTCCG---  
>tdbD00010157 *Symbiobacterium\_thermophilum* IAM 14863 292459 Ser CGA  
-GGAGGGTTGCCGAGT--GGTTAAGGTGCCGCTCTCGAAAAGCGGTGTGGCT---TAAC--GGCCAC-CGTGGGTTTCAATCCCACCCCTCCTCCGCCA  
>tdbD00010159 *Symbiobacterium\_thermophilum* IAM 14863 292459 Ser CGA  
-GGAGAGTTGCCGAGG--GGTTAAGGTGCCGCTCTCGAAAAGCGGTGTGGTG---ATG---AGCCAC-CGTGGGTTTCAATCCCACCCCTCCTCCGCCA  
>tdbD00010161 *Symbiobacterium\_thermophilum* IAM 14863 292459 Ser GCT  
-GGAGGATAACCCAAGT--GGTTGAAGGGGCGGCTTTGCTAAAGCTGTAGGGGGC--GCA--AGCCCG-CGAGGGTTTCAATCCCTCCTCCTCCGCCA  
>tdbD00010162 *Symbiobacterium\_thermophilum* IAM 14863 292459 Ser GCT  
-GGAGGATAACCCAAGT--GGCTGAAGGGGCGGCTTTGCTAAAGCTGTAGGGGGC--GCA--AGCCCG-CGAGGGTTTCAAATCCCTCCTCCTCCGCCA  
>tdbD00010158 *Symbiobacterium\_thermophilum* IAM 14863 292459 Ser GGA  
-GGAGAGTTGCCGAGT--GGTTAAGGTGCAGCATTGGAATGCTGTGTACGG---GAAA---CCGTAC-CGTGGGTTTCAATCCCACCCCTCCTCCGCCA  
>tdbD00010160 *Symbiobacterium\_thermophilum* IAM 14863 292459 Ser GGA  
-GGAGAGTTGCCGAGT--GGTFCGAAAGTGCAGCATTGGAATGCTGTGTACGG---ATA--ACCGTAC-CGTGGGTTTCAATCCCACCCCTCCTCCGCCA  
>tdbD00002666 *Synechococcus* sp. 1131 Ser GGA  
-GGAGAGTTGCCGAGC--GGTTGAAGGCGCAGCATTGGAATGCTGTGTAGGG---TAA---CTCTAA-CGAGGGTTTCAATCCCTCCTCCTCCG---  
>tdbD00002665 *Synechocystis* sp. 1143 Ser CGA

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>tdbD00009938 Thermosynechococcus\_elongatus\_BP-1\_197221 Ser CGA  
-GGAGAGGTGGCAGAGT--GGTTGAATGCGCTTGACTCGAAATCAAGTTTAGGG---TAAC--ACCTAA-CGGGGGTTTCAATCCCCCCTCTCCG---  
>tdbD00009937 Thermosynechococcus\_elongatus\_BP-1\_197221 Ser GCT  
-GGAGAGGTGGCTGAGT--GGTCAAAAGCGGAGATTGCTAATCTGTGTATAGGCAGGTAACCTCTATC-CGAGGGTTTCAATCCCTCCCTCTCCG---  
>tdbD00009935 Thermosynechococcus\_elongatus\_BP-1\_197221 Ser GGA  
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-GGAGAGATGGCAGAGT--GGTCAATGCGCTCGACTTGAATCGAGTGTGGCA---GTGA--TGCCAC-CGAGGGTTTCAATCCCTCTCTCCG---  
>tdbD00009687 Thermotoga\_maritima\_MSB8\_243274 Ser CGA  
-GGAGGCGTGTCCGAAGT--GGCT-AAGGAGCCGGTCTCGAAACCGGTGGGCC---GTGA---GGCCCTTGTGGGTTTCAATCCCACCCTCTCCGCCA  
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>tdbD00010200 Thermus\_thermophilus\_HB27\_262724 Ser CGA  
--GAGGGGTGCGGAGC--GGTTGAACCGGCGGTCTCGAAACCGGTAGGCCCC--TCGC-GGGGCCT-CGCGGGTTTCAATCCCACCCTCTCCGCCA  
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>tdbD00010203 Treponema\_denticola\_ATCC\_35405\_243275 Ser GGA  
-GGAGAGATGTCGAGT--GGTCAAGGTACACGATTGGAAGTCTGTGTGCCA---GAGA--TGGTAC-CGAGGGTTTCAATCCCTCTCTCCG---  
>tdbD00010204 Treponema\_denticola\_ATCC\_35405\_243275 Ser TGA  
-GGAGCGATGGCCGAGC--GGTTGAAGGCGGCGGTCTTGAACCGGTGTGCT---GATA---GGTAC-CGGGGGTTTCAATCCCTCTCGCTCCG---  
>tdbD00002630 Treponema\_pallidum\_160 Ser GGA  
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>tdbD00002633 Treponema\_pallidum\_160 Ser TGA  
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>tdbD00010028 Tropheryma\_whipplei\_str.\_Twist\_203267 Ser GCT  
-GGAGACGTCCATAGCCAGTCTAGTGCGCCACCTGCTAAGGTGGAGTGGCC---GAAA--GGGTAC-CGTGGGTTTCAATCCCACCCTCTCCG---  
>tdbD00010029 Tropheryma\_whipplei\_str.\_Twist\_203267 Ser GGA  
-GGAGGATTCGCTAGT--GGCTATGGCGCGGCTTGGAAAGCGCGTTGGGT---GCAA---GCCCT-CAGGGGTTTCAATCCCTATCTCCG---  
>tdbD00010027 Tropheryma\_whipplei\_str.\_Twist\_203267 Ser TGA  
-GGAGGGCTGTCCGAGC--GGCTAAGGAGCCGGTCTTGAACCGGTGAGCA---GAGA---TGCTC-CGTGGGTTTCAATCCCACGCCCTCCG---  
>tdbD00009623 Ureaplasma\_parvum\_serovar\_3\_38504 Ser TGA  
-GGAGAAATACCCAAGTCCGGCTGAAGGGATCAGTCTTGAACCTGAGAGGCGAT--GCA--AGTCGCG-CGGGGGTTTCAATCCCTCTTCTCCGCCA  
>tdbD00009612 Vibrio\_cholerae\_O1\_biovar\_El\_Tor\_str.\_N16961\_243277 Ser TGA  
-GGAGAGATGGCTGAGT--GGTTGAAAGCACCGGTCTTGAACCGGCGATGGTT--AAT--AGCTATC-CTAGGGTTTCAATCCCTATCTCTCCGCCA  
>tdbD00010207 Wolbachia\_endosymbiont\_of\_Drosophila\_melanogaster\_163164 Ser GCT  
-GGAAGGGTGGCCGAGC--GGCTGAAGGCGGCGGTTTGTCTAAACCGTTATACGACC-CAAAAGTCTGAT-CGAGGGTTTCAATCCCTCTCTCCG---  
>tdbD00010205 Wolbachia\_endosymbiont\_of\_Drosophila\_melanogaster\_163164 Ser GGA  
-GGAAGGGTGGCTGAGT--GGTCTAAAGCACAGCTTGGAAAGCGTGCACATAT--GAAA--ATATGT-CGGGGGTTTCAATCCCCCTTTTCCG---  
>tdbD00009951 Xanthomonas\_axonopodis\_pv.\_citri\_str.\_306\_190486 Ser CGA  
-GGAGAGGTGGCAGAGC--GGTTGAATGTACTGACTCGAAATCAGGCAGGCGTT--TAT--AGCGCT-CGGGGGTTTCAATCCCCCTCTCCGCCA  
>tdbD00009954 Xanthomonas\_axonopodis\_pv.\_citri\_str.\_306\_190486 Ser GCT  
-GGAGCGATGCCCCGAGC--GGCTGAAGGGGCTCCCTGCTAAGGGAGTATAGGGTC-AAA-AGCTCTAT-CGAGGGTTTCAATCCCTCTCGCTCCGCCA  
>tdbD00009952 Xanthomonas\_axonopodis\_pv.\_citri\_str.\_306\_190486 Ser GGA  
-GGAGAGGTGTCGAGT--GGTTGAAGGACAGCCTGGAAGTGTGTAAGCGTCT-AAA-CCGCGTCT-CGGGGGTTTCAATCCCTCTCTCCGCCA  
>tdbD00009953 Xanthomonas\_axonopodis\_pv.\_citri\_str.\_306\_190486 Ser TGA  
-GGAGAGATGGCCGAGC--GGTTTAAAGCACCGGTCTTGAACCGGCGAAGGG---TCAA--ACCTTC-CGTGGGTTTCAATCCCACCTCTCTCCGCCA  
>tdbD00009695 Xylella\_fastidiosa\_9a5c\_160492 Ser CGA  
-GGAGAGATGCGCGAGC--GGCTGAACGAGCAGCGTCTCGAAACCGGAGTAGGG---GCAA--CTCTAC-CGGGGGTTTCAATCCCCCTCTCTCCGCC-  
>tdbD00009692 Xylella\_fastidiosa\_9a5c\_160492 Ser GCT  
-GGAGTATGCCCCGAGA--GGCCGAAGGGGCTCCCTGCTAAGGGAGTATAGGGTC-AAA-ACTCTAT-CGAGGGTTTCAATCCCTCTACTCCGCCA  
>tdbD00009694 Xylella\_fastidiosa\_9a5c\_160492 Ser TGA  
-GGAAGCGTGGCAGAGT--GGTCAATGTCACCGGTCTTGAACCGGCAACGG---GCAA---CCGTT-CGTGAGTTTCAATCTCACCGCTTCCGCCA

>tdbD00009698 Xylella\_fastidiosa\_9a5c\_160492\_Ser\_TGA  
-GGAAGTGTGGCCGAGC--GGTTGAAGGCACCGGTCTTGAAACCCGGCACC---GAAA---GGGTT-CCAGAGTTTCAATCTCTGCGCTTCCGCC-  
>tdbD00010164 Yersinia\_pestis\_biovar\_Microtus\_str.\_91001\_229193\_Ser\_TGA  
-GGAAGGATGGCCGAGT--GGTTAAGGCAACGGTCTTGAAACCCGTCGACTG---TAA---CAGGTCCTAGAGTTTCAATCTCTATCCTTCCGCCA  
>tdbD00010165 Yersinia\_pestis\_biovar\_Microtus\_str.\_91001\_229193\_Ser\_TGA  
-GGAGGGTGGCCGAGT--GGCTGAAGGCAACCGGTCTTGAAACCCGTCGACGG---GTAA---CCGTT-CGAGAGTTTCAATCTCTCTCTCCGCCA  
>tdbD00010760 Acinetobacter\_sp.\_ADP1\_62977\_Thr\_GGT  
-GCTCTTATAGCTCAGT--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GTCTCGAGTTTCAATCTCGATAAGAGCTCCA  
>tdbD00010432 Agrobacterium\_tumefaciens\_str.\_C58\_176299\_Thr\_GGT  
-GCTGTATAGCTCAGG--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GCCGAGAGTTTCAATCTCTCTAGCAGCACCA  
>tdbD00010387 Aquifex\_aeolicus\_VF5\_224324\_Thr\_GGT  
-GCCAGGTAGCTCAGTC--GGT--AGAGCGCACCCCTTGGTAAGGGTGGAG-----GGCGCCGGTTTCAAGTCCGGTCTGGGCTCCA  
>tdbD00010670 Bacillus\_anthraxis\_str.\_Ames\_198094\_Thr\_GGT  
-GTTCCATAGCTCAGT--GGT--AGAGCACTTCCATGGTAAGGAAGAG-----GTCACCGGTTTCAAGCCCGGTTGGAAGCT---  
>tdbD00010604 Bacillus\_halodurans\_C-125\_272558\_Thr\_GGT  
-GTTCCATAGCTCAGTC--GGT--AGAGCACTACCATGGTAAGGTAGGG-----GTCAGCGGTTTCAAGTCCGGTGGGAAGCT---  
>tdbD00002950 Bacillus\_subtilis\_1423\_Thr\_GGT  
-GTTCCATAGCTCAGG--GGT--AGAGCACTTCCATGGTAAGGAAGAG-----GTCAGCGGTTTCAAGCCCGCTGGGAAGCT---  
>tdbD00010666 Bacteroides\_thetaiotaomicron\_VPI-5482\_226186\_Thr\_GGT  
-GCTGTATAGCTCAGC--GGT--AGAGCACTTCCCTTGGTAAGGAAGAG-----GTCCCGGTTTCAAGTCCCGGTAACAGCT---  
>tdbD00010676 Bartonella\_henselae\_str.\_Houston-1\_283166\_Thr\_GGT  
-GTCGCGTAGCTCAGT--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GTCGAGAGTTTCAATCTCTCTCGCAGCACCA  
>tdbD00010771 Bartonella\_quintana\_str.\_Toulouse\_283165\_Thr\_GGT  
-GTCGCGTAGCTCAGT--GGC--AGAGCACTCCCTTGGTAAGGGAGAG-----GTCGAGAGTTTCAATCTCTCTCGCAGCACCA  
>tdbD00002945 Borrelia\_burgdorferi\_139\_Thr\_GGT  
-GCCCTTATAGCTCAGT--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GTCGCGGTTTCAAGTCCGATTGAGGGCT---  
>tdbD00010608 Bradyrhizobium\_japonicum\_USDA\_110\_224911\_Thr\_GGT  
-GTCGCGTAGCTCAGT--GGT--AGAGCACTCCATGGTAAGGGAGAG-----GTCGAGAGTTTCAATCTGTCTGGCAGCACCA  
>tdbD00010306 Buchnera\_aphidicola\_str.\_APS\_(Acyrtosiphon\_pisum)\_107806\_Thr\_GGT  
-GCTGATATAGCTCAGTA--GGT--AGAGCACACCCTTGGTAAGGGAGAG-----GTCCCGAGTTTCAATCTGGGTATCAGCA---  
>tdbD00010644 Buchnera\_aphidicola\_str.\_Bp\_(Baizongia\_pistaciae)\_224915\_Thr\_GGT  
-GCTGATATAGCTCAGTTTGGT--AGAGCACACCCTCGGTAAGGGTGGAG-----GTTCCAGTTTCAACCTGGGTATCAGCA---  
>tdbD00010534 Buchnera\_aphidicola\_str.\_Sg\_(Schizaphis\_graminum)\_198804\_Thr\_GGT  
-GCTGATATAGCTCAGTA--GGT--AGAGCACACCCTTGGTAAGGGTGGAG-----GTCCCGAGTTTCAACCTGGGTATCAGCA---  
>tdbD00002966 Campylobacter\_jejuni\_197\_Thr\_GGT  
-GCTGTATAGCTCAGA--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GTCGCGGTTTCAATCCCGCTATGAGCTCCA  
>tdbD00010350 Campylobacter\_jejuni\_subsp.\_jejuni\_NCTC\_11168\_192222\_Thr\_GGT  
-GCTGTATAGCTCAGA--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GTCGCGGTTTCAATCCCGCTATGAGCTCCA  
>tdbD00010774 Candidatus\_Blochmannia\_floridanus\_203907\_Thr\_GGT  
-GCTGATATAGCTCAGG--GGC--AGAGCACTCCCTTGGTAAGGGTGGAG-----GTCGCGAGTTTCAATCTGCTTATCAGCA---  
>tdbD00010687 Candidatus\_Proteochlamydia\_amoebophila\_UWE25\_264201\_Thr\_GGT  
-GCCAGATAGCTCAGT--GGT--AGAGCACTTGCATGGTAAGCAAAAG-----GTCGTAGGTTTCAATCTCTATCTGGGCA---  
>tdbD00010353 Caulobacter\_crescentus\_CB15\_190650\_Thr\_GGT  
-GCCCGGTAGCTCAGT--GGT--AGAGCGCATCCTTGGTAAGGGTGGAG-----GTCGCGAGTTTCAATCTGCCGGCGGCACCA  
>tdbD00010399 Chlamydia\_muridarum\_Nigg\_243161\_Thr\_GGT  
-GCCAGGTAGCTCAGT--GGT--AGAGCACTTGCATGGTAAGCAAGTG-----GCCGTAGGTTTCAATCTCTATCTGGGCA---  
>tdbD00003085 Chlamydia\_trachomatis\_813\_Thr\_GGT  
-GCGCCGTAGCTCAT---GGT--AGAGCACTTGCATGGTAAGCAAGTG-----GCCGTAGGTTTCAATCTCTATCTGGGCA---  
>tdbD00010300 Chlamydia\_trachomatis\_813\_Thr\_GGT  
-GCCAGATAGCTCAGT--GGT--AGAGCACTTGCATGGTAAGCAAGCG-----GTCGTAGGTTTCAATCTCTATCTGGGCA---  
>tdbD00010291 Chlamydia\_pneumoniae\_AR39\_115711\_Thr\_GGT  
-GCCAGATAGCTCAGT--GGT--AGAGCACTTGCATGGTAAGCAAGCG-----GTCGTAGGTTTCAATCTCTATCTGGGCA---  
>tdbD00010528 Chlorobium\_tepidum\_TLS\_194439\_Thr\_GGT  
-GCTGATAGCTCAGTC--GGT--AGAGCACTTCCCTTGGTAAGGAAGAG-----GTCATCGGTTTCAAGTCCGATCATCAGCT---  
>tdbD00010405 Clostridium\_acetobutylicum\_ATCC\_824\_272562\_Thr\_GGT  
-GCCATGTGGCTCAGTA--GGT--AGAGCGTCACCTTGGTAAGGTGGAG-----GTCGCCAGTTTCAATCTGGTGGGCTCCA  
>tdbD00010396 Clostridium\_perfringens\_str.\_13\_195102\_Thr\_GGT  
-GTCACGTAGCTCAGTC--GGC--AGAGCGTCGCTTGGTAAGGGCGAG-----GTCGTGCGTTTCAATCCCGATCGTGGGCTCCA  
>tdbD00010611 Clostridium\_tetani\_E88\_212717\_Thr\_GGT  
-GCCATGTAGCTCAGTA--GGT--AGAGTGCACCTTGGTAAGGTGGAG-----GTCACCGGTTTCAATCCCGGTCATGGGCTCCA  
>tdbD00010680 Corynebacterium\_diphtheriae\_NCTC\_13129\_257309\_Thr\_GGT  
-GCCCCCTTAGCTCAGTC--GGC--AGAGCGTTTCCATGGTAAGGAAAAG-----GTCGACAGTTTCAATCTGTCTAGGGGCT---  
>tdbD00010577 Corynebacterium\_efficiens\_YS-314\_196164\_Thr\_GGT  
-GCCCCCTTAGCTCAGTC--GGC--AGAGCGTTTCCATGGTAAGGAAAAG-----GTCACAGTTTCAATCTGTCTAGGGGCT---  
>tdbD00010540 Corynebacterium\_glutamicum\_ATCC\_13032\_196627\_Thr\_GGT  
-GCCCCCTTAGCTCAGTC--GGT--AGAGCGTTTCCATGGTAAGGAAAAG-----GTCACAGTTTCAATCTGTCTAGGGGCT---  
>tdbD00010639 Coxiella\_burnetii\_RSA\_493\_227377\_Thr\_GGT  
-GCCACATAGCTCAGGC--GGT--AGAGCACTTCCCTTGGTAAGGAAGAG-----GTCACCGGTTTCAAGTCCGGTGTGGGCTCCA  
>tdbD00010356 Deinococcus\_radiodurans\_R1\_243230\_Thr\_GGT  
-GTCCTGTAGCTCAGC--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GTCATCGGTTTCAAGTCCGATCAGGAGCTCCA  
>tdbD00010740 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Thr\_GGT  
-GCCATGTGGCTCAGTC--GGT--AGAGCACATCCTTGGTAAGGATGAG-----GTCAGCAGTTTCAATCTGTCTAGGGGCTCCA  
>tdbD00010743 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Thr\_GGT  
-GCCACATAGCTCAGGC--GGT--AGAGCACTTCCCTTGGTAAGGAAGAG-----GTCATGAGTTTCAAGTCTCTATCTGGGCTCCA  
>tdbD00010613 Enterococcus\_faecalis\_V583\_226185\_Thr\_GGT

-GCCGCCCTTAGCTCAGTT-GGT--AGAGCACCACCATTGGTAAGGTGGGG-----GTCGCCGGTTCAAGCCCGGCAGGTGGCT---  
>tdbD00002956 Escherichia coli 562 Thr GGT  
-GCTGATATGGCTCAGTT-GGT--AGAGCGCACCCCTTGGTAGGGGTGGG-----GTCCCAGTTTCGACTCTGGGTATCAGCACCA  
>tdbD00002957 Escherichia coli 562 Thr GGT  
-GCTGATATAGCTCAGTT-GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCAATCTGCCTATCAGCACCA  
>tdbD00002960 Escherichia coli 562 Thr GGT  
-GCTGATATGGCTCAGTT-GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCCCAGTTTCGACTCTGGGTATCAGCACCA  
>tdbD00010705 Geobacter\_sulfurreducens\_PCA\_243231 Thr GGT  
-GCCACATAGCTCAGGA-GGT--AGAGCACTTCCCTTGGTAAGGAAGAG-----GTCACCGGTTTCGAGTCCGGTTGTGGGCTCCA  
>tdbD00002969 Haemophilus influenzae 727 Thr GGT  
-GCTGATATAGCTCAGTT-GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCGGCGGTTCAAATCCGCCTATCAGCACCA  
>tdbD00002949 Helicobacter pylori 210 Thr GGT  
-GCCTATATAGCTCAGA--GGC--AGAGCACTTCCCTTGGTAAGGAAGAG-----GTCGGCGGTTCAATTCGGCTTATAGGCTCCA  
>tdbD00010709 Lactobacillus\_johnsonii\_NCC\_533\_257314 Thr GGT  
-GCCGTTTTAGCTCAGGA-GGT--AGAGCACC GCCGTGGTAAGGAGGAG-----GTCCCAGTTCAAATCTGGGAAACGGCT---  
>tdbD00010618 Lactobacillus\_plantarum\_WCF51\_220668 Thr GGT  
-GCCGTTTTAGCTCAGCA-GGT--AGAGCACTTCCATGGTAAGGAAGAG-----GTCGGCAGTTCAAATCTGCTAAACGGCT---  
>tdbD00010580 Leptospira\_interrogans\_serovar\_Lai\_str.\_56601\_189518 Thr GGT  
-GCCCTCTTAGCTCAGC--GGT--AGAGCACTTCCATGGTAAGGAAGGG-----GTCACCAGTTCAAAGCTGGTAGAGGGCT---  
>tdbD00010391 Listeria\_innocua\_Clip11262\_272626 Thr GGT  
-GCCGCTTTAGCTCAGTT-GGT--AGAGCACTTCCATGGTAAGGAAGGG-----GTCGTCGGTTCAAATCCGACAAGTGGCT---  
>tdbD00002962 Listeria\_monocytogenes\_1639 Thr GGT  
-GCCGCTTTAGCTCAGTT-GGT--AGAGCACTTCCATGGTCCGGAAGGG-----GTCGTCGGTTCAAATCCGACAAGTGGCT---  
>tdbD00010632 Mycobacterium\_bovis\_AF2122/97\_233413 Thr GGT  
-GCCCCCTTAGCTCAGTC-GGC--AGAGCGTTTCCATGGTAAGGAAAAG-----GTCAACGGTTTCGATTCCGTTAGGGGGCT---  
>tdbD00010323 Mycobacterium\_leprae\_TN\_272631 Thr GGT  
-GCCCCCTTAGCTCAGTC-GGT--AGAGCGTTTCCATGGTAAGGAAAAG-----GTCAACGGTTTCGATTCCGTTAGGGGGCT---  
>tdbD00010631 Mycoplasma\_gallisepticum\_R\_233150 Thr GGT  
-GCCGAATTAGTTTGTAG--GGC--AAAACAGATGCATGGTAAGCATCAA-----A-GACAAGTTTCGATTCTCGTATTCCGGCACCA  
>tdbD00002933 Mycoplasma\_genitalium\_2097 Thr GGT  
-GCCGAATTGGTTTTAGG--GGC--AAAACAGATCCATGGTAAGGATCAG-----A-GAACAGTTTCGACTCTGTTATTCCGGCACCA  
>tdbD00002938 Mycoplasma\_pneumoniae\_2104 Thr GGT  
-GCCGAATTAGTTTGTAG--GGC--AAAACAGATCCATGGTAAGGATCAG-----G-AAACAGTTTCGACTCTGTTATTCCGGCACCA  
>tdbD00010362 Mycoplasma\_pneumoniae\_M129\_272634 Thr GGT  
-GCCGAATTAGTTTGTAG--GGC--AAAACAGATCCATGGTAAGGATCAG-----A-GAACAGTTTCGACTCTGTTATTCCGGCACCA  
>tdbD00010429 Mycoplasma\_pulmonis\_UAB\_CTIP\_272635 Thr GGT  
-GCCAATATAGCTCAGCA-GGC--AGAGCACATCCATGGTAAGGATGGG-----GTCGCTGGTTCAAGTCCAGTTATTGGCACCA  
>tdbD00010312 Neisseria\_meningitidis\_MC58\_122586 Thr GGT  
-GCCCATGTAGCTCAGG--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GTCGGCAGTTCAAATCTGCCATGGGCACCA  
>tdbD00010315 Neisseria\_meningitidis\_Z2491\_122587 Thr GGT  
-GCCCATGTAGCTCAGG--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GCCGGCAGTTCAAATCTGCCATGGGCACCA  
>tdbD00010661 Nitrosomonas\_europaea\_ATCC\_19718\_228410 Thr GGT  
-GCCCATGTAGCTCAGT--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GTCGCCAGTTCAAATCTGCCATGGGCACCA  
>tdbD00010427 Nostoc\_sp.\_PCC\_7120\_103690 Thr GGT  
-GCCCGTGTGGCTCAGT--GGT--AGAGCACACCCTTGGTAAGGGTGAG-----GTCACGAGTTCAAATCCTCGTCACGGGCT---  
>tdbD00010583 Oceanobacillus\_ihayensis\_HTE831\_221109 Thr GGT  
-GCTTCCATAGCTCAGTTCCGGT--AGAGCACTTCCATGGTAAGGAAGGG-----GTCAGCGGTTCAAAGTCCGCTTGAAGCT---  
>tdbD00010683 Onion\_yellow\_ phytoplasma\_OY-M\_262768 Thr GGT  
-GCCCTTATAGTTTAAAC--GGC--AGAACGTAGCAATGGTAATGCTGAA-----A-TACAAGTTCAAATCTGTAAAGGCACCA  
>tdbD00010690 Photorhabdus\_luminescens\_subsp.\_laumondii\_TTO1\_243265 Thr GGT  
-GCTGATATAGCTCAGTT-GGT--AGAGCACACCCTTGGTAAGGGTGAG-----GCCGGCAGTTTCAATCTGCCTATCAGCACCA  
>tdbD00010692 Photorhabdus\_luminescens\_subsp.\_laumondii\_TTO1\_243265 Thr GGT  
-GCTGATATAGCTCAGTT-GGT--AGAGCACACCCTTGGTAAGGGTGAG-----GTCCCAGTTTCAATCTGGGTATCAGCACCA  
>tdbD00010715 Porphyromonas\_gingivalis\_W83\_242619 Thr GGT  
-GCCAATGTAGCTCAGC--GGT--AGAGCACTTCCCTTGGTAAGGAAGAG-----GTCCCGGTTCAAAGTCCCGCATCGGCT---  
>tdbD00010751 Propionibacterium\_acnes\_KPA171202\_267747 Thr GGT  
-GCCCTATAGCTCAGTA-GGC--AGAGCGTCTCCATGGTAAGGAGAAG-----GTCAGCAGTTTCGATTCTGCTTGGGGGCT---  
>tdbD00002965 Pseudomonas\_aeruginosa\_287 Thr GGT  
-GCTCATGTAGCTCAGTT-GGT--AGAGCACACCCTTGGTAAGGGTGAG-----GTCAGCGGTTCAAATCCGCTCATGAGCTCCA  
>tdbD00010668 Pseudomonas\_syringae\_pv.\_tomato\_str.\_DC3000\_223283 Thr GGT  
-GCTCTGTAGCTCAGTT-GGT--AGAGCACACCCTTGGTAAGGGTGAG-----GTCAGCGGTTCAAATCCGCTCAAAGAGCTCCA  
>tdbD00010425 Ralstonia\_solanacearum\_GMI1000\_267608 Thr GGT  
-GCCCATGTGGCTCAGT--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GTCGGCAGTTTCGATCCTGCCATGGGCACCA  
>tdbD00002970 Rhizobium\_leguminosarum\_384 Thr GGT  
-GCTGCCGTAGCTCAGT--GGT--AGAGCACACCCTTGGTAAGGGTGAG-----GTCGGTGGTTCAAATCCCCTCGGCAGCACCA  
>tdbD00010659 Rhodopirellula\_baltica\_SH\_1\_243090 Thr GGT  
-GCTGCTGTAGCTCAGG--GGT--AGAGCGCCTCCTTGGTAAGGATGAG-----GTCATGGGTTCAAATCCCCTCAGCAGCT---  
>tdbD00010695 Rhodopseudomonas\_palustris\_CGA009\_258594 Thr GGT  
-GCTGCCGTAGCTCAGT--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GTCGACAGTTCAAATCCTGTCCGGCAGCACCA  
>tdbD00010408 Rickettsia\_conorii\_str.\_Malish\_7\_272944 Thr GGT  
-GCTACTATAGCTCAGG--GGT--AGAGCACTTCATGGTAATGAAGAG-----GTCGGGGGTTTCGATTCCCCTAGTAGCACCA  
>tdbD00010537 Rickettsia\_prowazekii\_str.\_Madrid\_E\_272947 Thr GGT  
-GCTACTATAGCTCAGG--GGT--AGAGCACTTCATGGTAATGAAGAG-----GCCGTGGGTTCAAATCCCCTAGTAGCACCA  
>tdbD00010718 Rickettsia\_typhi\_str.\_Wilmington\_257363 Thr GGT  
-GCTACTATAGCTCAGA--GGT--AGAGCACTTCATGGTAATGAAGAG-----GTCGTTGGTTCAAATCCCCTAGTAGCACCA



>tdbD00010589 *Shewanella oneidensis* MR-1 211586 Thr GGT  
-GCTGATATGGCTCAGTT-GGT--AGAGCACACCCCTGGTAAGGGTGAG-----GTCGGCAGTTTCAATCTGCCTATCAGCACCA  
>tdbD00010590 *Shewanella oneidensis* MR-1 211586 Thr GGT  
-GCTGATATGGCTCAGTC-GGT--AGAGCGCATCCCTGGTAAGGATGAG-----GTCCCCAGTTTCGATTCTGGGTATCAGCACCA  
>tdbD00002955 *Stigmatella aurantiaca* 41 Thr GGT  
-GCCCTGATAGCTCAGTT-GGT--AGAGCGCATCCCTGGTAAGGATGAG-----GTCACCAGTTTCAATCCTGGTTCAGGGCTCCA  
>tdbD00010600 *Streptococcus agalactiae* 2603V/R 208435 Thr GGT  
-GCCGTATAGTTAAAT--GGT--ATAATAGAGCAATGGTAATGCTCAG-----T-TCCGAGTTTCAATTCTCGGTGGTGCA---  
>tdbD00010544 *Streptococcus agalactiae* NEM316 211110 Thr GGT  
-GCCCTATAGCTTAAAT--GGT--ATAATAGAGCAATGGTAATGCTCAG-----T-TCCGAGTTTCAATTCTCGGTGGTGCA---  
>tdbD00010603 *Streptococcus mutans* UA159 210007 Thr GGT  
-GCCGTATAGTTAAAT--GGT--ATAATAGAGCAATGGTAATGCTCCG-----T-TCCGAGTTTCGATTCTCGGTGGTGCA---  
>tdbD00010402 *Streptococcus pneumoniae* TIGR4 170187 Thr GGT  
-GCTGATTTAGCTCAGTT-GGT--AGAGCGCATCCCTGGTAAGGATGAG-----GTCGCCGTTTCAATCCCGCAATTAGCA---  
>tdbD00010401 *Streptococcus pyogenes* M1 GAS 160490 Thr GGT  
-GCCGTGTAGTTAAAT--GGT--ATAATAAGCAATGGTAATGCTTCG-----T-TCCGAGTTTCGATTCTCGGTGGTGCA---  
>tdbD00010648 *Streptomyces avermitilis* MA-4680 227882 Thr GGT  
-GCCCCATAGCTCAGTC-GGC--AGAGCGTCTCCATGGTAAGGAGAAG-----GTCAACGTTTCGATTCCGTTTGGGGCTCCA  
>tdbD00010652 *Streptomyces avermitilis* MA-4680 227882 Thr GGT  
-GCCCCAATAGCTCAGTC-GGC--AGAGCGTCTCCATGGTAAGGAGAAG-----GTCTACGTTTCGATTCCGTTTGGGGCT---  
>tdbD00010586 *Streptomyces coelicolor* A3(2) 100226 Thr GGT  
-GCCCCAATAGCTCAGTC-GGC--AGAGCGTCTCCATGGTAAGGAGAAG-----GTCAACGTTTCGATTCCGTTTGGGGCT---  
>tdbD00010587 *Streptomyces coelicolor* A3(2) 100226 Thr GGT  
-GCCCTATAGCTCAGTC-GGT--AGAGCGTCTCCATGGTAAGGAGAAG-----GTCAACGTTTCGATTCCGTTTGGGGCTCCA  
>tdbD00010722 *Symbiobacterium thermophilum* IAM 14863 292459 Thr GGT  
-GCTGATGTAGCTCAGGA-GGT--AGAGCACGTCCTTGGTAAGGACGAG-----GTCACCGTTTCGAGCCCGGTATCAGCTCCA  
>tdbD00010723 *Symbiobacterium thermophilum* IAM 14863 292459 Thr GGT  
-GCTGATGTAGCTCAGGT-GGT--AGAGCACGTCCTTGGTAAGGACGAG-----GTCACCGTTTCGAGCCCGGTATCAGCTCCA  
>tdbD00002973 *Synechocystis* sp. 1143 Thr GGT  
-GCCCTGTAGCTCAGT--GGT--AGAGCACACCCCTGGTAAGGGTGAG-----GTCACGAGTTTCAATCCTCGTCAAGGGCT---  
>tdbD00010554 *Thermoanaerobacter tengcongensis* MB4 273068 Thr GGT  
-GCCACGTAGCTCAGTA-GGC--AGAGCGTCGCTTGGTAAGGCGGAG-----GTCACCGTTTCGATCCCGGTGCGGGCTCCA  
>tdbD00010548 *Thermosynechococcus elongatus* BP-1 197221 Thr GGT  
-GCCCGTGTAGCTCAGT--GGT--AGAGCACACCCCTGGTAAGGGTGAG-----GTCACGAGTTTCAATCCTCGTCAAGGGCT---  
>tdbD00010376 *Thermotoga maritima* MSB8 243274 Thr GGT  
-GCAGCGTAGCTTCAAGCGGT--GGAGCGCGCCTTGGTAAGGCGGAG-----GGTGTGGTTTCGAGTCCCACCGCTGCTCCA  
>tdbD00002953 *Thermus thermophilus* 274 Thr GGT  
-GTCGCGTAGCTCAGTA-GGT--AGAGCACACCCCTGGTAAGGGTGAG-----GTCGCCGTTTCGAGCCCGCGGAGCTCCA  
>tdbD00010757 *Treponema denticola* ATCC 35405 243275 Thr GGT  
-GCTCTGTAGCTCAGTC-GGC--AGAGCACAACCATGGTAAGGTTGGG-----GTCAGCAGTTTCAATCTGCTCGGGAGCT---  
>tdbD00002942 *Treponema pallidum* 160 Thr GGT  
-GTTCTGTAGCTCAGTT-GGC--AGAGCGCAACCATGGTAAGGTTGAG-----GTCAGCGTTTCAATCCCGCTCGGAAGCT---  
>tdbD00010621 *Tropheryma whippelii* str. Twist 203267 Thr GGT  
-GCCCCGTAGCTCAGT--GGC--AGAGCACTTCCATGGTAAGGAAGGG-----GTCGTAGTTTCAATCCTGACCCGGGGCT---  
>tdbD00010318 *Vibrio cholerae* O1 biovar El Tor str. N16961 243277 Thr GGT  
-GCTGATATAGCTCAGAT-GGT--AGAGCGCATCCCTGGTAAGGATGAG-----GTCGGCAGTTTCGATTCTGCCTATCAGCACCA  
>tdbD00010759 *Wolbachia endosymbiont of Drosophila melanogaster* 163164 Thr GGT  
-GCCGTGTAGCTCAGGT-GGT--AGAGTACGTCATTGGTAATGACGAG-----GTCCCAAGTTTCGAGTCTTGGTAACGGCA---  
>tdbD00010559 *Xanthomonas axonopodis* pv. *citri* str. 306 190486 Thr GGT  
-GTCACGTAGCTCAGTC-GGT--AGAGCACCTCCTTGGTAAGGAGGAG-----GTCGAAGTTTCGATTCTCTTTCGTGAGCACCA  
>tdbD00010379 *Xylella fastidiosa* 9a5c 160492 Thr GGT  
-GTCACGTAGCTCAGTC-GGT--AGAGCACCTCCTTGGTAAGGAGGAG-----GTCGATGGTTTCGATTCCATTCGTGAGCACCA  
>tdbD00008444 *Acinetobacter* sp. ADP1 62977 Pro TGG  
-CGGAGCATAGCACAGCCTGGT--AGTGCACCTGGTTTGGGACCAGGGG-----GTCGTAGTTTCGAATCCTACTGCTCCGACCA  
>tdbD00002118 *Aeromonas hydrophila* 644 Pro TGG  
-CGGTGATTAGCGCAGCCGGT--AGCGCATCTGGTTTGGGACCAGAGG-----GTCAAAGTTTCGAATCCTTTATCACCGACCA  
>tdbD00008167 *Agrobacterium tumefaciens* str. C58 176299 Pro CGG  
-CGGAGTGTAGCGCAGTCTGGT--AGCGCACGTCGTTCCGGGACGACGGG-----GTCGGAGTTTCGAATCCTCTCACTCCGACCA  
>tdbD00008168 *Agrobacterium tumefaciens* str. C58 176299 Pro GGG  
-CGGAGCGTAGCGCAGCCGGT--AGCGCACTTACTGGGGTCAAGGG-----GTCGTGGTTTCGAATCCCGCCGCTCCGACCA  
>tdbD00008169 *Agrobacterium tumefaciens* str. C58 176299 Pro TGG  
--GGAGTGTAGCGCAGTCTGGT--AGCGCATCTGGTTTGGGACCAGAGG-----GTCGGGAGTTTCGAATCCTCTCACTCCGACCA  
>tdbD00008134 *Aquifex aeolicus* VF5 224324 Pro CGG  
-CGGGCGTAGCGCAGGT-GGT--AGCGCGTGGCTTCCGGGAGCCAGAG-----GTCGCCGTTTCGAGTCCGGTCCGCCCGA---  
>tdbD00008135 *Aquifex aeolicus* VF5 224324 Pro GGG  
-CGGGGTGTAGCGCAGGT-GGT--AGCGCGTGGCATGGGGGGCCAGAG-----GTCGCCGTTTCGAGTCCGGTCAACCCGACCA  
>tdbD00008136 *Aquifex aeolicus* VF5 224324 Pro TGG  
-CGGGCGTAGCTCAGGT-GGT--AGAGCGTCCGCTTGGGAGCCGAAG-----GTCGCCGTTTCAGTCCGGCCGCCCGA---  
>tdbD00008382 *Bacillus anthracis* str. Ames 198094 Pro TGG  
-CGGGAAGTGGCTCAGCTTGGT--AGAGCACCTGGTTTGGGACCAGGGG-----GTCGCAGTTTCAATCCTGTCTTCCCGACCA  
>tdbD00008383 *Bacillus anthracis* str. Ames 198094 Pro TGG  
-CGGGAAGTGGCTCAGCTTGGT--AGAGCACCTGGTTTGGGACCAGGGG-----GTCGCAGTTTCAATCCTGTCTTCCCGA---  
>tdbD00002112 *Bacillus circulans* 1397 Pro GGG  
-CGGGGTATGGCGCAGTCTGGT--AGCGCGCACCCCTGGGGTGGGTGAG-----GCCGTGGTTTCAATCCCGCTACTCCGACCA  
>tdbD00008324 *Bacillus halodurans* C-125 272558 Pro TGG

-CGGGAAGTAGCTCAGCTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTCAAATCCTGTCTTCCCGACCA  
>tdbD00002111 Bacillus\_subtilis\_1423\_Pro\_TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGCACATGGTTTGGGACCATGGG-----GTCGCAGGTTCGAATCCTGTCTTCCCGACCA  
>tdbD00008378 Bacteroides\_thetaiotaomicron\_VPI-5482\_226186\_Pro\_CGG  
-CGGAATGTAGCGCAGTT--GGT--AGCGCACTACGTTCCGGGACGTAGGG-----GTCGGGGCTTCGAGTCGCCTCATCCGA---  
>tdbD00008379 Bacteroides\_thetaiotaomicron\_VPI-5482\_226186\_Pro\_GGG  
-CGGGATGTAGCTCAGCCCGT--AGAGTACGCGTCTGGGGGGCGTGTG-----GTCGCAAGTTCGAATCTTGTCATCCCGA---  
>tdbD00008376 Bacteroides\_thetaiotaomicron\_VPI-5482\_226186\_Pro\_TGG  
-CGGGGTGTAGCGCAGTCCGGT--AGCGCACCTGCTTTGGGAGCAGGG-----GTCGTGGGTTTCGAATCCCGCTACCCCGA---  
>tdbD00008384 Bartonella\_henselae\_str.\_Houston-1\_283166\_Pro\_GGG  
-CGGAGCGTAGCGCAGCCTGGT--AGCGCACTTACTGGGGGTCAAGGG-----GTCGTGGGTTTCGAATCCCGCCGCTCCGACCA  
>tdbD00008385 Bartonella\_henselae\_str.\_Houston-1\_283166\_Pro\_TGG  
-CGGAGCGTAGCGCAGCCTGGT--AGCGCACCTGATTTGGGATCAGGG-----GTCGTAGGTTTCGAATCCTATCGCTCCGACCA  
>tdbD00008450 Bartonella\_quintana\_str.\_Toulouse\_283165\_Pro\_GGG  
-CGGAGCGTAGCGCAGCCTGGT--AGCGCACTTACTGGGGGTCAAGGG-----GTCGTGGGTTCAAATCCCGCCGCTCCGACCA  
>tdbD00008387 Bdellovibrio\_bacteriovorus\_HD100\_264462\_Pro\_GGG  
-CTGCGCGTGGCTCAGCTTGGT--AGAGCACTTGTCTGGGGTGCAAGAG-----GTCGCTGGTTCAAATCCAGTCGCGCAGACCA  
>tdbD00008384 Bdellovibrio\_bacteriovorus\_HD100\_264462\_Pro\_TGG  
-CGGGGAGTAGCGCAGTCTGGT--AGCGCATCTGGTTTGGGACCAGAG-----GTCGTAGGTTTCGAATCCTATCTCCCGACCA  
>tdbD00008302 Bifidobacterium\_longum\_NCC2705\_206672\_Pro\_CGG  
-CGGGCTGTAGCGCAGCTTGGT--AGCGCGCTTCGTTCCGGGACGAAGAG-----GCCGCGGGTTCAAATCCCGCCAGCCCGA---  
>tdbD00008304 Bifidobacterium\_longum\_NCC2705\_206672\_Pro\_GGG  
-CGGGCCGTAGCGCAGTTGGT--AGCGCACTTACTGGGGGTCAAGGG-----GTCGCGGGTTCAAATCCCGCCGCCCCGA---  
>tdbD00008303 Bifidobacterium\_longum\_NCC2705\_206672\_Pro\_TGG  
-CGGGCTATAGCGCAGTTGGT--AGCGCGCTGCTTTGGGAGCAGGAT-----GTCGTGGGTTCAAATCCCGCTAGCCCGA---  
>tdbD00002104 Borrelia\_burgdorferi\_139\_Pro\_TGG  
-CGGGATGTGGCTAGT--GGCT--AAGGCACCTGCTTTGGGAGCAGGG-----ATCGTGAGTTCGAATCCACCATCCCGA---  
>tdbD00008325 Bradyrhizobium\_japonicum\_USDA\_110\_224911\_Pro\_CGG  
-CGGAGTGTGGCTCAGCCCGT--AGAGCACTGCGTTCGGGACGCAGGG-----GTCGCAGGTTTCGAATCCTGCCACTCCGACCA  
>tdbD00008327 Bradyrhizobium\_japonicum\_USDA\_110\_224911\_Pro\_GGG  
-CGGAGCGTGGCGCAGCCCGT--AGCGCACTAGTCTGGGAGACTAGGG-----GTCGAGGTTCAAATCCTCTCGCTCCGACCA  
>tdbD00008326 Bradyrhizobium\_japonicum\_USDA\_110\_224911\_Pro\_TGG  
-CGGGGTATAGCGCAGCCTGGT--AGCGCGGAGTTTGGGTACTGCAG-----GTCGTTGGTTTCGAATCCAGCTGCCCGACCA  
>tdbD00008150 Brucella\_melitensis\_16M\_224914\_Pro\_CGG  
-CGGAGTGTAGCGCAGCCTGGT--AGCGCACCTCGTTCGGGACGAGGG-----GTCGAGGTTTCGAATCCTCTCACTCCGACCA  
>tdbD00008149 Brucella\_melitensis\_16M\_224914\_Pro\_TGG  
-CGGAGCGTAGCGCAGTCTGGT--AGCGCACCTGATTTGGGATCAGGG-----GTCGCAGGTTTCGAATCCTGCCGCTCCGACCA  
>tdbD00008070 Buchnera\_aphidicola\_str.\_APS\_(Acyrtosiphon\_pisum)\_107806\_Pro\_TGG  
-CGGGCAATAGCGCAGCTTGGT--AGCGCAACTGGTTTGGGACCAGTAG-----GTCAGAGGTTCAAATCCTCTTTCGCCGACCA  
>tdbD00008356 Buchnera\_aphidicola\_str.\_Bp\_(Baizongia\_pistaciae)\_224915\_Pro\_TGG  
-CGGGAGTAGCGCAGTTTGGT--AGCGCAACTGGTTTGGGACCAGTAG-----GTCAGAGGTTCAAATCCTCTCTCGCCGA---  
>tdbD00008272 Buchnera\_aphidicola\_str.\_Sg\_(Schizaphis\_graminum)\_198804\_Pro\_TGG  
-CGGGCAATAGCGCAGCTTGGT--AGCGCAACTGGTTTGGGACCAGTAG-----GTCAGGGGTTCAAATCCTCTTTCGCCGACCA  
>tdbD00008106 Campylobacter\_jejuni\_subsp.\_jejuni\_NCTC\_11168\_192222\_Pro\_TGG  
-CGGGGTGTAGCGCAGTCTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GCCGAAGGTTTCGAATCCTTTTACCCCGACCA  
>tdbD00008452 Candidatus\_Blochmannia\_floridanus\_203907\_Pro\_TGG  
-CGGGAGTGGCGCAGTTTGGT--AGCGTGGCTGGTTTGGGACCAGTAG-----GTCGAGGTTTCGAATCCTCTCTCGCCGA---  
>tdbD00008396 Candidatus\_Protochlamydia\_amoebophila\_UWE25\_264201\_Pro\_GGG  
-CTGGTGTAGCGCAGCTTGGT--AGCGCACTTGCATGGGGTGCAAGGG-----GTCGGAAGTTCGAATCCTCTTCAACCAGA---  
>tdbD00008395 Candidatus\_Protochlamydia\_amoebophila\_UWE25\_264201\_Pro\_TGG  
-CGGAGTATAGCGCAGCTTGGT--AGCGCGGCTGCTTTGGGAGCAGTAG-----GTCGGGGGTTTCGAATCCTCTACTCCGA---  
>tdbD00008107 Caulobacter\_crescentus\_CB15\_190650\_Pro\_CGG  
-CGGAGTGTGGCTCAGTCTGGT--AGAGCACTGCGTTCGGGACGCAGGG-----GTCGCAGGTTCAAATCCTGCCACTCCGACCA  
>tdbD00008108 Caulobacter\_crescentus\_CB15\_190650\_Pro\_GGG  
-CGGAGCGTGGCGCAGCCTGGT--AGCGCACTTGCATGGGGGTCAAGGG-----GTCGCAGGTTTCGAATCCTGTGCTCCGACCA  
>tdbD00008109 Caulobacter\_crescentus\_CB15\_190650\_Pro\_TGG  
-CGGAGCGTAGCGCAGCCTGGT--AGCGCATCTGTTTGGGAGCAGAG-----GTCGCAGGTTCAAATCCTGCCGCTCCGACCA  
>tdbD00008141 Chlamydia\_muridarum\_Nigg\_243161\_Pro\_GGG  
-CTGGATGTAGCGCAGCCTGGT--AGCGCACTTGCATGGGGTGCAAGGG-----GGCGGAGGTTCAAATCCTCTCATCCAGA---  
>tdbD00008140 Chlamydia\_muridarum\_Nigg\_243161\_Pro\_TGG  
-CGGAGTATAGCGCAGCCTGGT--AGCGCGGTTGCTTTGGGAGCAATAG-----GTCGGGGGTTTCGAATCCCTCTACTCCGA---  
>tdbD00008061 Chlamydia\_pneumoniae\_AR39\_115711\_Pro\_GGG  
-CTGGGTGTAGCGCAGCCTGGT--AGCGCACTTGCATGGGGTGCAAGGG-----GGCGGAGGTTCAAATCCTCTCATCCAGA---  
>tdbD00008062 Chlamydia\_pneumoniae\_AR39\_115711\_Pro\_TGG  
-CGGAGTATAGCGCAGCCTGGT--AGCGCGGTTGCTTTGGGAGCAATAG-----GTCGGGGGTTTCGAATCCCTCTACTCCGA---  
>tdbD00008266 Chlorobium\_tepidum\_TLS\_194439\_Pro\_CGG  
-CGGGGTGTGGCTCAGCT--GGT--AGAGTGTGCTGCTTCGGGACGCAGAG-----GTCGTGGGTTTCGAGTCCCGCCACCCCGA---  
>tdbD00008264 Chlorobium\_tepidum\_TLS\_194439\_Pro\_GGG  
-CGGCTATAGCGCAGCCTGGT--AGCGCACTACCTGGGGTGGTAGGG-----GTCGTGGGTTCAAATCCCGCTACGCCGA---  
>tdbD00008265 Chlorobium\_tepidum\_TLS\_194439\_Pro\_TGG  
-CGGGCATGGCGCAGCT--GGT--AGCGTGCCTGCTTTGGGAGCAGAG-----GTCCCGAGTTCGAGTCTCGGTGCCCGACCA  
>tdbD00008146 Clostridium\_acetobutylicum\_ATCC\_824\_272562\_Pro\_CGG  
-CGGGGTGTAGCGCAGT--GGT--AGCGCGCATGCTTCGGGAGCATGAT-----GTCGCAAGTTCAACTCTGTACCCCGA---  
>tdbD00008145 Clostridium\_acetobutylicum\_ATCC\_824\_272562\_Pro\_TGG  
-CGGGGTGTGGCGCAGAT--GGG--AGCGCGCGTGGTTTGGGACCATGAG-----GTCGCAGGTTCAAATCCTGTACCCCGACCA

>tdbD00008139 Clostridium\_perfringens\_str.\_13 195102 Pro TGG  
-CGGGGTGTGGCGCAGAT-GGG--AGCGCGCTGGTTTGGGACCATAGAG-----GTCGCAGGTTTCGATCCCTGTACCCCGACCA  
>tdbD00008328 Clostridium\_tetani\_E88 212717 Pro GGG  
-CTGGGTATAGCGCAGAT-GGT--AGCGCGCATGCATGGGGTGCATAGAG-----GTCGCAGGTTCAAGTCTGTACTCAGACCA  
>tdbD00008329 Clostridium\_tetani\_E88 212717 Pro TGG  
-CGGGGTGTGGCGCAGAT-GGG--AGCGCGCTGGTTTGGGACCATAGAG-----GTCGCAGGTTCAAGCCTGTACCCCGACCA  
>tdbD00008388 Corynebacterium\_diphtheriae\_NCTC\_13129 257309 Pro CGG  
-CGGGATATGGCGCAGCTTGGT--AGCGCGCTCGTTCGGGACGAGGAG-----GTCGCAGGTTCAAATCCTGTATCCCGACCA  
>tdbD00008389 Corynebacterium\_diphtheriae\_NCTC\_13129 257309 Pro GGG  
-CGGACTATGGCGCAGCTTGGT--AGCGCACTGACTTGGGGTCAAGGG-----GTCGCAGGTTCAAATCCTGTTAGTCCGA---  
>tdbD00008390 Corynebacterium\_diphtheriae\_NCTC\_13129 257309 Pro TGG  
-CGGGACGTGGCGCAGTTTGGT--AGCGCACCTGCTTTGGGAGCAGGGG-----GTCGCAGGTTCAAATCCTGTCTGCCGA---  
>tdbD00008310 Corynebacterium\_efficiens\_YS-314 196164 Pro GGG  
-CGGACTATGGCGCAGCTTGGT--AGCGCACTACACTGGGGTGTAGGG-----GTCGCAGGTTCAAATCCTGTCTAGTCCGA---  
>tdbD00008309 Corynebacterium\_efficiens\_YS-314 196164 Pro TGG  
-CGGGGCGTGGCGCAGTTTGGT--AGCGCACCTGCTTTGGGAGCAGGGG-----GTCGCAGGTTCAAATCCTGTCTGCCGA---  
>tdbD00008274 Corynebacterium\_glutamicum\_ATCC\_13032 196627 Pro CGG  
-CGGGATATGGCGCAGCTTGGT--AGCGCGTCCCTCGGGAGCAGGG-----GTCGCAGGTTCAATCCTGTATCCCGA---  
>tdbD00008275 Corynebacterium\_glutamicum\_ATCC\_13032 196627 Pro GGG  
-CGGACTATGGCGCAGCTTGGT--AGCGCACTACACTGGGGTGTAGGG-----GTCGCAGGTTCAAATCCTGTAGTCCGA---  
>tdbD00008276 Corynebacterium\_glutamicum\_ATCC\_13032 196627 Pro TGG  
-CGGGGCGTGGCGCAGCTTGGT--AGCGCACTGCTTTGGGAGCAGGGG-----GTCGCAGGTTCAAATCCTGTCTGCCGA---  
>tdbD00008351 Coxiella\_burnetii\_RSA\_493 227377 Pro CGG  
-CGGGGTGTAGCTCAGCTTGGT--AGAGCACTGCCTTCGGGAGGCAGGG-----GCCGGAGGTTCAATCCTCTCACCCCGA---  
>tdbD00008352 Coxiella\_burnetii\_RSA\_493 227377 Pro GGG  
-CGGGGTATAGCGCAGCTTGGT--AGCGCGCTGCTTTGGGAGCAGGAT-----GTCGGGGGTTCAAATCCTCTCACCCCGA---  
>tdbD00008353 Coxiella\_burnetii\_RSA\_493 227377 Pro GGG  
-CGGGGCGTAGCGCAGCTTGGT--AGCGCACTTGCATGGGGTCAAGGG-----GTCGCAGGTTCAAATCCTGCCGTCCCGA---  
>tdbD00008110 Deinococcus\_radiodurans\_R1\_243230 Pro CGG  
-CGGGGCGTAGCGCAGCTTGGT--AGCGCACGTCTCGTTGGGAGCAGGG-----GTCGGAGGTTCAATCCTCTCGCCCGACCA  
>tdbD00008111 Deinococcus\_radiodurans\_R1\_243230 Pro GGG  
-CGAGGCGTAGCGCAGCTTGGT--AGCGCACTACCTTGGGGTGGTAGGG-----GTCGTGAGTTCAAATCCTCGCCCGCTCGACCA  
>tdbD00008112 Deinococcus\_radiodurans\_R1\_243230 Pro TGG  
-CGGGAAGTAGCGCAGCCGGT--AGCGCACTGGTTTGGGACCAAGGG-----GTCGCAGGTTCAATCCTGTCTTCCCGACCA  
>tdbD00008430 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882 Pro CGG  
-CGGGATGTGGCTCAGTTTGGT--AGAGCGCAGCGTTCGGGAGCCTGAG-----GCCGGAGGTTCAATCCTCTCATCCCGACCA  
>tdbD00008431 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882 Pro GGG  
-CGGGATGTAGCGCAGCTTGGT--AGCGCACTTGAATGGGGTCAAGGG-----GTCGAAGGTTCAAATCCTTCTCATCCCGACCA  
>tdbD00008429 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882 Pro TGG  
-CGGAACTAGCGCAGCTTGGT--AGCGCACCTGCCTTGGGAGCAGGG-----GTCGTGTTTCAATCCTAGTCTCGACCA  
>tdbD00008330 Enterococcus\_faecalis\_V583 226185 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTCAATCCTGTCTTCCCGA---  
>tdbD00002114 Escherichia\_coli\_562 Pro CGG  
-CGGTGATTGGCGCAGCTTGGT--AGCGCACTTCTGTTGGGAGCAAGGG-----GTCGGAGGTTCAATCCTCTATCACCGACCA  
>tdbD00002115 Escherichia\_coli\_562 Pro GGG  
-CGGCACGTAGCGCAGCTTGGT--AGCGCACCTCATGGGGTCTCGGG-----GTCGGAGGTTCAAATCCTCTCGTGCCGACCA  
>tdbD00002113 Escherichia\_coli\_562 Pro TGG  
-CGGCGAGTAGCGCAGCTTGGT--AGCGCACTGGTTTGGGACCAAGTTG-----GTCGGAGGTTCAATCCTCTCTCGCCGACCA  
>tdbD00008267 Fusobacterium\_nucleatum\_subsp.\_nucleatum\_ATCC\_25586 190304 Pro TGG  
-CGGAATATAGCGCAGCCCGT--AGCGCACCTGCCTTGGGAGCAGGG-----GTCGCAAGTTCAAATCCTGTCTATCCGACCA  
>tdbD00008268 Fusobacterium\_nucleatum\_subsp.\_nucleatum\_ATCC\_25586 190304 Pro GGG  
-CGGAATATAGCGCAGCCCGT--AGCGCACCTGCCTTGGGAGCAGGG-----GCCGCAAGTTCAAATCCTGTCTATCCGACCA  
>tdbD00008406 Geobacter\_sulfurreducens\_PCA\_243231 Pro CGG  
-CGGGGCGTAGCGCAGCTTGGT--AGCGCACCTGCTTCGGGAGCAGGG-----GTCGGAGGTTCAAATCCTCTCGCCCGACCA  
>tdbD00008407 Geobacter\_sulfurreducens\_PCA\_243231 Pro GGG  
-CGGGGCGTAGCGCAGCTTGGT--AGCGCACCACTGGGGTCTGGTG-----GTCGTGTTTCAATCCTAGTCTCGCCCGACCA  
>tdbD00008408 Geobacter\_sulfurreducens\_PCA\_243231 Pro TGG  
-CGGGGTGTAGCGCAGCTTGGT--AGCGCACCTGCCTTGGGAGCAGGG-----GTCGGAGGTTCAATCCTCTCACCCCGACCA  
>tdbD00002120 Haemophilus\_influenzae\_727 Pro TGG  
-CGGCGAGTAGCGCAGCTTGGT--AGCGCACTGGTTTGGGACCAAGTTG-----GTCGTAGGTTCAAATCCTATCTCGCCGACCA  
>tdbD00008346 Helicobacter\_hepaticus\_ATCC\_51449 235279 Pro GGG  
-CGGAGTATAGCGCAGCTTGGT--AGCGCGCACCTTGGGGTGGGTGAG-----GTCGTGGGTTTGAATCCCGCTACTCCGACCA  
>tdbD00008345 Helicobacter\_hepaticus\_ATCC\_51449 235279 Pro TGG  
-CGGGGCGTAGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGAAGGTTCAATCCTTCTCGCCCGACCA  
>tdbD00002109 Helicobacter\_pylori\_210 Pro GGG  
-CGGAGTATGGCGCAGCTTGGT--AGCGCGCACCTTGGGGTGGGTGAG-----GTCGTGGGTTTGAATCCCGCTACTCCGACCA  
>tdbD00002108 Lactobacillus\_delbrueckii\_subsp.\_bulgaricus\_1585 Pro TGG  
-CGGGAAGTGGCTCAGTTTGGT--AGAGCACCTGGTTTGGGACCAAGGG-----GTCGCAGGTTCAAATCCTGTCTTCCCGA---  
>tdbD00008410 Lactobacillus\_johnsonii\_NCC\_533 257314 Pro TGG  
-CGGGAAGTGGCTCAGTTTGGT--AGAGCACCTGGTTTGGGACCAAGGG-----GTCGCAGGTTCAATCCTGTCTTCCCGA---  
>tdbD00008332 Lactobacillus\_plantarum\_WCF51\_220668 Pro CGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGCACTACGTTTGGGACGTTAGGG-----GTCGCAGGTTCAAATCCTGTCTTCCCGA---  
>tdbD00008331 Lactobacillus\_plantarum\_WCF51\_220668 Pro TGG  
-CGGGAATAGCTCAGCTTGGT--AGAGCACCTGGTTTGGGACCAAGGG-----GTCGCAGGTTCAATCCTGTCTTCCCGA---  
>tdbD00008411 Leifsonia\_xyli\_subsp.\_xyli\_str.\_CTCB07 281090 Pro CGG

-CGGGGTGTGGCGCAGCTTGGT--AGCGCGCTTCGTTCCGGGACGAAGAG-----GCCGCAGGTTCAAATCCTGTCAACCCGACCA  
>tdbD00008412 Leifsonia\_xyli\_subsp.\_xyli\_str.\_CTCB07\_281090 Pro GGG  
-CGGGGTGTGGCGCAGCTTGGT--AGCGCACTTGACTGGGGGTCAAGGG-----GTCGCAGGTTCAAATCCTGTGTCAGCCCGACCA  
>tdbD00008413 Leifsonia\_xyli\_subsp.\_xyli\_str.\_CTCB07\_281090 Pro TGG  
-CGGGGCGTAGCTCAGCTTGGCT--AGAGCGCCCGCTTTGGGAGCGGGAG-----GTCGCAGGTTCAAATCCTGTGTCGCCCCGA---  
>tdbD00008312 Leptospira\_interrogans\_serovar\_Lai\_str.\_56601\_189518 Pro GGG  
-CGGGGTGTAGCGCAGT--GGT--AGCGCACTTCTCTGGGGGGGAAGGG-----GTCGTGGTTCAAATCCAGTCACTCCGA---  
>tdbD00008311 Leptospira\_interrogans\_serovar\_Lai\_str.\_56601\_189518 Pro TGG  
-CGGGATGTAGCGCAGG--GGT--AGCGCATCTGCCTTTGGGAGCAGAGG-----GTCGTAGGTTCAAATCCTATCATCCCGA---  
>tdbD00008433 Mesoplasma\_florum\_L1\_265311 Pro TGG  
-CGGGAAGTGGCTCAGCTTGGT--AGAGCATTCGGTTTGGGACCGAAGG-----GTCGCAGGTTCAAATCCTGTCTTCCCGACCA  
>tdbD00008151 Mesorhizobium\_loti\_MAFF303099\_266835 Pro CGG  
-CGGAGTGTAGCGCAGCTTGGT--AGCGCACCTCGTTCCGGGACGAGGG-----GTCGCAGGTTCAAATCCTGCCACTCCGACCA  
>tdbD00008153 Mesorhizobium\_loti\_MAFF303099\_266835 Pro GGG  
-CGGAGTGTAGCGCAGCCCGGT--AGCGCACTTGACTGGGGGTCAAGGG-----GTCGTGGTTCAAATCCGGCCACTCCGACCA  
>tdbD00008152 Mesorhizobium\_loti\_MAFF303099\_266835 Pro TGG  
-CGGAGTGTAGCGCAGGCTGGT--AGCGCATCTGGTTTGGGACCGAGG-----GTCGGGAGTTCAAATCTCTCCACTCCGACCA  
>tdbD00008349 Mycobacterium\_bovis\_AF2122/97\_233413 Pro CGG  
-CGGGGTGTGGCGCAGCTTGGT--AGCGCGCTTCGTTCCGGGACGAAGAG-----GCCGTGGGTTCAAATCCCGCCACCCCGA---  
>tdbD00008347 Mycobacterium\_bovis\_AF2122/97\_233413 Pro GGG  
-CGGGTGTGGCGCAGTTTGGT--AGCGCACTTGACTGGGGGTCAAGTG-----GTCGCAGGTTCAAATCCTGTGTCAGCCCGA---  
>tdbD00008348 Mycobacterium\_bovis\_AF2122/97\_233413 Pro TGG  
-CGGGGTGTAGCGCAGCTTGGT--AGCGCATCCGCTTTGGGAGCGGAAG-----GCCGCAGGTTCAAATCCTGTCAACCCGACCA  
>tdbD00002096 Mycoplasma\_capricolum\_2095 Pro TGG  
-CGGGAAGTGGCTCAGTTTGGT--AGAGCATTCGGTTTGGGACCGAAGG-----GTCGCAGGTTCAAATCCTGTCTTCCCGACCA  
>tdbD00008344 Mycoplasma\_gallisepticum\_R\_233150 Pro TGG  
-CGGGAAGTAGCTTAGCTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTCAAATCCTGTCTTCCCGACCA  
>tdbD00002097 Mycoplasma\_genitalium\_2097 Pro TGG  
-CGGGAAGTAGCTTAGTTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTCAAATCCTGTCTTCCCGACCA  
>tdbD00002099 Mycoplasma\_pneumoniae\_2104 Pro TGG  
-CGGGAAGTAGCTTAGTTTGGTA-GAAGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTCAAATCCTGTCTTCCCGACCA  
>tdbD00008074 Neisseria\_meningitidis\_MC58\_122586 Pro CGG  
-CGGAATGTAGCGCAGCCCGGT--AGCGCACTTCGTTCCGGGACGAAGGG-----GGCGGAGGTTCAAATCCTCTCATTCCGACCA  
>tdbD00008075 Neisseria\_meningitidis\_MC58\_122586 Pro GGG  
-CGGAGTGTGGCGCAGTCTGGT--AGCGCACTTGCAATGGGGTGCAAGGG-----GTCGAAGGTTCAAATCCTTTCACTCCGACCA  
>tdbD00008076 Neisseria\_meningitidis\_MC58\_122586 Pro TGG  
-CGGGGCGTAGCGCAGCCCGGT--AGCGCATCTGCCTTTGGGAGCAGAGG-----GTCGTGAGTTCAAATCCACCCCGCCGACCA  
>tdbD00008077 Neisseria\_meningitidis\_Z2491\_122587 Pro CGG  
-CGGAATGTAGCGCAGCCCGGT--AGCGCACTTCGTTCCGGGACGAAGGG-----GTCGGAGGTTCAAATCCTCTCATTCGACCA  
>tdbD00008375 Nitrosomonas\_europaea\_ATCC\_19718\_228410 Pro CGG  
-CGGGTGTAGCTCAGCCTGGT--AGAGTACTGCGTTCCGGGACGAGGA-----GCCGGAGGTTCAAATCCTCTCACCCCGACCA  
>tdbD00008373 Nitrosomonas\_europaea\_ATCC\_19718\_228410 Pro GGG  
-CGGGGCGTAGCGCAGCCTGGT--AGCGTACTTGCAATGGGGTGCAAGTG-----GTCGGAGGTTCAAATCCTCTCGCCCCGACCA  
>tdbD00008374 Nitrosomonas\_europaea\_ATCC\_19718\_228410 Pro TGG  
-CGGGTGTAGCGTAGCCTGGT--AGCGCGCCTGGTTTGGGACCGAGGAT-----GTCGGGAGTTCAAATCTCTCCACCCCGACCA  
>tdbD00008164 Nostoc\_sp.\_PCC\_7120\_103690 Pro CGG  
-CGGGATGTAGCGCAGCTTGGT--AGCGCACTTCGTTCCGGGACGAAGGG-----GCCGTGGTTCAAATCCAGTCACTCCCGA---  
>tdbD00008165 Nostoc\_sp.\_PCC\_7120\_103690 Pro GGG  
-CGGGGCGTAGCGCAGCTTGGT--AGCGCGCCACTTTGGGGTAGTGGAG-----GTCGTGGGTTCAAATCCCGCCGCTCCGA---  
>tdbD00008162 Nostoc\_sp.\_PCC\_7120\_103690 Pro TGG  
-CGGGATGTAATTTCAGT--GGTCTAGAAGCCTTGTTTGGGGACAAGGA-----GTCGTAGGTTCAAATCCTACCATCCCGACCA  
>tdbD00008163 Nostoc\_sp.\_PCC\_7120\_103690 Pro TGG  
-CGGGATGTAGCGCAGCTTGGT--AGCGCGCCTGCCTTTGGGAGCAGGAT-----GCCGCAGGTTCAAATCCTGTCACTCCCGA---  
>tdbD00008313 Oceanobacillus\_heyensis\_HTE831\_221109 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTCAAATCCTGTCTTCCCGACCA  
>tdbD00008391 Onion\_yellows\_phytoplasma\_OY-M\_262768 Pro TGG  
-CGGGAAGTAGCTTAGCTTGGT--ATAGCGCCTGGTTTGGGACCGAGG-----GTCGCGGGTTCAAATCCTGCCTTCCCGACCA  
>tdbD00002117 Photobacterium\_phosphoreum\_659 Pro TGG  
-CGGTGAATAGCGCAGTTTGGT--AGCGCATCTGGTTTGGGACCGAGG-----GTCGGGGGTTCAAATCCCTCTTACCAGACCA  
>tdbD00008398 Photorhabdus\_luminescens\_subsp.\_laumondii\_TT01\_243265 Pro GGG  
-CGGCATGTAGCGCAGCTTGGT--AGCGCACCGTCAATGGGGTGTGGGG-----GTCGGAGGTTCAAATCCTCTCATGCCGACCA  
>tdbD00008416 Porphyromonas\_gingivalis\_W83\_242619 Pro CGG  
-CGGGATGTAGCACAGTT--GGT--AGCGGCCACGTTCCGGGACGTTGGAG-----GTCGGAAGTTTCGAGTCTTCTCATCCCGA---  
>tdbD00008415 Porphyromonas\_gingivalis\_W83\_242619 Pro GGG  
-CGGGTGTAGCTCAGCCCGGT--AGAGTACCGCTTGGGGGCGTGTG-----GTCGTGGTTCAAATCCAGTCAACCCCGA---  
>tdbD00008436 Propionibacterium\_acnes\_KP171202\_267747 Pro CGG  
-CGGGTGTGGCGCAGTTTGGT--AGCGCACTTGACTGGGGGTCAAGGG-----GTCGCAGGTTCAAATCCTGTCAACCCGACCA  
>tdbD00008434 Propionibacterium\_acnes\_KP171202\_267747 Pro GGG  
-CGGGTGTGGCGCAGTTTGGT--AGCGCACTTGACTGGGGGTCAAGGG-----GTCGCAGGTTCAAATCCTGTGTCAGCCCGA---  
>tdbD00008435 Propionibacterium\_acnes\_KP171202\_267747 Pro TGG  
-CGGGGCGTAGCGTAGT--GGT--AGCGCGCCTGCTTTGGGAGCAGGAG-----ATCGCAGGTTTCGAGTCTGTGCCCCGACCA  
>tdbD00008119 Pseudomonas\_aeruginosa\_PA01\_208964 Pro CGG  
-CGGAGCGTAGCGCAGCTTGGT--AGCGCGTCTCGTTCCGGGACGAGAAG-----GTCGTGGTTCAAATCCAGTCTGCTCCGACCA  
>tdbD00008120 Pseudomonas\_aeruginosa\_PA01\_208964 Pro GGG  
-CGGGGCGTAGCGCAGCTTGGT--AGCGCACTTGCAATGGGGTCAAGGG-----GTCGAGTGTTCGAATCACTCCGTCGACCA

>tdbD00008121 *Pseudomonas aeruginosa*\_PAO1\_208964\_Pro\_TGG  
-CGGGGTATAGCGCAGTCCGGT--AGCGCGCTGCTTTGGGAGCAGGAT-----GTCGGGAGTTTCAATCTCTCTACCCCGACCA  
>tdbD00008381 *Pseudomonas syringae*\_pv.\_tomato\_str.\_DC3000\_223283\_Pro\_GGG  
-CGGGGCGTAGCGCAGTCCGGT--AGCGCACTAGCATGGGGTGCTAGGG-----GTCGAGTGTTCGAATCACTCCGTCGCCGACCA  
>tdbD00008380 *Pseudomonas syringae*\_pv.\_tomato\_str.\_DC3000\_223283\_Pro\_TGG  
-CGGGGTATAGCGCAGTCCGGT--AGCGCGCTGCTTTGGGAGCAGGAT-----GTCAGGAGTTTCAATCCCTTACCCCGACCA  
>tdbD00008161 *Ralstonia solanacearum*\_GMI1000\_267608\_Pro\_CGG  
-CGGGGTGTAGCTTAGCCTGGT--AGAGCGCTACGTTGGGACGTAGAG-----GCCGGAGGTTTCAATCCTCTCACCCCGACCA  
>tdbD00008160 *Ralstonia solanacearum*\_GMI1000\_267608\_Pro\_GGG  
-CGGGGCGTAGCGCAGCCTGGT--AGCGTACCTGCATGGGGTGCAGGTG-----GTCGGGAGTTTCAATCCTCTCGCCCCGACCA  
>tdbD00008159 *Ralstonia solanacearum*\_GMI1000\_267608\_Pro\_TGG  
-CGGGGCGTAGCGCAGCCTGGT--AGCGCATCTGATTTGGGATCAGAGG-----GTCGCATGTTTCAATCATGTGCCCCGACCA  
>tdbD00008369 *Rhodopirellula baltica*\_SH\_1\_243090\_Pro\_CGG  
-CGGGGCGTAGCGCAGCCTGGT--AGCGCATCTGATTTGGGATCAGAGG-----GTCGCATGTTTCAATCATGTGCCCCGACCA  
>tdbD00008372 *Rhodopirellula baltica*\_SH\_1\_243090\_Pro\_GGG  
-CGGGGCGTAGCGCAGCCTGGT--AGCGCATCTGATTTGGGATCAGAGG-----GTCGCATGTTTCAATCATGTGCCCCGACCA  
>tdbD00008370 *Rhodopirellula baltica*\_SH\_1\_243090\_Pro\_TGG  
-CGGGGCGTAGCGCAGCCTGGT--AGCGCATCTGATTTGGGATCAGAGG-----GTCGCATGTTTCAATCATGTGCCCCGACCA  
>tdbD00008401 *Rhodopseudomonas palustris*\_CGA009\_258594\_Pro\_GGG  
-CGGAGCGTAGCGCAGCCGGT--AGCGCACTAGTCTGGGAGACTAGGG-----GTCGAAGGTTTCAATCCTTTGCTCCGACCA  
>tdbD00008147 *Rickettsia conorii*\_str.\_Malish\_7\_272944\_Pro\_TGG  
-CGGGGCGTAGCGCAGCCTGGT--AGCGCATCTGATTTGGGATCAGAGG-----GTCGGGAGTTTCAATCTCTCCGCCCGACCA  
>tdbD00008317 *Shewanella oneidensis*\_MR-1\_211586\_Pro\_GGG  
-CGGTATGTAGCGCAGCCGGT--AGCGCACTGTATGGGGTGCAGGG-----GTCGGGAGTTTCAATCCTCTCATACCGACCA  
>tdbD00008318 *Shewanella oneidensis*\_MR-1\_211586\_Pro\_TGG  
-CGGTGATTAGCGCAGCCTGGT--AGCGCATCTGATTTGGGATCAGAGG-----GTCAGAGGTTTCAATCCTCTATCACCGACCA  
>tdbD00008320 *Shigella flexneri*\_2a\_str.\_301\_198214\_Pro\_GGG  
-CGGCACGTAGCGCAGCCTGGT--AGCGCACGTATGGGGTGCAGAG-----G-----GTCGGGAGTTTCAATCCTCTCGTCCCGACCA  
>tdbD00002119 *Sinorhizobium meliloti*\_382\_Pro\_AGG  
-CGGAGTGTAGCGCAGTCTGGT--AGCGCACACGTTAGGGACGTGGGG-----GTCGAGTGTTCGAATCACTCCACTCCGACCA  
>tdbD00008173 *Sinorhizobium meliloti*\_1021\_266834\_Pro\_CGG  
-CGGAGTGTAGCGCAGTCTGGT--AGCGCACACGTTAGGGACGTGGGG-----GTCGAGTGTTCGAATCACTCCACTCCGACCA  
>tdbD00008175 *Sinorhizobium meliloti*\_1021\_266834\_Pro\_TGG  
-CGGAGTGTAGCGCAGTCTGGT--AGCGCATCTGATTTGGGATCAGAGG-----GTCGGGAGTTTCAATCTCTCCACTCCGACCA  
>tdbD00002100 *Spiroplasma melliferum*\_2134\_Pro\_TGG  
-CGGAAAGTAGCTTAGCTTGGT--AGAGCACTCGGTTTGGGACCGAGGG-----GTCGCAGGTTTCAATCCTGTCTTTCCGACCA  
>tdbD00008333 *Staphylococcus epidermidis*\_ATCC\_12228\_176280\_Pro\_TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GTCGTAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00008334 *Staphylococcus epidermidis*\_ATCC\_12228\_176280\_Pro\_TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GCCCGAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00008322 *Streptococcus agalactiae*\_2603V/R\_208435\_Pro\_TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGTACTTGGTTTGGGACCAAGGT-----GTCGCAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00002121 *Streptococcus mutans*\_1309\_Pro\_TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGTACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00008144 *Streptococcus pneumoniae*\_TIGR4\_170187\_Pro\_TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGTACTTGGTTTGGGACCAAGGT-----GTCGCAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00002105 *Streptomyces ambofaciens*\_1889\_Pro\_CGG  
-CGGGGTGTGGCGCAGCTTGGT--AGCGCGCTTCGTTCCGGACGAAGAG-----GTCGTGGGTTTCAATCCCGCCACCCCGA---  
>tdbD00008362 *Streptomyces avermitilis*\_MA-4680\_227882\_Pro\_CGG  
-CGGGGTGTAGCGCAGCTTGGT--AGCGCGCTTCGTTCCGGACGAAGAG-----GTCGTGGGTTTCAATCCCGCCACCCCGA---  
>tdbD00008360 *Streptomyces avermitilis*\_MA-4680\_227882\_Pro\_GGG  
-CGGGACGTGGCGCAGCTTGGT--AGCGCACTTACTGGGGTCAAGGG-----GTCGCAGGTTTCAATCCTGTCTCCCGA---  
>tdbD00008363 *Streptomyces avermitilis*\_MA-4680\_227882\_Pro\_TGG  
-CGGGGTGTGGCGCAGCTTGGT--AGCGCGTCCGTTTGGGACCGGAAG-----GCCGTGGGTTTCAATCCCGCCACCCCGACCA  
>tdbD00008420 *Symbiobacterium thermophilum*\_IAM\_14863\_292459\_Pro\_CGG  
-CGGGGTGTGGCTCAGCTTGGT--AGAGCGCACGGTTCGGGACCGTGAG-----GTCGCAGGTTTCAATCCTGTCAACCCCGACCA  
>tdbD00008419 *Symbiobacterium thermophilum*\_IAM\_14863\_292459\_Pro\_GGG  
-CGGGCTGTGGCGCAGCTTGGT--AGCGCGCTTCTTGGGGTGAAGAG-----GTCGCAGGTTTCAATCCTGTCAACCCCGACCA  
>tdbD00008418 *Symbiobacterium thermophilum*\_IAM\_14863\_292459\_Pro\_TGG  
-CGGGGTGTGGCGCAGCTTGGT--AGCGCGCTTCTTGGGGTGAAGAG-----GTCGCAGGTTTCAATCCTGTCAACCCCGACCA  
>tdbD00002123 *Synechocystis*\_sp.\_1143\_Pro\_CGG  
-CGGGATGTAGCGCAGCTTGGT--AGCGCACTTCTTGGGACGAAGGG-----GCCCGAGGTTTCAATCCTGTCTATCCCGA---  
>tdbD00002122 *Synechocystis*\_sp.\_1143\_Pro\_GGG  
-CGGGGCGTAGCGCAGCTTGGT--AGCGCACCACTTTGGGGTAGTGGGG-----GTCGTGGGTTTCAATCCCGCCGCTCCGA---  
>tdbD00002124 *Synechocystis*\_sp.\_1143\_Pro\_TGG  
-CGGGATGTAGCGCAGCTTGGT--AGCGCGCTTCTTGGGACGAAGGG-----GTCGCAGGTTTCAATCCTGTCTATCCCGA---  
>tdbD00008287 *Thermoanaerobacter tengcongensis*\_MB4\_273068\_Pro\_CGG  
-CGGGGCATGGCGCAGC--GGT--AGCGCGCGGGTTCGGGACCGTGAG-----GTCGCAGGTTTCAATCCTGTGCCCCGACCA  
>tdbD00008288 *Thermoanaerobacter tengcongensis*\_MB4\_273068\_Pro\_GGG  
-CTGGTGTGGCGCAGCT--GGT--AGCGCGCCAGATGGGGTCTGGAG-----GCCGGGGGTTTCAAGTCCCCCACTCAGACCA  
>tdbD00008286 *Thermoanaerobacter tengcongensis*\_MB4\_273068\_Pro\_TGG  
-CGGGATGTAGCGCAGCT--GGT--AGCGCACGTGCTTTGGGACGATGGG-----GTCGGGGGTTTCAAGTCCCCCACTCAGACCA  
>tdbD00008281 *Thermosynechococcus elongatus*\_BP-1\_197221\_Pro\_CGG  
-CGGGATGTAGCGCAGCTTGGT--AGCGCACTTCTTGGGACGAAGGG-----GTCGCAGGTTTCAATCCTGTCTATCCCGA---  
>tdbD00008280 *Thermosynechococcus elongatus*\_BP-1\_197221\_Pro\_TGG

-CGGGATGTAGCGCAGCTTGGT--AGCGCATCTGCTTTGGGAGCAGAGG-----GTCGCAGGTTCAAATCCTGTTCATCCCGA---  
>tdbD00008125 Thermotoga\_maritima\_MSB8\_243274\_Pro\_CGG  
-CGGGGAGTAGCTCAGAC-GGCC-AGAGCGCCAGAATCGGGATCTGGAG-----GTCGCGGGTTCAAGTCCCGCCTCCCGACCA  
>tdbD00008126 Thermotoga\_maritima\_MSB8\_243274\_Pro\_GGG  
-CGGGGCGTAGCGCAGGT-GGCT-AGCGCGCTTGATGGGGCGCAAGAG-----GTCGCTGGTTCAAGTCCAGTCGCCCCGACCA  
>tdbD00008127 Thermotoga\_maritima\_MSB8\_243274\_Pro\_TGG  
-CGGGGCGTAGCGCAGGT-GGCT-AGCGCGCTGCCTTGGGAGCAGGAG-----GTCGCTGGTTCAAGTCCAGTCGCCCCGACCA  
>tdbD00008438 Thermus\_thermophilus\_HB27\_262724\_Pro\_CGG  
---GGGAGTAGCGCAGCCCGT--AGCGCACCTCGTTGGGACGAGGGG-----GTCGCTGGTTCAAATCCAGTCTCCCGACCA  
>tdbD00008439 Thermus\_thermophilus\_HB27\_262724\_Pro\_GGG  
-CGGGGAGTAGCGCAGCCTGGT--AGCGCACACGCTTGGGGTGCCTGGG-----GTCGTCGGTTCAAATCCCGCCTCCCGACCA  
>tdbD00008437 Thermus\_thermophilus\_HB27\_262724\_Pro\_TGG  
-CGGGGCGTAGCGCAGGCCGGT--AGCGCACCTGCTTTGGGAGCAGGGG-----GTCGCCCGTTCAAATCGGGCCGCCCCGACCA  
>tdbD00008442 Treponema\_denticola\_ATCC\_35405\_243275\_Pro\_CGG  
-CGGGCAGTAGCGCAGG--GGT--AGCGCGCTTGGTTCCGGGACCAAGAA-----GTCGGGGTTCAAATCCCCCTGCCCGA---  
>tdbD00008440 Treponema\_denticola\_ATCC\_35405\_243275\_Pro\_GGG  
-CGGGCAATAGCGCAGTT-GGTT-AGCGTACAAGTCTGGGGGACTTGGG-----GTCCCGGTTCAAATCCGGGTGCCCGA---  
>tdbD00008441 Treponema\_denticola\_ATCC\_35405\_243275\_Pro\_TGG  
-CGGGATGTAGCCTAGG--GGCT-AAGGCGTCTGGTTTGGGACCAGAAG-----ATCGGGGTTCAAATCCCTCCATCCCGA---  
>tdbD00002101 Treponema\_pallidum\_160\_Pro\_CGG  
-CGGGTGGTAGCGCAGT--GGT--AGCGCGCTCGGTTCCGGGACTGAGAG-----GTCGGGGTTCAAATCCCCCTCGCCCCGACCA  
>tdbD00002103 Treponema\_pallidum\_160\_Pro\_GGG  
-CGGGCAATGGCGCAGTA-GGTT-AGCGTACAAGTCTGGGGGACTTGGG-----GTCCCGGTTTCGAGTCCGGGTGCCCGA---  
>tdbD00002102 Treponema\_pallidum\_160\_Pro\_TGG  
-CGGGACGTGGCCTAGG--GGCT-AGGGCACCCGGTTTGGGACCGGAAG-----ATCGAGGGTTCAAATCCCTCCGTCCCGA---  
>tdbD00008337 Tropheryma\_whipplei\_str\_Twist\_203267\_Pro\_CGG  
-CGGGGTGTGGCGCAGCTTGGT--AGCGCGCTCGTTCGGGACGAGGAG-----GTCGTGGTTCAAATCCCGCCACCCCGA---  
>tdbD00008335 Tropheryma\_whipplei\_str\_Twist\_203267\_Pro\_GGG  
-CGGGCTGTGGCGCAGCTTGGT--AGCGCACTTACTGGGGGTCAAGGG-----GTCGTGGTTCAAATCCCGCCAGCCCGA---  
>tdbD00008336 Tropheryma\_whipplei\_str\_Twist\_203267\_Pro\_TGG  
-CGGGGTGTAGCTCAGTTTGGT--AGAGCGCCCGCTTTGGGAGCGGGAG-----GTCGCAGGTTCAAATCCTGTGCGCCCCGA---  
>tdbD00008087 Ureaplasma\_parvum\_serovar\_3\_38504\_Pro\_TGG  
-CGGGAAGTAGCACAGCTTGGT--AGTGCATTTGGTTTGGGACCAAGGG-----GTCGCAGGTTCGAATCCTGTCTTCCCGACCA  
>tdbD00008080 Vibrio\_cholerae\_O1\_biovar\_El\_Tor\_str\_N16961\_243277\_Pro\_GGG  
-CGGACTGTAGCGCAGCTTGGT--AGCGCACCGTCATGGGGTGTGCGGG-----GTCGGAGGTTCAAATCCTCTCAGTCCGACCA  
>tdbD00008082 Vibrio\_cholerae\_O1\_biovar\_El\_Tor\_str\_N16961\_243277\_Pro\_TGG  
-CGGTGAATAGCGCAGTTTGGT--ARCGCATCTGGTTTGGGACCAAGGG-----GTCGGGGTTCGAATCCTCTTACCAGACCA  
>tdbD00008443 Wolbachia\_endosymbiont\_of\_Drosophila\_melanogaster\_163164\_Pro\_TGG  
-CGGGGCGTAGCGCAGCCTGGT--AGCGCATTTGGTTTGGGACCAAGGG-----GTCGGGAGTTCAAATCCTCTCCGCCCGA---  
>tdbD00008293 Xanthomonas\_axonopodis\_pv\_citri\_str\_306\_190486\_Pro\_CGG  
-CGGGGTGTAGCTCAGTCTGGT--AGAGCGCTACGTTCCGGGACGTAGAG-----GTCGCAGGTTCGAATCCTGTCTCCCGACCA  
>tdbD00008294 Xanthomonas\_axonopodis\_pv\_citri\_str\_306\_190486\_Pro\_GGG  
-CGGGGTATAGCGCAGCCTGGT--AGCGCACTAGTCTGGGGGACTAGTG-----GTCGTCGGTTCGAATCCGGTACCCCGACCA  
>tdbD00008292 Xanthomonas\_axonopodis\_pv\_citri\_str\_306\_190486\_Pro\_TGG  
-CGGGGTATAGCGCAGTCTGGT--AGCGCGCTGCTTTGGGAGCAGGAT-----GTCGGGGTTTCGAATCCCTCTACCCCGACCA  
>tdbD00008129 Xylella\_fastidiosa\_9a5c\_160492\_Pro\_GGG  
-CGGGGTATAGCGCAGCCTGGT--AGCGCACAGTCTGGGGGACTGGTG-----GTCGTCGGTTCAAATCCGGTACCCCGACCA  
>tdbD00008130 Xylella\_fastidiosa\_9a5c\_160492\_Pro\_TGG  
-CGGGGTATAGCGCAGTCTGGC--AGCGCGCTGCTTTGGGAGCAGGAT-----GTCGGGGTTTCGAATCCCTCTACCCCGACCA  
>tdbD00008421 Yersinia\_pestis\_biovar\_Microtus\_str\_91001\_229193\_Pro\_GGG  
-CGGATGTAGCGCAGCTTGGT--AGCGCACCGTCATGGGGTGTGCGGG-----GTCGAAGGTTCAAATCCTTTTCATGCCGACCA  
>tdbD00005590 Acinetobacter\_sp\_ADPl\_62977\_Gly\_GCC  
-GCGGGAATAGCTCAGTT-GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGCAGGTTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005591 Acinetobacter\_sp\_ADPl\_62977\_Gly\_TCC  
-GCGGGAGTAAGTCAAGT-GGT--AGAGTGGCAGCCTTCCAAGCTGCAT-----GTCGCAGGTTTCGATCCTCGTCTCCCGCTCCA  
>tdbD00005261 Agrobacterium\_tumefaciens\_str\_C58\_176299\_Gly\_CCC  
-GCGGGTGTAGCTCAAT--GGT--AGAGCAGCAGCTTCCCAAGCTGAAT-----A-CGAGGGTTTCGATTCCCTTACCCGCTCCA  
>tdbD00005263 Agrobacterium\_tumefaciens\_str\_C58\_176299\_Gly\_GCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGAGGGTTCAAATCCCTTCCCGCTCCA  
>tdbD00005216 Aquifex\_aeolicus\_VF5\_224324\_Gly\_CCC  
-GCGGGCGTAGCTCAGA--GGT--AGAGCACCTGCTTCCCAAGCAGGAG-----GTCGCGGGTTTCGAGTCCCGTCCCGCTCCA  
>tdbD00005217 Aquifex\_aeolicus\_VF5\_224324\_Gly\_GCC  
-GCGGGCGTAGCTCAGT--GGT--AGAGCGGCTGCTTGCCATGCAGCAG-----GTCGCGGGTTTCGAGTCCCGTCCCGCTCCA  
>tdbD00005218 Aquifex\_aeolicus\_VF5\_224324\_Gly\_TCC  
-GCGGGCGTAGCTCAGTT-GGT--AGAGCAGCGGCTTCCAAGCCGCGAG-----GTCGCGGGTTTCGAGTCCCGTCCCGCTCCA  
>tdbD00008043 Azorhizobium\_caulinodans\_7\_Gly\_GCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGAGGGTTTCGAATCCCTTCCCGCTCCA  
>tdbD00005592 Bacillus\_anthraxis\_str\_A2012\_191218\_Gly\_GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAATACAACCTTGCCAAGGTTGGG-----GTCGCGGGTTTCGAATCCCGTCTTCCGCTCCA  
>tdbD00005504 Bacillus\_anthraxis\_str\_Ames\_198094\_Gly\_GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAATACAACCTTGCCAAGGTTGGG-----GTCGCGGGTTTCGAATCCCGTCTTCCGCT---  
>tdbD00005505 Bacillus\_anthraxis\_str\_Ames\_198094\_Gly\_TCC  
-GCGGGTGTAGTTTGT--GGT--AAAACAAGAGCCTTCCAAGCTCTGG-----T-CGAGAGTTTCGATTCTCTTACCCGCT---  
>tdbD00005507 Bacillus\_anthraxis\_str\_Ames\_198094\_Gly\_TCC  
-GCGGGTGTAGTTTGT--GGT--AAAACAAGAGCCTTCCAAGCTCTGG-----T-CGAGAGTTTCGATTCTCTTACCCGCTCCA

>tdbD00005436 *Bacillus\_halodurans\_C-125* 272558 Gly GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAACACCACCTTGCCAAGGTGGGG-----GTCGCGGGTTCGAATCCCCTCTCCGCTCCA  
>tdbD00005437 *Bacillus\_halodurans\_C-125* 272558 Gly TCC  
-GCGGGTGTAGTTTGTAGT--GGT--AAAACCTCAGCCTTCCAAGCTGATG-----T-CGTGGGTTTCGATTCATCACCCTCCGCT---  
>tdbD00005438 *Bacillus\_halodurans\_C-125* 272558 Gly TCC  
-GCGGGTGTAGTTTGTAGT--GGT--AAAACCTCAGCCTTCCAAGCTGATG-----T-CGTGGGTTTCGATTCATCACCCTCCGCTCCA  
>tdbD00005439 *Bacillus\_halodurans\_C-125* 272558 Gly TCC  
-GCGGGTGTAGTTTGTAGT--GGT--AAAACCTCAGCCTTCCAAGCTGATG-----T-CGTGGGTTTCGATTCATCACCCTCCGCTCCA  
>tdbD00000831 *Bacillus\_subtilis* 1423 Gly GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAACACCACCTTGCCAAGGTGGGG-----GTCGCGGGTTCGAATCCCCTCTCCGCTCCA  
>tdbD00000833 *Bacillus\_subtilis* 1423 Gly GCC  
-GCGGAAGTAGTTCAGT--GGT--TGAACACCACCTTGCCAAGGTGGGG-----GTCGCGGGTTCGAATCCCCTCTCCGCTCCA  
>tdbD00005499 *Bacteroides\_thetaiotaomicron\_VPI-5482* 226186 Gly CCC  
-GCGGTAGTAGCTCAGTT--GGT--AGAGCATTAGCTTCCAAGCTGAGG-----GTCGCGAGTTTCGAGCCTCGTTTACCCTGCT---  
>tdbD00005497 *Bacteroides\_thetaiotaomicron\_VPI-5482* 226186 Gly GCC  
-GCGGAAATAGCTCAGTT--GGT--AGAGCATAACCTTGCCAAGGTTAGG-----GTCGCGAGTTTCGAGTCTCGTTTCCGCT---  
>tdbD00005500 *Bacteroides\_thetaiotaomicron\_VPI-5482* 226186 Gly TCC  
-GCGGAAGTAGCTCAGTT--GGT--AGAGCATTAGCTTCCAAGCTGAGG-----GTCGCGGGTTTTCGAGCCCCGCTCTCCGCT---  
>tdbD00005509 *Bartonella\_henselae\_str.\_Houston-1* 283166 Gly GCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCACAACTTGCCAAGGTTGGG-----GTCGTGGGTTTCGAATCCCCTCCGCTCCA  
>tdbD00005508 *Bartonella\_henselae\_str.\_Houston-1* 283166 Gly TCC  
-GCGGTATAGCTCAAT--GGT--AGAGCAGCAGCCTTCCAAGCTGAAT-----A-TGCGGGTTCGATTCCTCCGCTACCCTCCGCTCCA  
>tdbD00005510 *Bdellovibrio\_bacteriovorus\_HD100* 264462 Gly GCC  
-GCGGGAGTAGCTCAGTT--GAT--AGAGCGATGCCTTGCCAAGGCATAG-----GTCGCGGGTTTTCGAGCCCCGCTCTCCGCTCCA  
>tdbD00005511 *Bdellovibrio\_bacteriovorus\_HD100* 264462 Gly TCC  
-GCGGAATAGCTCAAT--GGT--AGAGTATCTGCCTTCCAAGCAGAGG-----GTTGCGGGTTCGAGACCCGTTTCCGCTCCA  
>tdbD00005410 *Bifidobacterium\_longum\_NCC2705* 206672 Gly CCC  
-GCGGACATAGTTCATC--GGT--AGAATGAAAGCTTCCAAGCTTTAG-----A-GGCGGGTTCGACTCCCCTGTCCGCTCCA  
>tdbD00005407 *Bifidobacterium\_longum\_NCC2705* 206672 Gly GCC  
-GCGGACATAGCTTCAAT--GGT--AAAGCGCAACCTTGCCAAGGTTGAG-----ACCGGGGTTTCGAGTCCCCTGTCCGCT---  
>tdbD00005409 *Bifidobacterium\_longum\_NCC2705* 206672 Gly GCC  
-GCGGACATAGCTTCAAT--GGT--AAAGCGCAACCTTGCCAAGGTTGAG-----ACCGGGGTTTCGAGTCCCCTGTCCGCTCCA  
>tdbD00005406 *Bifidobacterium\_longum\_NCC2705* 206672 Gly TCC  
-GCGGATGTAGCTCAAT--GGT--AGAGCCTCAGTCTTCCAAGCTGAT-----A-CGCGGGTTCGATTCCTCCGCTACCCTCCGCTCCA  
>tdbD00000819 *Borrelia\_burgdorferi* 139 Gly GCC  
-GCGAAAGTAACTCAGG--GGT--AGAGTGTACCTCGCCAAGGTGGAA-----GTCGCGGGTTCGAATCCCCTCTTCCGCT---  
>tdbD00000818 *Borrelia\_burgdorferi* 139 Gly TCC  
-GCTCTTCGTATAAT--GGCT--ATTACCTTAGCCTTCCAAGCTAATG-----A-TGTCGGTTCGATTCGGATAGGACGCT---  
>tdbD00005185 *Borrelia\_burgdorferi\_B31* 224326 Gly GCC  
-GCGAAAGTAACTCAGG--GGT--AGAGTGTACCTTGCCAAGGTGGAA-----GTCGCGGGTTCGAATCCCCTCTTCCGCT---  
>tdbD00005441 *Bradyrhizobium\_japonicum\_USDA\_110* 224911 Gly CCC  
-GCGGGCGTAGTTCAT--GGT--AGAAGCGCAGCTTCCAAGCTGCAT-----A-CGAGGGTTCGATTCCTTCGCCCCGCTCCA  
>tdbD00005440 *Bradyrhizobium\_japonicum\_USDA\_110* 224911 Gly GCC  
-GCGGGTGTAGCTCAGT--GGT--AGAGCAGCAGCTTGCCAAGGTCGGG-----GTCGAGGGTTCGAGCCCCCTTCGCCCCGCTCCA  
>tdbD00005442 *Bradyrhizobium\_japonicum\_USDA\_110* 224911 Gly TCC  
-GCGGGTGTAGCTCAAT--GGT--AGAGCAGCAGCCTTCCAAGCTGAAT-----A-CGAGGGTTCGATTCCTTCACCCGCTCCA  
>tdbD00005242 *Brucella\_melitensis\_16M* 224914 Gly CCC  
-GCGGGTATGATGTAAT--GGT--AGCCTGTCACTTCCAAGCTGAAC-----G-CGCGGGTTCGATTCCTCCGCTACCCTCCGCTCCA  
>tdbD00005241 *Brucella\_melitensis\_16M* 224914 Gly TCC  
-GCGGGTATAGCTCAAT--GGT--AGAGCAGCAGCCTTCCAAGCTGAAT-----A-CGCGGGTTCGATTCCTCCGCTACCCTCCGCTCCA  
>tdbD00005147 *Buchnera\_aphidicola\_str.\_APS\_(Acyrtosiphon\_pisum)* 107806 Gly GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGCGAGTTCAAGTCTCGTTTCCGCTCCA  
>tdbD00005148 *Buchnera\_aphidicola\_str.\_APS\_(Acyrtosiphon\_pisum)* 107806 Gly TCC  
-GCGGACATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-CGCGGGTTCGAATTCCTCCGCTGTTCCGCT---  
>tdbD00005479 *Buchnera\_aphidicola\_str.\_Bp\_(Baizongia\_pistaciae)* 224915 Gly GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGTACAACCTTGCCAAGGTTGGG-----GTCGCGAGTTCAAACTCTCGTTTCCGCT---  
>tdbD00005478 *Buchnera\_aphidicola\_str.\_Bp\_(Baizongia\_pistaciae)* 224915 Gly TCC  
-GCGAATCGTATAAT--GGAT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGAATTCCTCCGCTGTTCCGCTCCA  
>tdbD00005368 *Buchnera\_aphidicola\_str.\_Sg\_(Schizaphis\_graminum)* 198804 Gly GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGCGAGTTTCGAATCTCGTTTCCGCTCCA  
>tdbD00005367 *Buchnera\_aphidicola\_str.\_Sg\_(Schizaphis\_graminum)* 198804 Gly TCC  
-GCGGACATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGAATTCCTCCGCTGCCCCGCT---  
>tdbD00000841 *Campylobacter\_jejuni* 197 Gly TCC  
-GCGGGAGTAGCTCAGTT--GGCT--AGAGCATCAGCCTTCCAAGCTGAGG-----GTCGCGGGTTCGAGTCCCCTTCCGCTCCA  
>tdbD00005187 *Campylobacter\_jejuni\_subsp.\_jejuni\_NCTC\_11168* 192222 Gly GCC  
-GCGGGAATAGCTCAGG--GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGCGAGTTTCGAATCTCGTTTCCGCTCCA  
>tdbD00005603 *Candidatus\_Blochmannia\_floridanus* 203907 Gly GCC  
-GCGGGAATAGCTCAGAT--GGTT--AGAGTGAACCTTGCCAAGGTTGAG-----GTCGCGAGTTTCGAATCTCGTTTCCGCT---  
>tdbD00005521 *Candidatus\_Proteochlamydia\_amoebophila\_UWE25* 264201 Gly GCC  
-GCGGGTGTAGCTCAGT--GGT--AGAGCATCAGTTTGCCAACGTTGAGA-----GTCGTGAGTTTCGAATCTCATCACCCTGCT---  
>tdbD00005520 *Candidatus\_Proteochlamydia\_amoebophila\_UWE25* 264201 Gly TCC  
-GCGCCTGTAGTTCAAT--GGT--AGAACAGTAGCCTTCCAAGCTACGA-----G-TGTCAGTTTCGATTCGATCAGGCGCT---  
>tdbD00005189 *Caulobacter\_crescentus\_CB15* 190650 Gly CCC  
-GCGGGCGTAGTTCAGA--GGT--AGAACGTGAGCTTCCAAGCTGAAT-----GTCGCGGGTTCGATTCCTCCGCTGCCCCGCTCCA  
>tdbD00005190 *Caulobacter\_crescentus\_CB15* 190650 Gly GCC

-GCGGGCGTAGCTCAGT--GGT--AGAGCGCCACCTTGCCAAGGTGGAT-----GTCGAGAGTTCGAATCTCTTCGCCCGCTCCA  
>tdbD00005191 *Caulobacter crescentus*\_CB15 190650 Gly TCC  
-GCGGGTATAGCACAAAT--GGT--AGTGCAGCAGCCTTCCAAGCTGAGG-----A-TGCGGGTTCGATTCCCGTACCCGCTCCA  
>tdbD00005231 *Chlamydia muridarum*\_Nigg 243161 Gly GCC  
-GCGGGTGTAGCTCAGT--GGT--AGAGCGCCACGTTGCCAACGTGAAG-----GTCGTGAGTTCAGCCTCATCACCCGCT---  
>tdbD00005230 *Chlamydia muridarum*\_Nigg 243161 Gly TCC  
-GCGCCCGTAGCTCAAT--GGT--AGAGCTGTAGCCTTCCAAGCTACCG-----G-TGTCAGTTCGATTCTGATCGGGCGCT---  
>tdbD00005136 *Chlamydophila pneumoniae*\_AR39 115711 Gly GCC  
-GCGGGTGTAGCTCAGT--GGT--AGAGCGTCACGTTGCCAACGTGAAG-----GTCGTGAGTTCAGCCTCATCACCCGCT---  
>tdbD00005359 *Chlorobium tepidum*\_TLS 194439 Gly CCC  
-GCGGGTGTAACTCAGTT--GGT--AGAGTGTGTTGCTTCCCAAGCAAAAT-----GTCGCGAGTTCGAATCTCGTACCCGCT---  
>tdbD00005358 *Chlorobium tepidum*\_TLS 194439 Gly GCC  
-GCGGGAATAGCTCAGCT--GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCT---  
>tdbD00005236 *Chlorobium tepidum*\_TLS 194439 Gly TCC  
-GCGGGAGTAACTCAGCT--GGT--AGAGTCAACGCTTCCAAGCTGTTG-----GTCGCGGGTTCGAGTCCCGTCTCCCGCT---  
>tdbD00005238 *Clostridium acetobutylicum*\_ATCC\_824 272562 Gly CCC  
-GCGGGAATAGCTCAGT--GGT--AGAGCACTAGCTTCCCAAGCTGGGT-----GCCGCGGGTTCGATACCCGTTTCCCGCTCCA  
>tdbD00005237 *Clostridium acetobutylicum*\_ATCC\_824 272562 Gly GCC  
-GCGGGAGTGGCTCAGT--GGT--AGAGCGTCACCTTGCCAAGGTGAAC-----GTCGCGAGTTCGAATCTCGTCTTCCGCTCCA  
>tdbD00005237 *Clostridium acetobutylicum*\_ATCC\_824 272562 Gly TCC  
-GCGGGTGTAACTCAAT--GGT--AGAGTGTAGCCTTCCAAGCTAGTT-----A-CGAGGGTTCGATTCCCTCTACCCGCTCCA  
>tdbD00005228 *Clostridium perfringens*\_str.\_13 195102 Gly GCC  
-GCGGGAGTACTCAAT--GGT--AGAGTGTACCTTGCCAAGGTGAAA-----GTTGCGAGTTCGAGTCTCGTCTTCCGCTCCA  
>tdbD00005229 *Clostridium perfringens*\_str.\_13 195102 Gly GCC  
-GCGGGAGTACTCAAT--GGT--AGAGTGTACCTTGCCAAGGTGAAA-----GTTGCGGGTTCGAGTCCCGTCTTCCGCTCCA  
>tdbD00005227 *Clostridium perfringens*\_str.\_13 195102 Gly TCC  
-GCGGGTGTAGTTCAAT--GGT--AGAACACCAGCCTTCCAAGCTGGAT-----A-CCCGGGTTCGATTCCCGGTACCCGCTCCA  
>tdbD00005443 *Clostridium tetani*\_E88 212717 Gly GCC  
-GCGGGAGTGGCTCAGT--GGT--AGAGCGTCACCTTGCCAAGGTGAAC-----GTCGTGGGTTCGAATCCCATCTTCCGCTCCA  
>tdbD00005444 *Clostridium tetani*\_E88 212717 Gly TCC  
-GCGGGTGTAGCTCAAT--GGT--AGAGTTCACGCTTCCAAGCTGGCT-----G-TGAGAGTTCGATTCTCTTACCCGCTCCA  
>tdbD00005512 *Corynebacterium diphtheriae*\_NCTC 13129 257309 Gly GCC  
-GCGGATGTAGCGCAGTT--GGT--AGCGCATCACCTTGCCAAGGTGAGG-----GTCGCGAGTTCGAGTCTCGTCATCCGCT---  
>tdbD00005472 *Coxiella burnetii*\_RSA 493 227377 Gly CCC  
-GCGGGTGTAGTTCAAT--GGT--AGAACATAAGCTTCCCAAGCTTAGA-----A-CGTGGGTTCGATTCCCATCACCCGCT---  
>tdbD00005473 *Coxiella burnetii*\_RSA 493 227377 Gly GCC  
-GCGGGAATAGCTCAGCT--GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGCGAGTTCGAATCTCGTTTCCCGCTCCA  
>tdbD00005471 *Coxiella burnetii*\_RSA 493 227377 Gly TCC  
-GCGGGTGTAGTTCAAC--GGT--AGAACTTCAGCCTTCCAAGCTGATA-----G-CGTGGGTTCGACTCCCATCACCCGCT---  
>tdbD00005192 *Deinococcus radiodurans*\_R1 243230 Gly CCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCGTCAGCTTCCCAAGCTGAAT-----GTCGCGAGTTCGAGTCTCGTTTCCCGCT---  
>tdbD00005193 *Deinococcus radiodurans*\_R1 243230 Gly GCC  
-GCGGGAGTACTCAGCT--GGT--AGAGCACTACCTTGCCAAGGTAGAT-----GTCGCGAGTTCGAATCTCGTCTCCCGCTCCA  
>tdbD00005194 *Deinococcus radiodurans*\_R1 243230 Gly TCC  
-GCGGGATTGTTAGT--GGT--AGCACAGCAGCCTTCCAAGCTTCTG-----G-CCTCGGTTTCGAATCCCGTATCCCGCTCCA  
>tdbD00005573 *Desulfovibrio vulgaris*\_subsp.\_vulgaris\_str.\_Hildenborough 882 Gly CCC  
-GCGGGAATAACTCAGC--GGT--AGAGTGTACGCTTCCCAAGCTGAAG-----GTCGCGGGTTCAAATCCCGTTTCCCGCTCCA  
>tdbD00005572 *Desulfovibrio vulgaris*\_subsp.\_vulgaris\_str.\_Hildenborough 882 Gly GCC  
-GCGGGAGTAACTCAGT--GGT--AGAGTGAACCTTGCCAAGGTTGAA-----GTCGCGGGTTCAAATCCCGTCTCCCGCTCCA  
>tdbD00005574 *Desulfovibrio vulgaris*\_subsp.\_vulgaris\_str.\_Hildenborough 882 Gly TCC  
-GCGGGAATACTCAGT--GGT--AGAGTGAACCTTGCCAAGGTTGAGG-----GTTGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005445 *Enterococcus faecalis*\_V583 226185 Gly GCC  
-GCGGAAATAGCTCAGT--GGT--AGAGCACCACCTTGCCAAGGTGGGG-----GTCGCGGGTTCGAACCCCGTTTCCCGCT---  
>tdbD00005446 *Enterococcus faecalis*\_V583 226185 Gly TCC  
-GCGGGTGTAGTTTGT--GGT--AAAACCACAGCCTTCCAAGCTGTTG-----T-CGCGAGTTCGATTCTCGTACCCGCT---  
>tdbD00000839 *Escherichia coli* 562 Gly CCC  
-GCGGGCGTAGTTCAAT--GGT--AGAACGAGAGCTTCCCAAGCTCTAT-----A-CGAGGGTTCGATTCCCTTCGCCCGCTCCA  
>tdbD00000838 *Escherichia coli* 562 Gly GCC  
-GCGGGAATACTCAGT--GGT--AGAGCACGACCTTGCCAAGGTGCGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00000837 *Escherichia coli* 562 Gly TCC  
-GCGGGCATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCGTTCGCCGCTCCA  
>tdbD00005362 *Fusobacterium nucleatum*\_subsp.\_nucleatum\_ATCC\_25586 190304 Gly GCC  
-GCGGGAATACTCAGT--GGT--AGAGCATAACCTTGCCAAGGTTAGG-----GTCGCGAGTTCGAGCCTCGTTTCCCGCTCCA  
>tdbD00005361 *Fusobacterium nucleatum*\_subsp.\_nucleatum\_ATCC\_25586 190304 Gly TCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCGTCAGCCTTCCAAGCTGAAT-----GTCGCGAGTTCGAACCTCGTTTCCCGCTCCA  
>tdbD00005540 *Geobacter sulfurreducens*\_PCA 243231 Gly CCC  
-GCGGGAATACTCAGT--GGT--AGAGTGTACGCTTCCCAAGCTGAAG-----GTCGCGGGTTCGAATCCCGTTTCCCGCTCCA  
>tdbD00005539 *Geobacter sulfurreducens*\_PCA 243231 Gly GCC  
-GCGGGAATACTCAGT--GGT--AGAGTGAACCTTGCCAAGGTTGAA-----GTCGCGGGTTCGAATCCCGTTTCCCGCTCCA  
>tdbD00000844 *Haemophilus influenzae* 727 Gly GCC  
-GCGGGAATACTCAGT--GGT--AGAGCACGACCTTGCCAAGGTGCGG-----GTCGCGAGTTCGAGCCTCGTTTCCCGCTCCA  
>tdbD00000846 *Haemophilus influenzae* 727 Gly TCC  
-GCGGGCATCGTATAAT--GGCT--ATTACCTTAGCCTTCCAAGCTAATG-----A-TGCGGGTTCGATTCCCGTTCGCCGCTCCA  
>tdbD00000827 *Helicobacter pylori* 210 Gly GCC  
-GCGGGAATACTCAGT--GGT--AGAGCACGACCTTGCCAAGGTGCGG-----GCCGCGGGTTCGATCCCGTTTCCCGCTCCA



>tdbD00000828 *Helicobacter pylori* 210 Gly TCC  
-GCGGAATAGCTCAGTT-GGCT-AGAGCATCAGCCTTCCAAGCTGAGG-----GTCGCGGGTTTCGAGTCCCCTTTCCCGCTCCA  
>tdbD00005180 *Helicobacter pylori*\_J99 85963 Gly GCC  
-GCGGAATAGCTCAGT--GGTA-GAAGCACGACCTTGCCAAGGTGCGG-----GCCGCGGGTTTCGATCCCCTTTCCCGCTCCA  
>tdbD00000826 *Lactobacillus delbrueckii*\_subsp.\_*bulgaricus* 1585 Gly GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAACATCACCTTGCCATGGTGGGG-----GTCGCGGGTTTCGAATCCCCTTCCCGCT---  
>tdbD00005542 *Lactobacillus johnsonii*\_NCC\_533 257314 Gly CCC  
-GCGGGTATAGTTAAT--GGT--AAAATGTGAGCTTCCAAGCTGAAG-----A-TGCGGGTTTCGATTACCGTATCCGCT---  
>tdbD00005543 *Lactobacillus johnsonii*\_NCC\_533 257314 Gly GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAACATCACCTTGCCATGGTGGGG-----GTCGCGGGTTTCGAATCCCCTTCCCGCTCCA  
>tdbD00005545 *Lactobacillus johnsonii*\_NCC\_533 257314 Gly GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAACACCACCTTGCCATGGTGGGG-----GTCGCGGGTTTCGAATCCCCTTCCCGCT---  
>tdbD00000829 *Lactococcus lactis* 1358 Gly TCC  
-GCGGATGTAGTTAAT--GGT--AGAACCACCTTGCCATGGTGGCT-----A-CGCGAGTTTCGATTCTCGTCATCCGCT---  
>tdbD00005548 *Leifsonia xyli*\_subsp.\_*xyli*\_str.\_CTCB07 281090 Gly CCC  
-GCGAGTGTAGTTCAAT--GGT--AGAACTTCAGCTTCCAAGCTGATA-----G-CGCGGGTTTCGATTCCCCTCACTCGCTCCA  
>tdbD00005416 *Leptospira interrogans*\_serovar\_*Lai*\_str.\_56601 189518 Gly GCC  
-GCGGAATAGCTCAGT--GGT--AGAGCACCTTCCCAAGGTGGGG-----GTCGCGGGTTTCGAATCCCCTTTCCCGCT---  
>tdbD00005219 *Listeria innocua*\_Climpl1262 272626 Gly GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAACATCACCTTGCCAAGGTGGGG-----GTCGCGGGTTTCGAACCCCCTTCCCGCT---  
>tdbD00005221 *Listeria innocua*\_Climpl1262 272626 Gly GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAACATCACCTTGCCAAGGTGGGG-----GTCGCGGGTTTCGAACCCCCTTCCCGCTCCA  
>tdbD00005222 *Listeria innocua*\_Climpl1262 272626 Gly GCC  
-GCGGAAGTAGTTCAGC--GGT--AGAACATCACCTTGCCAAGGTGGGG-----GTCGCGGGTTTCGAACCCCCTTCCCGCT---  
>tdbD00005220 *Listeria innocua*\_Climpl1262 272626 Gly TCC  
-GCGGGTGTAGTTTAAAT--GGT--AAAACACTACGCTTCCAAGGTGGT-----T-CGTGGGTTTCGATTCCCATCACCCGCT---  
>tdbD00005245 *Mesorhizobium loti*\_MAFF303099 266835 Gly GCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCACACCTTGCCAAGGTGGG-----GTCGAGCGTTTCGAATCGCTTACCCGCTCCA  
>tdbD00005244 *Mesorhizobium loti*\_MAFF303099 266835 Gly TCC  
-GCGGGTATAGCTCAGT--GGT--AGAGCAGCAGCCTTCCAAGCTGAAT-----A-TGCGGGTTTCGATTCCCCTACCCGCTCCA  
>tdbD00005468 *Mycobacterium bovis*\_AF2122/97 233413 Gly GCC  
-GCGGATGTAGCGCAGTT--GGT--AGCGCATCACCTTGCCAAGGTGAGG-----GTCGCGGGTTTCGAATCCCCTCATCCGCT---  
>tdbD00005467 *Mycobacterium bovis*\_AF2122/97 233413 Gly TCC  
-GCGGGCGTAGCTCAAT--GGT--AGAGCCCTAGTCTTCCAAGCTAGCC-----A-CGCGGGTTTCGATTCCCCTCGCCCGCT---  
>tdbD00005164 *Mycobacterium leprae*\_TN 272631 Gly TCC  
-GCGGGCGTAGCTCAAT--GGT--AGAGCCCTAGTCTTCCAAGCTAGCT-----A-CACGGGTTTCGATTCCCCTCGCCCGCT---  
>tdbD00005464 *Mycoplasma gallisepticum*\_R 233150 Gly TCC  
-GCGGGTGTAGTTCAAT--GGT--AGAAGTGCAGCCTTCCAAGCTGTTA-----A-TGTGGGTTTCGATTCCCCTACCCGCTCCA  
>tdbD00000811 *Mycoplasma genitalium* 2097 Gly TCC  
-GCGAGTATAGTTAAT--GGT--AGAACATCAGCCTTCCAAGCTGATC-----G-TGTCGGTTTCGATTCCGATTACTCGCTCCA  
>tdbD00000813 *Mycoplasma pneumoniae* 2104 Gly TCC  
-GCGAGTATAGTTTAAAT--GGT--AGAACATCAGCCTTCCAAGCTGATC-----G-TGTCGGTTTCGATTCCGATTACTCGCTCCA  
>tdbD00005152 *Neisseria meningitidis*\_MC58 122586 Gly GCC  
-GCGGAATAGCTCAGTT--GGT--AGAGCGCAACCTTGCCAAGGTGAG-----GTCGCGAGTTTCGAGACTCGTTTCCCGCTCCA  
>tdbD00005153 *Neisseria meningitidis*\_MC58 122586 Gly TCC  
-GCGGGTGTAGCTCAAT--GGT--AGAGCAGAAGCCTTCCAAGCTTACG-----G-TGAGGGTTTCGATTCCCCTTACCCGCTCCA  
>tdbD00005495 *Nitrosomonas europaea*\_ATCC 19718 228410 Gly CCC  
-GCGGGTGTAGTTCAAT--GGC--AGAACGGTAGCTTCCAAGCTGCAT-----A-CGAGGGTTTCGATTCCCCTTACCCGCTCCA  
>tdbD00005496 *Nitrosomonas europaea*\_ATCC 19718 228410 Gly TCC  
-GCGGGTGTAGCTCAAT--GGT--AGAGCAGAAGCCTTCCAAGCTTACG-----A-CGAGGGTTTCGATTCCCCTTACCCGCTCCA  
>tdbD00005257 *Nostoc*\_sp.\_PCC 7120 103690 Gly CCC  
-GCGGGCGTAATTCAGT--GGT--AGAATGTACCTTCCAAGGTGAAC-----GTCGTGGGTTTCGAGTCCCCTCGCCCGCT---  
>tdbD00005259 *Nostoc*\_sp.\_PCC 7120 103690 Gly GCC  
-GCGGGTATAGCTCAGT--GGT--AGAGCGTCACCTTGCCAAGGTGAAT-----GTCGCGGGTTTCGAATCGCGTTACCCGCT---  
>tdbD00005256 *Nostoc*\_sp.\_PCC 7120 103690 Gly TCC  
-GCGATCGTGGTGTAAC--GGC--AGCATCAGAGTCTTCCAAGCTCAG-----G-TACGAGTTTCGAGTCTCGTCGATCGCT---  
>tdbD00005258 *Nostoc*\_sp.\_PCC 7120 103690 Gly TCC  
-GCGGGCGTAGTTTAAAT--GGT--AAAACCTATAGCCTTCCAAGCTATTA-----A-TGCGGGTTTCGATTCCCCTCGCCCGCT---  
>tdbD00005418 *Oceanobacillus iheyensis*\_HTE831 221109 Gly TCC  
-GCGGGTGTAGTTAAT--GGT--AAAACCTCAGCCTTCCAAGCTGATG-----A-CGAGGGTTTCGATTCCCCTTACCCGCTCCA  
>tdbD00005515 *Onion yellows phytoplasma*\_OY-M 262768 Gly TCC  
-GCGGGCGTCGTATAAT--GGCC-ATTACCTTAGCCTTCCAAGCTAAA-----A-CGTGGGTTTCGATTCCCCTCGCCCGCTCCA  
>tdbD00005199 *Pasteurella multocida*\_subsp.\_*multocida*\_str.\_Pm70 272843 Gly GCC  
-GCGGAATAGCTCAGTT--GGT--AGAGCACACCTTGCCAAGGTGGG-----GTCGCGAGTTTCGAGCTCGTTTCCCGCTCCA  
>tdbD00005523 *Photobacterium luminescens*\_subsp.\_*laumondii*\_TTO1 243265 Gly CCC  
-GCGAGCGTAGTTCAAT--GGC--AGAACGAGAGCTTCCAAGCTCTAT-----A-CGAGGGTTTCGATTCCCCTTCGCTCGCTCCA  
>tdbD00005551 *Porphyromonas gingivalis*\_W83 242619 Gly CCC  
-GCGGTAGTAGCTCAGTT--GGT--AGAGCATCAGCTTCCAAGCTGAGG-----GTCACGAGTTTCGAGCTCGCTACCCGCT---  
>tdbD00005550 *Porphyromonas gingivalis*\_W83 242619 Gly GCC  
-GCGGAAGTAGCTCAGTT--GGT--AGAGCATAACCTTGCCAAGGTTAGG-----GTCGCGGGTTTCGAGTCCCCTTCCCGCT---  
>tdbD00005552 *Porphyromonas gingivalis*\_W83 242619 Gly GCC  
-GCGGAAGTAGCTCAGTT--GGT--AGAGCATAACCTTGCCAAGGTTAGG-----GTCGCGGGTTTCGAGTCCCCTTCCCGCTCCA  
>tdbD00005549 *Porphyromonas gingivalis*\_W83 242619 Gly TCC  
-GCGGAAGTAGCTCAGTC--GAT--AGAGCATCAGCCTTCCAAGCTGAGG-----GTCGCGGGTTTCGAGCCCCTTCCCGCT---  
>tdbD00005581 *Propionibacterium acnes*\_KPA171202 267747 Gly CCC

-GCGGGCGTAGCTCAAT--GGT--AGAGCGTCAGCTTCCCAAGCTGGAT-----A-CGCGGGTTCGATTCCCCTCGCCCCTCCA  
>tdbD00005579 Propionibacterium\_acnes\_KP171202\_267747\_Gly\_GCC  
-GCGGACGTGGCTCAGTT--GGT--AGAGCATCACCTTGCCAAGGTGAGG-----GTCGCGGGTTCGAGTCCCCTCGTCCGCT---  
>tdbD00005580 Propionibacterium\_acnes\_KP171202\_267747\_Gly\_TCC  
-GCGGATGTAGCTCAAT--GGT--AGAGCCCAGTCTTCCAACTGGCT-----A-CGCGGGTTCGATTCCCCTCATCCGCTCCA  
>tdbD00000840 Pseudomonas\_aeruginosa\_287\_Gly\_TCC  
-GCGGGTATAGTTCAGT--GGT--AGAACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCCTACCCGCTCCA  
>tdbD00005203 Pseudomonas\_aeruginosa\_PA01\_208964\_Gly\_CCC  
-GCGGGCGTCGTATAAT--GGC--ATTACCTGAGCTTCCCAAGCTCATG-----A-CGAGGGTTCGATTCCCCTCGCCCCTCCA  
>tdbD00005503 Pseudomonas\_syringae\_pv\_tomato\_str\_DC3000\_223283\_Gly\_CCC  
-GCGGGTATAGTTGAAT--GGT--ACAACCTATTGCTTCCCAAGCAATCG-----G-TGAGGGTTCGATTCCCCTACCCGCTCCA  
>tdbD00005501 Pseudomonas\_syringae\_pv\_tomato\_str\_DC3000\_223283\_Gly\_TCC  
-GCGGGTATAGTTTGT--GGT--AGAACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCCTACCCGCTCCA  
>tdbD00005253 Ralstonia\_solanacearum\_GMI1000\_267608\_Gly\_CCC  
-GCGGGCGTCGTATAAT--GGT--AATACCCTAGCTTCCCAAGCTAGAG-----C-CGTGGGTTCGATTCCCCTACCCGCTCCA  
>tdbD00005254 Ralstonia\_solanacearum\_GMI1000\_267608\_Gly\_GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCGCAACCTTGCCAAGGTTGAG-----GTCGCGAGTTCGAGCCTCGTTTCCCGCTCCA  
>tdbD00005490 Rhodopirellula\_baltica\_SH\_1\_243090\_Gly\_GCC  
-GCGCCCATGATGTAGC--GGT--AGCCTGTGCCTTGCCATGGCGGAA-----G-TGTGGGTTCGACTCCCCTGCGGCT---  
>tdbD00005491 Rhodopirellula\_baltica\_SH\_1\_243090\_Gly\_GCC  
-GCGGCTGTAGCTCAGTT--GGC--AGAGCATCACCTTGCCAACGTGATT-----GTCGTGCGTTCGAATCCGATCAGCCGCT---  
>tdbD00005492 Rhodopirellula\_baltica\_SH\_1\_243090\_Gly\_TCC  
-GCGGGTGTAGCTCAAT--GGT--AGAGCAGCAGCCTTCCAAGCTGAAT-----A-CGAGGGTTCGATTCCCCTACCCGCT---  
>tdbD00005239 Rickettsia\_conorii\_str\_Malish\_7\_272944\_Gly\_GCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCGCCACCTTGCCAAGGTTGAA-----GTCGAGGGTTCGAATCCCCTACCCGCTCCA  
>tdbD00005240 Rickettsia\_conorii\_str\_Malish\_7\_272944\_Gly\_TCC  
-GCGGGTGTAGCTCAAT--GGT--AGAGTTCAGCCTTCCAAGCTGGCT-----G-TGTGGGTTCGATTCCCCTACCCGCTCCA  
>tdbD00005369 Rickettsia\_prowazekii\_str\_Madrid\_E\_272947\_Gly\_GCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCGCTACCTTGCCAAGGTCGAA-----GTCGAGGGTTCGAATCCCCTACCCGCTCCA  
>tdbD00005554 Rickettsia\_typhi\_str\_Wilmington\_257363\_Gly\_TCC  
-GCGGGTGTAACTCAAT--GGT--AGAGTTCAGCCTTCCAAGCTGGCT-----G-TGTGGGTTCGATTCCCCTACCCGCTCCA  
>tdbD00005424 Shewanella\_oneidensis\_MR-1\_211586\_Gly\_GCC  
-GCGACATTAGCTCAGTT--GGT--AGAGCGATACCTTGCCAAGGTATAG-----GTCATCGGTTTCGAACCCGATATGTCGCTCCA  
>tdbD00005425 Shewanella\_oneidensis\_MR-1\_211586\_Gly\_TCC  
-GCGGGCATCGTATAAT--GGT--ATTACTCCAGCCTTCCAAGCTGATA-----A-CGCGGGTTCGATTCCCCTGCCCCCTCCA  
>tdbD00005429 Shigella\_flexneri\_2a\_str\_301\_198214\_Gly\_GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCAGCAGCTTGCCAAGGTCGAG-----GTCTCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005268 Sinorhizobium\_meliloti\_1021\_266834\_Gly\_CCC  
-GCGGGTGTAGTTCAGT--GGT--AGAACCGCCAGCTTCCCAAGCTTGAT-----GTCGTGCGTTCGATCCCCTACCCGCTCCA  
>tdbD00005270 Sinorhizobium\_meliloti\_1021\_266834\_Gly\_GCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGGGGTTCGAATCGCCTACCCGCTCCA  
>tdbD00005530 Staphylococcus\_aureus\_subsp\_aureus\_MRSA252\_282458\_Gly\_TCC  
-GCGGGTGTAGTTTAAAT--GGC--AAAACCTCAGCCTTCCAAGCTGATG-----T-TGTGGGTTCGATTCCCCTACCCGCTCCA  
>tdbD00000836 Stigmatella\_aurantiaca\_41\_Gly\_TCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCGTCAGCCTTCCAAGCTGAAT-----GTCGTGGGTTTCGAGTCCCATTCCCGCTCCA  
>tdbD00005430 Streptococcus\_agalactiae\_2603V/R\_208435\_Gly\_GCC  
-GCGAACGTAGTTCAGT--GGT--AGAACATCACCTTGCCAAGGTGAGG-----GTCGCGGGTTCGAACCCCTCGTTCGCT---  
>tdbD00005431 Streptococcus\_agalactiae\_2603V/R\_208435\_Gly\_TCC  
-GCGGGTGTAGTTTGT--GGT--AAAACCTCAGCCTTCCAAGCTGTTG-----T-CGCGAGTTCGATTCTCGTACCCGCT---  
>tdbD00005432 Streptococcus\_mutans\_UA159\_210007\_Gly\_GCC  
-GCGAACGTAGTTCAGT--GGT--AGAACATCACCTTGCCAAGGTGGGG-----GTCGCGGGTTCGAATCCCCTCGTTCGCT---  
>tdbD00005235 Streptococcus\_pneumoniae\_TIGR4\_170187\_Gly\_GCC  
-GCGAACGTAGTTCAGT--GGT--AGAACACCACCTTGCCAAGGTGGGG-----GTCGCGGGTTCGAATCCCCTCGTTCGCT---  
>tdbD00005484 Streptomyces\_avermitilis\_MA-4680\_227882\_Gly\_CCC  
-GCGGGTGTAGTTTAAAT--GGT--AGAACATGAGCTTCCCAAGCTCAGA-----G-CGCGAGTTCGATTCTCGTACCCGCTCCA  
>tdbD00005483 Streptomyces\_avermitilis\_MA-4680\_227882\_Gly\_GCC  
-GCGGACGTAGCTCAGTT--GGT--AGAGCGCAACCTTGCCAAGGTTGAG-----GTCGCGAGTTCGAGCCTCGTTCGCTCCA  
>tdbD00005486 Streptomyces\_avermitilis\_MA-4680\_227882\_Gly\_GCC  
-GCGGACGTAGCTCAGTT--GGT--AGAGCGCAACCTTGCCAAGGTTGAG-----GTCGCGAGTTCGAGCCTCGTTCGCTCCA  
>tdbD00005485 Streptomyces\_avermitilis\_MA-4680\_227882\_Gly\_TCC  
-GCGGGCGTAGCTCAAT--GGT--AGAGCCCTAGCTTCCAACTAGCT-----A-CGCGGGTTCGATTCCCCTCGCCCCTCCA  
>tdbD00005420 Streptomyces\_coelicolor\_A3(2)\_100226\_Gly\_CCC  
-GCGGGTGTAGTTTAAAT--GGT--AGAACATGAGCTTCCCAAGCTGAGA-----G-CGCGAGTTCGATTCTCGTACCCGCTCCA  
>tdbD00005421 Streptomyces\_coelicolor\_A3(2)\_100226\_Gly\_GCC  
-GCGAACGTAGCTCAGTT--GGT--AGAGCGCAACCTTGCCAAGGTTGAG-----GTCGCGAGTTCGAACCTCGTTCGCTCCA  
>tdbD00005423 Streptomyces\_coelicolor\_A3(2)\_100226\_Gly\_TCC  
-GCGGGCGTAGCTCAAT--GGT--AGAGCACCAGCTTCCAACTGGCT-----A-CGCGGGTTCGATTCCCCTCGCCCCT---  
>tdbD00005557 Symbiobacterium\_thermophilum\_IAM\_14863\_292459\_Gly\_CCC  
-GCGGGTGTAGTTCAAT--GGT--AGAACGTGAGCTTCCCAAGCTGAAG-----A-CGTGGGTTTCGATTCCCCTACCCGCTCCA  
>tdbD00005558 Symbiobacterium\_thermophilum\_IAM\_14863\_292459\_Gly\_CCC  
-GCGGGTGTAGTTCAAT--GGT--AGAACATGAGCTTCCCAAGCTGAGA-----A-CGTGGGTTTCGATTCCCCTACCCGCTCCA  
>tdbD00005555 Symbiobacterium\_thermophilum\_IAM\_14863\_292459\_Gly\_GCC  
-GCGGGTTTGTAGCTCAGTT--GGT--AGAGCGCCACCTTGCCAAGGTTGAG-----GTCGCGAGTTCGAGTCTCGTAAACCCGCTCCA  
>tdbD00005556 Symbiobacterium\_thermophilum\_IAM\_14863\_292459\_Gly\_TCC  
-GCGGGTGTAGCTTAGT--GGT--AAAGCTCCAGCCTTCCAAGCTGGCG-----A-CGAGGGTTCGATTCCCCTACCCGCTCCA

>tdbD00000849 *Synechocystis*\_sp. 1143 Gly CCC  
-GCGGTATAGTTTAGT--GGT--AAAACGAAAGCCTCCCAATGCTTTAG-----T-TGGGGGTTTCGATTCCCCCTACCCGCT---  
>tdbD00000850 *Synechocystis*\_sp. 1143 Gly GCC  
-GCGGTATAGCTCAGT--GGT--AGAGCGCAACCTTGCCAAGGTTGAT-----GTCGCGGTTTCGAATCGCGTTACCCGCT---  
>tdbD00000848 *Synechocystis*\_sp. 1143 Gly TCC  
-GCGGTGTAGTTTAGT--GGT--AAAACCTTAGCCTTCCAAGCTAATG-----A-TAGGGGTTTCGATTCCCCCTACCCGCT---  
>tdbD00005389 *Thermoanaerobacter*\_tengcongensis\_MB4\_273068 Gly CCC  
-GCGGATGTAGCTCAGC--GGT--AGAGCATCAGCTTCCCAAGCTGAGG-----GCCCGGGGTTCAAATCCCGTCATCCGCTCCA  
>tdbD00005390 *Thermoanaerobacter*\_tengcongensis\_MB4\_273068 Gly GCC  
-GCGGCATAGCTCAGTT--GGC--AGAGCATCACCTTGCCAAGGTGAGG-----GTCGCGAGTTTCGAGTCTCGTTGCCGCTCCA  
>tdbD00005391 *Thermoanaerobacter*\_tengcongensis\_MB4\_273068 Gly TCC  
-GCGGTGTAGCTCAAT--GGT--AGAGCCCCAGCCTTCCAAGCTGGTT-----G-CGTGGGTTTCGATTCCCATCACCCGCTCCA  
>tdbD00005384 *Thermosynechococcus*\_elongatus\_BP-1\_197221 Gly CCC  
-GCGGACGTAATTCAGT--GGT--AGAATGTCAGCTTCCCAAGGTGAAC-----GTCGTGGGTTTCGAGTCCCATCGTCCGCT---  
>tdbD00005383 *Thermosynechococcus*\_elongatus\_BP-1\_197221 Gly TCC  
-GCGGCATGTTTTAAT--GGT--AAAACCTTAGCCTTCCAAGCTAGAG-----A-CGCGGGTTTCGATTCCCGTCCCGCT---  
>tdbD00005209 *Thermotoga*\_maritima\_MSB8\_243274 Gly CCC  
-GCGGTGTAGCTCAGT--GGT--AGAGCACCAGCTTCCCAAGGTGAGG-----GTCGCGGGTTTCGAATCCCGTCGCCCCTCCA  
>tdbD00005210 *Thermotoga*\_maritima\_MSB8\_243274 Gly GCC  
-GCGGTGTAGCTCAGT--GGT--AGAGCACCAGCTTCCCAAGGTGAGG-----GTCGCGGGTTTCGAATCCCGTCGCCCCTCCA  
>tdbD00005211 *Thermotoga*\_maritima\_MSB8\_243274 Gly TCC  
-GCGGTGTAGCTCACT--GGT--AGAGCATCGCCTTCCCAAGGTGAGG-----GTTGCGGGTTTCGAGTCCCCTCGCCCCTCCA  
>tdbD00000835 *Thermus*\_thermophilus\_274 Gly CCC  
-GCGGAGTAGCTCAGTT--GGT--AGAGCATCGGCTTCCCAAGCCGAGG-----GTCGCGGGTTTCGAGTCCCCTCGCCCCTCCA  
>tdbD00000834 *Thermus*\_thermophilus\_274 Gly GCC  
-GCGGAGTAGCTCAGT--GGT--AGAGCAGCACCTTGCCAAGGTGAGG-----GTCGCGGGTTTCAGTCCCCTCGCCCCTCCA  
>tdbD00005582 *Thermus*\_thermophilus\_HB27\_262724 Gly TCC  
-GCGGAGTAGCTCAGTTGGT--AGAGCATCGGCTTCCCAAGCCGAGG-----GTCGCGGGTTTCGAATCCCGTCTCCCGCTCCA  
>tdbD00005586 *Treponema*\_denticola\_ATCC\_35405\_243275 Gly GCC  
-GCGGAATAGCTCAGT--GGT--AGAGCGCACCTTGCCAAGGTGAGG-----GTCGCGAGTTCAATCCTCGTTTCCCGCT---  
>tdbD00005587 *Treponema*\_denticola\_ATCC\_35405\_243275 Gly TCC  
-GCGGATGTCGTATAAC--GGCT--ATTACCCAGCCTTCCAAGCTGGAG-----A-CGTGGGTTTCGACTCCCATCATCCGCT---  
>tdbD00000817 *Treponema*\_pallidum\_160 Gly GCC  
-GCGGAATAGCTCAGT--GGT--AGAGCGCACCTTGCCAAGGTGAGG-----GTCGCGGGTTTCGATCCCCGTTTCCCGCT---  
>tdbD00000816 *Treponema*\_pallidum\_160 Gly TCC  
-GCGGATGTTGTATAAC--GGCT--ATTACCCAGCCTTCCAAGCTGGAG-----A-CGTGGGTTTCGACTCCCATCATCCGCT---  
>tdbD00005457 *Tropheryma*\_whipplei\_str. Twist\_203267 Gly CCC  
-GCGAGTGTAGTTCAAT--GGC--AGAATTCAGCTTCCCAAGCTGAGC-----G-CGCGGGTTTCGATTCCCGTCACTCGCT---  
>tdbD00005456 *Tropheryma*\_whipplei\_str. Twist\_203267 Gly GCC  
-GCGGATGTGGCGCAGT--GGT--AGCGCATCACCTTGCCAAGGTGAGG-----GTCGCGAGTTTCGAATCTCGTATCCGCT---  
>tdbD00005166 *Ureaplasma*\_parvum\_serovar\_3\_38504 Gly TCC  
-GCGGTGTAGTTCAAT--GGT--AGAATATAGCCTTCCAAGCTATTA-----G-TGTGGGTTTCGATTCCCATCACCCGCTCCA  
>tdbD00005156 *Vibrio*\_cholerae\_O1\_biov. El Tor\_str. N16961\_243277 Gly GCC  
-GCGACTAGCTCAGTT--GGT--AGAGCGCAACCTTGCCAAGGTGAG-----GTCAGGATTCGAACCTCGTGTGTCGCTCCA  
>tdbD00005589 *Wolbachia*\_endosymbiont\_of\_Drosophila\_melanogaster\_163164 Gly GCC  
-GCGGAGTAGCTCAGTT--GGT--AGAGCGCAACCTTGCCAAGGTGAG-----GTCGAGGTTTCGAACCCCTTCTCCCGCT---  
>tdbD00005588 *Wolbachia*\_endosymbiont\_of\_Drosophila\_melanogaster\_163164 Gly TCC  
-GCGGTATAGCTCAAT--GGT--AGAGCTTAGCCTTCCAAGCTAGTG-----A-CGTGGGTTCAATTCACCTATCCGCT---  
>tdbD00005397 *Xanthomonas*\_axonopodis\_p. citri\_str. 306\_190486 Gly CCC  
-GCGGGCTAGCTCAAT--GGT--AGAGCTGTAGCTTCCCAAGCTACTG-----A-CGTGGGTTTCGATTCCCATCGCCCCTCCA  
>tdbD00005396 *Xanthomonas*\_axonopodis\_p. citri\_str. 306\_190486 Gly GCC  
-GCGGAATAGCTCAGTT--GGT--AGAGCGCAACCTTGCCAAGGTGAG-----GTCGCGAGTTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005395 *Xanthomonas*\_axonopodis\_p. citri\_str. 306\_190486 Gly TCC  
-GCGGAGTAGTTCAAC--GGT--AGAACCTCAGCCTTCCAAGCTGATG-----G-TGCGGGTTTCGATTCCCGTCTCCCGCTCCA  
>tdbD00005212 *Xylella*\_fastidiosa\_9a5c\_160492 Gly CCC  
-GCGGGCTAGCTCAAT--GGT--AGAGCTGTAGCTTCCCAAGCTACCG-----A-CGTGGGTTTCGATTCCCATCGCCCCTCCA  
>tdbD00005215 *Xylella*\_fastidiosa\_9a5c\_160492 Gly TCC  
-GCGGAGTAGTTCAAA--GGT--AGAACCTCAGCCTTCCAAGCTGATG-----G-TGCGGGTTTCGATTCCCGTCTCCCGCTCCA  
>tdbD00005561 *Yersinia*\_pestis\_biov. Microtus\_str. 91001\_229193 Gly CCC  
-GCGGTGTAGTTCAAT--GGT--AGAACGAGAGCTTCCCAAGCTCTAT-----A-CGAGGGTTTCGATTCCCTTACCCGCTCCA  
>tdbD00005560 *Yersinia*\_pestis\_biov. Microtus\_str. 91001\_229193 Gly TCC  
-GCGGCATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGTGGGTTTCGATTCCCCTGCCCCTCCA  
>tdbD00000981 *Acholeplasma*\_laidlawii\_2148 His GTG  
GGCGTTGTGGCGAAGT--GGTT--AACGCATCGGCTTGTGGCGCCGACA-----CTCGGGGTTCAATTCCTCCGCGCCCA  
>tdbD00005818 *Acinetobacter*\_sp. ADP1\_62977 His GTG  
GGTGGATGTAGCTCAGTT--GGT--AGAGCCTGGATTGTGATTCCAGTT-----GTCGCGGGTTTCGAATCCCGTCATTCACCCCA  
>tdbD00000991 *Aeromonas*\_hydrophila\_644 His GTG  
GGTGGCTGTAGCTCAGTT--GGT--AGAGTCCCGATTGTGATTCCGGTT-----GTCGTGGGTTTCGAGCCCCATCAGCCACCCCA  
>tdbD00005681 *Aquifex*\_aeolicus\_VF5\_224324 His GTG  
GGAGGTGTAGCTCAGTT--GGT--AGAGCGGGGACTGTGGATCCCGT-----GTCGCGGGTTTCGAGTCCCGTCAACCTCCCA  
>tdbD00005784 *Bacillus*\_anthracis\_str. Ames\_198094 His GTG  
GGCGTTGTGGCGAAGT--GGTT--AACGCACCGATTGTGGCTCCGGCA-----TTCGTGGGTTTCGATTCCCATCAGTCGCCCCA  
>tdbD00005759 *Bacillus*\_halodurans\_C-125\_272558 His GTG  
GGGACTGTGGCGAAGT--GGTT--AACGCACCGATTGTGGCTCCGGCA-----CTCGTGGGTTTCGATTCCCATCAGTCGCCCCA  
>tdbD00000986 *Bacillus*\_subtilis\_1423 His GTG

GGCGGTTGTGGCGAAGT--GGTT-AACGCACCAGATTGTGGCTCTGGCA-----CTCGTGGGTTTCGATTCCCATCAATCGCCCCA  
>tdbD00000987 *Bacillus subtilis* 1423 His GTG  
GGCGGTTGTGGCGAAGT--GGTT-AACGCACCAGATTGTGGCTCTGGCA-----TTCGTGGGTTTCGATTCCCATCAATCGCCCCA  
>tdbD00005782 *Bacteroides thetaiotaomicron* VPI-5482 226186 His GTG  
GGTGGATGTAGTTCAGTT--GGTT-AGAGCGTCAGATTGTGGTTCTGAAT-----GTCGCCGGTTTCGAGTCCGGTCTTCCACC---  
>tdbD00005786 *Bdellovibrio bacteriovorus* HD100 264462 His GTG  
GGTGGGTATAGCTCAGTT--GGT--AGAGCATCGGATTGTGATTCCGAGT-----GTCGCCGGTTCAAGCCCCGTTACTCACCCEA  
>tdbD00005748 *Bifidobacterium longum* NCC2705 206672 His GTG  
GGTGGCCATAGCTCAGTT--GGT--AGAGCATCTGATTGTGGTTCAGAAG-----GTCGCCGGTTTCGAGCCCGGTTGGCCACCCCA  
>tdbD00000983 *Borrelia burgdorferi* 139 His GTG  
GGTGGTTGTAGCTCAGTT--GGT--AGAGCGTCGGGTTGTGGTTCGCAAT-----GTCGCCGGTTCAAGCCCCGTTCAATCACC---  
>tdbD00005653 *Buchnera aphidicola* str. APS (*Acyrtosiphon pisum*) 107806 His GTG  
GGTGGCTATAGCTCAGTT--GGT--AGAGTGTGGATTGTGATTCCAGTG-----GTCATGGGTTCAAGTCCCATTAGCCACCCCA  
>tdbD00005775 *Buchnera aphidicola* str. Bp (*Baizongia pistaciae*) 224915 His GTG  
GGTGGCTATAGCTCAGTT--GGT--AGAGTCTGGATTGTGATTCCAGTT-----GTCATGGGTTCAAGTCCCATTAGCCACC---  
>tdbD00005733 *Buchnera aphidicola* str. Sg (*Schizaphis graminum*) 198804 His GTG  
GGTGGCTATAGCTCAGTT--GGT--AGAGTCTGGATTGTGATTCCAGTG-----GTCATGGGTTCAAGTCCCATTAGCCACC---  
>tdbD00005790 *Candidatus jejuni* subsp. *jejuni* NCTC\_11168 192222 His GTG  
GGTGGTGTAGCTCAGTC--GGTT-AGAGCATCAGATTGTGGTCTGAGG-----GTCGTGGGTTCAATCCCATCACTCACCCEA  
>tdbD00005823 *Candidatus Blochmannia floridanus* 203907 His GTG  
GGTGGTGTAGCTCAGTT--GGT--AGAGCTCTGATTGTGGTTCGAGT-----GTCGTGGGTTTCGAATCCCATCAGTCACC---  
>tdbD00005790 *Candidatus Protochlamydia amoebophila* UWE25 264201 His GTG  
GGCGGTCGTAGCTCAGTT--GGTT-AGAGCGTGGATTGTGGTTCGCAAT-----GTCGCCGGTTTCGAATCCCCTCGATCGCC---  
>tdbD00005687 *Chlamydia muridarum* Nigg 243161 His GTG  
GGCGAAGCTAGCTCAGTT--GGTT-AGAGCGTCGGATTGTGGTTCGCAAG-----GTCGCCGGTTTCGAACCCCGTTCGTTCCGCC---  
>tdbD00005647 *Chlamydia pneumoniae* AR39 115711 His GTG  
GGCGAAGCTAGCTCAGTT--GGTT-AGAGCGTCGGATTGTGGTTCGCAAG-----GTCGCCGGTTTCGAACCCCGTTCGTTCCGCC---  
>tdbD00005730 *Chlorobium tepidum* TLS 194439 His GTG  
GGTGGTGTAGCTCAGTT--GGTT-AGAGCGCCAGGTTGTGGCCCTGGAG-----GTCGGGGGTTTCGAGTCCCCTCATTACCCCG  
>tdbD00005690 *Clostridium acetobutylicum* ATCC\_824 272562 His GTG  
GGTGGGTATAGCTCAGTT--GGT--AGAGCGCCAGATTGTGGTTCGCAAT-----GTCTAGGGTTTCGAGACCCTATATTACC---  
>tdbD00005686 *Clostridium perfringens* str. 13 195102 His GTG  
GGTGGGCGTAGTTCAGTT--GGT--AGAGCACCAGATTGTGGTCTGGGT-----GTCGCCGAGTTTCGAGTCTCGTCGCTCACCCEA  
>tdbD00005761 *Clostridium tetani* E88 212717 His GTG  
GGTGGGTATAGCTCAGTT--GGT--AGAGCGCCAGATTGTGGTTCGCAAT-----GCCAAGGGTTTCGAGTCCCCTTATCCACCCCA  
>tdbD00005787 *Corynebacterium diphtheriae* NCTC\_13129 257309 His GTG  
GGTGGCTGTAGTTCAGTT--GGT--AGAGCACCAGGTTGTGATCCTGGGT-----GTCGCCGGTTTCGAGCCCCGTCAGCCACC---  
>tdbD00005773 *Coxiella burnetii* RSA\_493 227377 His GTG  
GGTGGGCGTAGCTCAGTT--GGT--AGAGCCCCGATTGTGATTCCGGTT-----GTCGTGGGTTTCAGTCCCATCGTCCACCCCA  
>tdbD00005672 *Deinococcus radiodurans* R1 243230 His GTG  
GGTGGAAATTAGCTCAGTC--GGTT-AGAGCGCCGCTCTGTGGAAGCGGAG-----GCCGTGGGTTTCAGTCCCATATTCCACCCCA  
>tdbD00005810 *Desulfovibrio vulgaris* subsp. *vulgaris* str. *Hildenborough* 882 His GTG  
GGCGGATGTAGCTCAGCA--GGT--AGAGCACCTGGTTGTGGCCAGGTC-----GCCGTGGGTTTCAGTCCCATCATTCCGCCCCA  
>tdbD00005762 *Enterococcus faecalis* V583 226185 His GTG  
GGCGATCGTGGTGAAGT--GGTT-AACACACCAGATTGTGGCTCTGGCA-----TTCGTGGGTTTCGATTCCCATCGGTCCGCC---  
>tdbD00000988 *Escherichia coli* 562 His GTG  
GGTGGCTATAGCTCAGTT--GGT--AGAGCCCTGGATTGTGATTCCAGTT-----GTCGTGGGTTTCGAATCCCATTAGCCACCCCA  
>tdbD00005731 *Fusobacterium nucleatum* subsp. *nucleatum* ATCC\_25586 190304 His GTG  
GGTGGCCGTAGTTCAGTT--GGT--AGAGCGCCAGTTGTGGCACTGGTT-----GTCGCCGAGTTTCGAGCCTCGTCGCTCACCCEA  
>tdbD00005797 *Geobacter sulfurreducens* PCA 243231 His GTG  
GGTGGCTATGGTGAAGG--GGTCTAACACACATGACTGTGACTCAGCA-----TTCGTGGGTTTCGAATCCCCTAGCCACCCCA  
>tdbD00005770 *Helicobacter hepaticus* ATCC\_51449 235279 His GTG  
GGTGGGTGTAGCTCAGTT--GGTT-AGAGCATCAGGTTGTGGCTCTGAGG-----GTCGTGGGTTTCGAGCCCCATCTCCACCCCA  
>tdbD00000985 *Helicobacter pylori* 120 His GTG  
GGTGGGAGTAGCTCAGTC--GGTT-AGAGCATCAGATTGTGGTCTGAGG-----GTCGTGGGTTTCGATTCCCATCTTCCACCCCA  
>tdbD00005798 *Lactobacillus johnsonii* NCC\_533 257314 His GTG  
GGCGGAATTGGTGAAGT--GGTT-AACACACCAGGTTGTGGATCCGGCA-----TGCCTGGGTTTCGATCCCACATTCCGCC---  
>tdbD00005763 *Lactobacillus plantarum* WCFS1 220668 His GTG  
GGCGGTAGTGGCGAAGT--GGTT-AACGCACCAGATTGTGGTCCGGCA-----CGCGTGGGTTTCGATTCCCACCTACCGCC---  
>tdbD00005799 *Leifsonia xyli* subsp. *xyli* str. *CTCB07* 281090 His GTG  
GGTGGGTATAGCTCAGCT--GGT--AGAGCGCCTGGTTGTGGTCCAGGAG-----GTCGCCGGTTTCAGCCCCGTTACTCACCCEA  
>tdbD00005751 *Leptospira interrogans* serovar *Lai* str. 56601 189518 His GTG  
GGAGAAGCTAGCTCAGTT--GGT--AGAGTCCAGTTGTGGTACTGGCC-----GTCGCCGGTTTCGATTCCCCTCGTTCTCCCA  
>tdbD00005682 *Listeria innocua* Clip11262 272626 His GTG  
GGCGGATATGGCGAAGT--GGTT-AACGCACCCTGATTGTGGTTCAGGCA-----TTCGTGGGTTTCGATTCCCATTATCCGCC---  
>tdbD00005683 *Listeria innocua* Clip11262 272626 His GTG  
GGCGGATGTGGCGAAGT--GGTT-AACGCACCCTGATTGTGGTTCAGGCA-----TTCGTGGGTTTCGATTCCCATCATCCGCC---  
>tdbD00005813 *Mesoplasma florum* L1 265311 His GTG  
GGCGCGGTGGTGAAGT--GGTT-AACACATCAGGTTGTGGTCTGAGCA-----TTCGCCGGTTTCGATTCCCCTCGGCCACCCCA  
>tdbD00005771 *Mycobacterium bovis* AF2122/97 233413 His GTG  
GGTGGTGTAGTTCAGTT--GGT--AGAGCACAGGTTGTGATCCTGGGT-----GTCGCCGGTTTCGAGTCCCCTCACTCACCCEA  
>tdbD00000978 *Mycoplasma capricolum* 2095 His GTG  
GGCGTAGGTGGTGAAGT--GGTT-AACACATCAGGTTGTGGTCTGAGCA-----TACGCCGGTTTCGATCCCCTTCTACGCCCEA  
>tdbD00005769 *Mycoplasma gallisepticum* R 233150 His GTG  
GGCGGTTGTGGCGAAGC--GGTTTAAACGCACCCTGACTGTGAATCAGGCA-----TGCACGGGTTTCGAATCCCCTCAATCGCCCCA

>tdbD00000979 Mycoplasma genitalium 2097 His GTG  
GGCGATTGTGGCGAAGT--GGTT-AACGCACCTGATTGTGGATCAGGCA-----TTCGTGGGTTCAATTCCCATCAGTCGCCCA-  
>tdbD00005673 Mycoplasma genitalium G37 243273 His GTG  
GGCGATTGTGGCGAAGT--GGTT-AACGCACCTGATTGTGGATCAGGCA-----TTCGTGGGTTCAATTCCCATCAGTCGCCCA  
>tdbD00000980 Mycoplasma pneumoniae 2104 His GTG  
GGCGATTGTGGCGAAGT--GGTT-AACGCACCTGATTGTGGATCAGGCA-----T-----GTCGTGGGTTCAATTCCCATCAGTCGCCCA  
>tdbD00005698 Mycoplasma pulmonis\_UAB\_CTIP 272635 His GTG  
GGTGAATATGGCGAAGG--GGTC-AACGCATCGGGTTGTGGTCCGACA-----TTCGCGGGTTTCAATCCCCTTATTCACCCCA  
>tdbD00005655 Neisseria meningitidis MC58 122586 His GTG  
GGTGGCTGTAGCTCAGTT--GGT--AGAGCCCCGATTGTGATCCGGTT-----GTCGTGGGTTTCGAGCCCCATCAGCCACCCCA  
>tdbD00005781 Nitrosomonas europaea ATCC 19718 228410 His GTG  
GGTGGCTGTAGCTCAGTT--GGT--AGAGTCCCGATTGTGATCCGGTT-----GTCGTGGGTTTCGAGTCCCATCAGCCACCCCA  
>tdbD00005697 Nostoc sp. PCC 7120 103690 His GTG  
GGCGGGCTAGGCAAGT--GGTT-AAGGCAGTGGATTGTGGATCCAGCA-----TTCGCGGGTTTCAAGTCCCCTCGTTCGCC---  
>tdbD00005752 Oceanobacillus\_ihayensis\_HTE831 221109 His GTG  
GGCGGTTCGTGGCGAAGT--GGTT-AACGCACCGATTGTGGTCCGACA-----TTCGTGGGTTCAATCCCACCGGTCCGCCCA  
>tdbD00005753 Oceanobacillus\_ihayensis\_HTE831 221109 His GTG  
GGCGGTTCGTGGCGAAGT--GGTT-AACGCACCGATTGTGGTCCGACA-----CACGTGGGTTTCGATCCCATCGATCGCC---  
>tdbD00005788 Onion yellows phytoplasma OY-M 262768 His GTG  
GGCGGTTCGTGGCGAAGT--GGTT-AACGCACCGATTGTGGTCCGACA-----TTCGTGGGTTTCGATCCCATCGATCGCC---  
>tdbD00005675 Pasteurella multocida subsp. multocida str. Pm70 272843 His GTG  
GGTGGCTATAGCTCAGTT--GGT--AGAGCCCCGATTGTGATCCGGTT-----GTCGTGGGTTTCAAGTCCCATTAGCCACCCCA  
>tdbD00000990 Photobacterium phosphoreum 659 His GTG  
GGTGGCTATAGCTCAGTT--GGT--AGAGTCCCGATTGTGATCCGGTT-----GTCGCGAGTTTCAAGCCTCGTTAGCCACCCCA  
>tdbD00005791 Photorhabdus luminescens subsp. laumondii\_TTO1 243265 His GTG  
GGTGGCTATAGCTCAGTT--GGT--AGAGCCTGGATTGTGATCCAGTT-----GTCGTGGGTTTCGAGTCCCATTAGCCACCCCA  
>tdbD00005800 Porphyromonas gingivalis W83 242619 His GTG  
GGTGGCGTAGTTCAGT--GGT--AGAGCAACGGATTGTGGTCCGACT-----GTCGTGGGTTTCGAGTCCCATCGTCCACCCCA  
>tdbD00005814 Propionibacterium acnes KP171202 267747 His GTG  
GGTGGCTATAGCTCAGTT--GGT--AGAGCACCTGGTTGTGGTCCAGGGG-----GTCGCGGGTTTCAAGTCCCCTTAGCCACCCCA  
>tdbD00005677 Pseudomonas aeruginosa PAO1 208964 His GTG  
GGTGGCGTAGCTCAGTT--GGT--AGAGCACAGATTGTGGTCCCTGGT-----GTCGTGGGTTTCGATCCCATCGTCCACCCCA  
>tdbD00005783 Pseudomonas syringae pv. tomato str. DC3000 223283 His GTG  
GGTGGCGTAGCTCAGTT--GGT--AGAGCACAGATTGTGACTCCTCGC-----GTCGTGGGTTTCGAACCCCATCGTCCACCCCA  
>tdbD00005696 Ralstonia solanacearum GMI1000 267608 His GTG  
GGTGGCTGTAGCTCAGTT--GGT--AGAGTCCAGATTGTGATCTGGTC-----GTCGTGGGTTTCGAGTCCCATCAGCCACCCCA  
>tdbD00005780 Rhodopirellula baltica SH 1 243090 His GTG  
GGTGGTTGTAGTTTCAAGT--GGT--AGAACGTCGGATTGTGATCCGGAAG-----GTCGCGGGTTTCGAGTCCCCTCAGCCACC---  
>tdbD00005691 Rickettsia conorii str. Malish 7 272944 His GTG  
GGCGGGTGTAGCTCAGTT--GGTT--AGAGCATCAGTTGTGGTCTGAGG-----GTCGCGGGTTTCGAATCCCCTACTCGCCCA  
>tdbD00005734 Rickettsia prowazekii str. Madrid E 272947 His GTG  
GGCGAGTGTAGCTCAGTT--GGTT--AGAGCATCAGTTGTGGTCTGAGG-----GCCACGGGTTTCGAATCCCCTACTCGCCCA  
>tdbD00005755 Shewanella oneidensis MR-1 211586 His GTG  
GGTGTATGTAGCTCAGTT--GGT--AGAGTCCCGATTGTGATCCGGTT-----GTCGTGGGTTTCGAGCCCCATCAGTCCACCCCA  
>tdbD00000984 Staphylococcus aureus 1280 His GTG  
GGCGGCTGTGGTGAAGT--GGTT-AACACATCGGATTGTGGTCCGACA-----TTCGAGGGTTTCGATCCCCTTACGCCGCC---  
>tdbD00005793 Staphylococcus aureus subsp. aureus MRSA252 282458 His GTG  
GGCGGTTGTGGTGAAGT--GGTT-AACACATCGGATTGTGGTCCGACA-----TTCGAGGGTTTCGATCCCCTTACGCCGCCCA  
>tdbD00005764 Staphylococcus epidermidis ATCC 12228 176280 His GTG  
GGCGGTTGTGGCGAAGT--GGTT-AACGCATCGGATTGTGGTCCGACA-----CTCGAGGGTTTCGATCCCCTTCAACGCCCA  
>tdbD00005765 Staphylococcus epidermidis ATCC 12228 176280 His GTG  
GGCGGTTGTGGCGAAGT--GGTT-AACGCATCGGATTGTGGTCCGACA-----CTCGAGGGTTTCGATCCCCTTCAACGCC---  
>tdbD00005757 Streptococcus agalactiae 2603V/R 208435 His GTG  
GGCGGTTGTGGTGAAGT--GGTT-AACACATCAGATTGTGGTCTGACA-----TTCGTGGGTTTCGATCCCATCACTCGCC---  
>tdbD00005758 Streptococcus mutans UA159 210007 His GTG  
GGCGGTTGTGGTGAAGT--GGTT-AACACACCAGATTGTGGTCTGGCA-----TTCGTGGGTTTCGATCCCATCACTCGCC---  
>tdbD00005777 Streptomyces avermitilis MA-4680 227882 His GTG  
GGTGGGTGTAGCTCAGCT--GGT--AGAGCACCTGGTTGTGGTCCAGGAT-----GCCGCGGGTTTCAAGTCCCCTACTCACC---  
>tdbD00005802 Symbiobacterium thermophilum IAM 14863 292459 His GTG  
GCTGACCGTAGCTCAGCT--GGTT--AGAGCGCCAGATTGTGGTCTGGAG-----GTCGCGGGTTTCGATCCCCTCGGTTCAGCCCA  
>tdbD00005803 Symbiobacterium thermophilum IAM 14863 292459 His GTG  
GCAGACCGTAGCTCAGTT--GGCT--AGAGCGCCAGATTGTGGTCTGGAG-----GTCGCGGGTTTCGACCCCGGTTCGCTGCCCCA  
>tdbD00000993 Synechocystis sp. 1143 His GTG  
GGCGAGCGTAGCCAAGG--GGTT-AAGGCAGAGATTGTGGTCCCTCCA-----CTCGTGGGTTTCGAATCCCATCGTTCGCC---  
>tdbD00005742 Thermoanaerobacter tengcongensis MB4 273068 His GTG  
GGTGGATATAGTTTCAAGT--GGCA--AGAAGCCAGATTGTGGTCTGGAG-----GTCGTGGGTTTCAAGTCCCCTACTCACCACCCCA  
>tdbD00005740 Thermosynechococcus elongatus BP-1 197221 His GTG  
GGCGAGCGTAGCCAAGT--GGTT-AAGGCAGTGGATTGTGGTCCACCA-----TTCGTGGGTTTCGAGTCCCATCGCTCGCC---  
>tdbD00005679 Thermotoga maritima MSB8 243274 His GTG  
GGTGACCATAGCTCAGTT--GGT--AGAGCGCCTGACTGTGGATCAGGTG-----GTCGCGGGTTTCGAGTCCCCTGGTTCACCCCA  
>tdbD00005815 Thermus thermophilus HB27 262724 His GTG  
GGTGAGCGTAGCTCAGCT--GGTT--AGAGCACCGACTGTGGATCCGGGG-----GTCGTGGGTTTCAAGTCCCATCGCTCACCACCCCA  
>tdbD00005816 Treponema denticola ATCC 35405 243275 His GTG  
GGTGGGTATAGTTTCAAG--GGT--AGAGCGCCAGATTGTGGTCTGGTT-----GTCGTGGGTTTCAATCCCCTACTCACCACC---  
>tdbD00000982 Treponema pallidum 160 His GTG

GGTGGGTGTAGTTCAGT--GGT--AGAGCGCCAGATTGTGGATCTGGTT-----GTCGTGGGTTTCGAATCCCATCACTCACC---  
>tdbD00005766 Tropheryma\_whipplei\_str.\_Twist\_203267\_His\_GTG  
GGTGGATATAGCTCAGCT--GGT--AGAGCACCTGGTTGTGGTCCAGGAT-----GTCGCGGGTTCGAGTCCCCTTATCCACC---  
>tdbD00005661 Ureaplasma\_parvum\_serovar\_3\_38504\_His\_GTG  
GGCGGTTATGGTGAAGTT--GGTT--AACACGCCTGATTGTGGCTCAGGTA-----TT-----TTCGCGGGTTCGAGTCCCCTAATCGCCCCA  
>tdbD00005657 Vibrio\_cholerae\_O1\_biovar\_El\_Tor\_str.\_N16961\_243277\_His\_GTG  
GGTGGCTATAGCTCAGTT--GGT--AGAGCCCAGATTGTGATTCCGGTT-----GTCGTGGGTTTCGAGCCCCATTAGCCACCCCA  
>tdbD00005817 Wolbachia\_endosymbiont\_of\_Drosophila\_melanogaster\_163164\_His\_GTG  
GGCGGGCGTAGCTCAGTT--GGT--AGAGCGCTCAGTTTGTGGTACTGAAT-----GTTGCCAGTTTCGATCCTGGTCGCTCGCCCCA  
>tdbD00005744 Xanthomonas\_axonopodis\_pv.\_citri\_str.\_306\_190486\_His\_GTG  
GGTGGCTGTAGCTCAGCT--GGTT--AGAGTACTGGATTGTGATTCCAGAT-----GTCGGGGGTTTCGAGTCCCCTCAGCCACCCCA  
>tdbD00005680 Xylella\_fastidiosa\_9a5c\_160492\_His\_GTG  
GGTGGCTGTAGCTCAGTT--GGTT--AGAGTACTGGATTGTGATTCCAGTT-----GTCGGGGGTTTCGAGTCCCCTCAGCCACCCCA  
>tdbD00000393 Acholeplasma\_laidlawii\_2148\_Asp\_GTC  
-GGTCCGGTGGTGTAGG--GGTT--AACATGCCTGCCTGTACGCAGGAG-----ATCGCGGGTTCAAATCCCCTCCGGACCCCA  
>tdbD00004573 Bacillus\_anthraxis\_str.\_A2012\_191218\_Asp\_GTC  
-GGTCCCGTGGTGTAGT--GGTT--AACATGCCTGCCTGTACGCAGGAG-----ATCGCGGGTTCGACCCCGTCCGGACCCCA  
>tdbD00004506 Bacillus\_halodurans\_C-125\_272558\_Asp\_GTC  
-GGTCCGGTAGTTCAGTT--GGTT--AGAATGCCTGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGGACCCCA  
>tdbD00004531 Bacteroides\_thetaiotaomicron\_VPI-5482\_226186\_Asp\_GTC  
-GGTGCCTTAGTTCAGTT--GGTT--AGAATACATGCCTGTACGCATGGG-----GTCACGGGTTTCGAGTCCCCTACGCACCG---  
>tdbD00004392 Bacteroides\_thetaiotaomicron\_VPI-5482\_226186\_Asp\_GTC  
-GGTTCGGTAGTTCAGTT--GGTT--AGAATACATGCCTGTACGCATGGG-----GTCGCGGGTTCGAGTCCCCTCCGGACCCG---  
>tdbD00004536 Bdellovibrio\_bacteriovorus\_HD100\_264462\_Asp\_GTC  
-GGGGTGGTAGTAAAGTT--GGTT--ATAACGTCGCCCTGTACGCAGGAG-----GCCGCGGGTTCGAGTCCCCTCCACCCCGCCA  
>tdbD00000396 Borrelia\_burgdorferi\_139\_Asp\_GTC  
-GGGGCGTAGTTCAGTT--GGTT--AGAACGCCTGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGACCCGTCGCTCCCG---  
>tdbD00004547 Borrelia\_garinii\_PBi\_290434\_Asp\_GTC  
-GGGGCGTAGTTCAGTT--GGTT--AGAACGCCTGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGACCCGTCGCTCCCG---  
>tdbD00004383 Buchnera\_aphidicola\_str.\_APS\_(Acyrtosiphon\_pisum)\_107806\_Asp\_GTC  
-GGTGTGGTAGTTCAGTT--GGTT--AGAATACCGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGCACCG---  
>tdbD00004525 Buchnera\_aphidicola\_str.\_Bp\_(Baizongia\_pistaciae)\_224915\_Asp\_GTC  
-GGTGCCTTAGTTCAGTT--GGTT--AGAATACCGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGCACCG---  
>tdbD00004476 Buchnera\_aphidicola\_str.\_Sg\_(Schizaphis\_graminum)\_198804\_Asp\_GTC  
-GGTGCCTTAGTTCAGTT--GGTT--AGAATACCGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGCACCG---  
>tdbD00004577 Candidatus\_Blochmannia\_floridanus\_203907\_Asp\_GTC  
-GGTGCCTTAGTTCAGTT--GGTT--AGAATACCGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGCACCG---  
>tdbD00004472 Chlorobium\_tepidum\_TLS\_194439\_Asp\_GTC  
-GGAGCTGTAGCTCAGTCTGGTT--AGAGCGCCTGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGACCCGTCAGTCCG---  
>tdbD00004523 Coxiella\_burnetii\_RSA\_493\_227377\_Asp\_GTC  
-GGAGTGGTAGTTCAGTT--GGTT--AGAATACCGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCACTCCGCCA  
>tdbD00004404 Deinococcus\_radiodurans\_R1\_243230\_Asp\_GTC  
-GGTCCGGTAGTGTAGC--GGTT--AGCATATCTGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGCACCG---  
>tdbD00004563 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Asp\_GTC  
-GGAGCGTAGTAAAGAC--GGTT--ATAACGCGCCCTGTACGCAGGAG-----GCCGAGGGTTCGAGTCCCCTCCGCACCG---  
>tdbD00004564 Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Asp\_GTC  
-GGAGCGTAGTAAAGAC--GGTT--ATAACGCGCCCTGTACGCAGGAG-----GCCGAGGGTTCGAGTCCCCTCCGCACCG---  
>tdbD00004509 Enterococcus\_faecalis\_V583\_226185\_Asp\_GTC  
-GGTTTGGTAGTTCAGCT--GGTT--AGAATGCCTGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCAGACCCCA  
>tdbD00004510 Enterococcus\_faecalis\_V583\_226185\_Asp\_GTC  
-GGTTTGGTAGTTCAGCT--GGTT--AGAATGCCTGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCAGACCCG---  
>tdbD00004511 Enterococcus\_faecalis\_V583\_226185\_Asp\_GTC  
-GGTTCCGTGGTGTAGG--GGTT--AACATGCCTGCCTGTACGCAGGAG-----ATCGCGGGTTCGAGTCCCCTCCAGACCCCA  
>tdbD00000404 Escherichia\_coli\_562\_Asp\_GTC  
-GGAGCGTAGTTCAGTTCAGTTC--GGTT--AGAATACCTGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004394 Escherichia\_coli\_O157H7\_83334\_Asp\_GTC:  
-GGAGCGTAGTTCAGTTCAGTTC--GGTT--AGAATACCTGCCTGTACGCAGGAG-----T-CGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004473 Fusobacterium\_nucleatum\_subsp.\_nucleatum\_ATCC\_25586\_190304\_Asp\_GTC  
-GGGGTGTAGCTCAGCTCAGTT--GGTT--AGAGCGCCTGCCTGTACGCAGGAG-----GTCGCGAGTTCGAGTCTCGTCACTCCGCCA  
>tdbD00004474 Fusobacterium\_nucleatum\_subsp.\_nucleatum\_ATCC\_25586\_190304\_Asp\_GTC  
-GGGGTGTAGCTCAGCTCAGTT--GGTT--AGAGCGCCTGCCTGTACGCAGGAG-----GTCGCGAGTTCGAGTCTCGTCACTCCGCCA  
>tdbD00004548 Geobacter\_sulfurreducens\_PCA\_243231\_Asp\_GTC  
-GGGGTGTAGCTCAGCTCAGTT--GGTT--AGAGCGCCTGCCTGTACGCAGGAG-----GTCGCGAGTTCGAGTCTCGTCACTCCGCCA  
>tdbD00000405 Haemophilus\_influenzae\_727\_Asp\_GTC  
-GGAGTGGTAGTTCAGCT--GGTT--AGAATACCTGCCTGTACGCAGGAG-----T-CGCGGGTTCGAGTCCCCTCCATTCCGCCA  
>tdbD00000406 Haemophilus\_influenzae\_727\_Asp\_GTC  
-GGAGTGGTAGTTCAGCT--GGTT--AGAATACCTGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCATTCCGCCA  
>tdbD00000407 Haemophilus\_influenzae\_727\_Asp\_GTC  
-GGAGTGGTAGTTCAGCT--GGTT--AGAATACCTGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCATTCCGCCA  
>tdbD00000401 Helicobacter\_pylori\_210\_Asp\_GTC  
-GGAGCGTAGTTCAGCTCAGTT--GGTT--AGAATACCTGCCTGTACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00000400 Lactobacillus\_delbrueckii\_subsp.\_bulgaricus\_1585\_Asp\_GTC  
-GGTCCATTGGAGCAGT--GGTCTATCTCGCCTCCCTGTACGCAGGAG-----ATCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004550 Lactobacillus\_johnsonii\_NCC\_533\_257314\_Asp\_GTC  
-GGTCCATTGGAGCAGT--GGTCTATCTCGCCTCCCTGTACGCAGGAG-----ATCGCGGGTTCGAGTCCCCTCCGTTCCGCCA

>tdbD00004512 *Lactobacillus plantarum* WCFS1 220668 Asp GTC  
-GGTCCGTTGGTCTAGTT--GGTTTAGGACGCCTGCCTGTCACGCAGGAG-----ATCACGAGTTCGAGTCTCGTACGGACCG---  
>tdbD00004499 *Leptospira interrogans* serovar Lai str. 56601 189518 Asp GTC  
-GGAGCTGTAGCTCAGCT--GGTT-AGAGTGCCTGCCTGTCACGCAGGAT-----GTCGCGGGTTCGAGTCCCCTCAGCTCCG---  
>tdbD00004416 *Listeria innocua* Clipl1262 272626 Asp GTC  
-GGTCCGTTGGTGTAGG--GGTT-AACATGCCTGCCTGTCACGCAGGAG-----ATCGCGGGTTCAAATCCCCTCGGGACCG---  
>tdbD00004417 *Listeria innocua* Clipl1262 272626 Asp GTC  
-GGTCCGTTGGTGTAGG--GGTT-AACATGCCTGCCTGTCACGCAGGAG-----ATCGCGGGTTCAAATCCCCTCGGGACCGCCA  
>tdbD00004520 *Mycoplasma gallisepticum* R 233150 Asp GTC  
-GGTTCCTTGGTGTAGT--GAT--AACATACCTCCCTGTCACGGAGGGG-----T-TGCGGGTTTGATTCCCCTAGGAACCGCCA  
>tdbD00004405 *Mycoplasma genitalium* G37 243273 Asp GTC  
-GGTCCATGTTGTAGT--GAT--AACATATCTCCCTGTCACGGAGGGG-----T-TGCGGGTTTGATTCCCCTTGAACCGCCA  
>tdbD00000392 *Mycoplasma pneumoniae* 2104 Asp GTC  
-GGTTCATGTTGTAGT--GGTT-AACATATCTCCCTGTCACGGAGGGG-----T-TGCGGGTTCGATTCCCCTTGAACCGCCA  
>tdbD00004434 *Mycoplasma pulmonis* UAB CTIP 272635 Asp GTC  
-GGTCCAGTGTAAAGT--GGTTGACTACGCCTCCCTGTCACGGAGGAG-----ATCGCGGGTTCGATTCCCCTCTGGACCGCCA  
>tdbD00004433 *Nostoc* sp. PCC 7120 103690 Asp GTC  
-GGACTGTAGTTCAGT--GGTT-AGAGCACCGCCCTGTCACGGCGGGG-----GTTGCGGGTTCGAGCCCCGTAGTCCCG---  
>tdbD00004538 *Onion yellows phytoplasma* OY-M 262768 Asp GTC  
-GGTCCGTTGGTGTAGT--GGTT-AACATGCCTGCCTGTCACGCAGGAG-----ATCGCGGGTTCAGTCCCCTCCGACCGCCA  
>tdbD00004408 *Pasteurella multocida* subsp. *multocida* str. Pm70 272843 Asp GTC  
-GGAGCGGTAGTTCAGT--GGTT-AGAATACCTGCCTGTCACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004541 *Phototribadus luminescens* subsp. *laumondii* T101 243265 Asp GTC  
-GGTCCGTTAGTTCAGT--GGTT-AGAATACCGCCCTGTCACGGCGGGG-----GTCGCGGGTTCGAGCCCCGTCCGACCGCCA  
>tdbD00004542 *Phototribadus luminescens* subsp. *laumondii* T101 243265 Asp GTC  
-GGTCCGTTAGTTCAGT--GGTT-AGAATACCGCCCTGTCACGGCGGGG-----GTCGCGGGTTCGAGTCCCCTCCGACCGCCA  
>tdbD00004552 *Porphyromonas gingivalis* W83 242619 Asp GTC  
-GGTGTGGTGTAGT--GGTT-AGAATACCTGCCTGTCACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCATACCG---  
>tdbD00004411 *Pseudomonas aeruginosa* PA01 208964 Asp GTC  
-GGAGCGGTAGTTCAGT--GGTT-AGAATACCGCCCTGTCACGGCGGGG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004431 *Ralstonia solanacearum* GMI1000 267608 Asp GTC  
-GGAGTGGTGTAGT--GGTT-AGAATACCGCCCTGTCACGGCGGGG-----GTCGCGGGTTCGAGTCCCCTCCACTCCGCCA  
>tdbD00004437 *Salmonella enterica* subsp. *enterica* serovar Typhi str. CT18 220341 Asp GTC  
-GGAGCGGTAGTTCAGT--GGTT-AGAATACCTGCCTGTCACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004502 *Shewanella oneidensis* MR-1 211586 Asp GTC  
-GGAGCGGTAGTTCAGT--GGTT-AGAATACCGCCCTGTCACGGCGGGG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00000394 *Spiroplasma melliferum* 2134 Asp GTC  
-GGTCTGTAGTGAAGT--GGTT-ATCATGCCTCTCTGTACACAGAGGAG-----ATCGCGGGTTCAGTCCCCTCAAGACCGCCA  
>tdbD00000399 *Staphylococcus aureus* 1280 Asp GTC  
-GGTCTGTAGTGTAGC--GGTT-AACACGCCTGCCTGTCACGCAGGAG-----ATCGCGGGTTCGATTCCCCTCGAGACCGCCA  
>tdbD00004544 *Staphylococcus aureus* subsp. *aureus* MRSA252 282458 Asp GTC  
-GGTCTGTAGTGTAGC--GGTT-AACACGCCTGCCTGTCACGCAGGAG-----ATCGCGGGTTCGATTCCCCTCGAGACCG---  
>tdbD00004514 *Staphylococcus epidermidis* ATCC 12228 176280 Asp GTC  
-GGTCCCGTAGTGTAGC--GGTT-AACACGCCTGCCTGTCACGCAGGAG-----ATCGCGGGTTCGATTCCCCTCGGGACCG---  
>tdbD00004516 *Staphylococcus epidermidis* ATCC 12228 176280 Asp GTC  
-GGTCCCGTAGTGTAGC--GGTT-AACACGCCTGCCTGTCACGCAGGAG-----ATCGCGGGTTCGATTCCCCTCGGGACCGCCA  
>tdbD00004504 *Streptococcus agalactiae* 2603V/R 208435 Asp GTC  
-GGTCCCGTAGTGTAGC--GGTT-ATCAGTCGCCCTGTCACGGCGAAG-----ATCGCGGGTTCGATTCCCCTCGGGACCG---  
>tdbD00004505 *Streptococcus mutans* UA159 210007 Asp GTC  
-GGTCCCGTTGGTGTAGC--GGTT-ATCAGTCGCCCTGTCACGGCGAAG-----ATCGCGGGTTCGATTCCCCTCGGGACCG---  
>tdbD00004554 *Symbiobacterium thermophilum* IAM 14863 292459 Asp GTC  
-GGAGCGGTGTAGTAGA--GGCTAACATGCGGCCCTGTCACGGCCGAG-----ATCGCGGGTTCGAATCCCCTCGCTCCGCCA  
>tdbD00004555 *Symbiobacterium thermophilum* IAM 14863 292459 Asp GTC  
-GGAGCGGTGTAGTAGA--GGCTAACATGCGGCCCTGTCACGGCCGAG-----ATCGCGGGTTCGAATCCCCTCGCTCCGCCA  
>tdbD00000408 *Synechocystis* sp. 1143 Asp GTC  
-GGTCTGTAGTTCAT--GGTT-AGAGCACCGCCCTGTCACGGCGGAA-----GTTGCGGGTTCGAGCCCCGTAGACCCG---  
>tdbD00004483 *Thermosynechococcus elongatus* BP-1 197221 Asp GTC  
-GGGACTGTAGTTCAT--GGTT-AGAGCACCGCCCTGTCACGGCGGAA-----GTTGCGGGTTCGAGCCCCGTAGTCCCG---  
>tdbD00004413 *Thermotoga maritima* MSB8 243274 Asp GTC  
-GGGAGCGTGTGACGCTGGTT--AGCATGCCGGTCTGTACACCGGTG-----GTCGCGGGTTCAAATCCCCTCGTCCCGCCA  
>tdbD00004570 *Treponema denticola* ATCC 35405 243275 Asp GTC  
-GGGGCGTAGCGAAGCT--GGTTTATCGCGCTGGCCTGTCACGGCGGAG-----ATCGCGGGTTCGAGCCCCGTGCTCCCG---  
>tdbD00000395 *Treponema pallidum* 160 Asp GTC  
-GGGGCGTAGCGAAGTT--GGTT-ATCGCGCCAGCCTGTCACGGCGGAG-----ATCGCGGGTTCGAGCCCCGTGCTCCCG---  
>tdbD00004391 *Ureaplasma parvum* serovar 3 38504 Asp GTC  
-GGTCTGTGGTGTAGT--GATT-AACATGCCTCTCTGTCACAGAGGAG-----ATCGCGGGTTCGACTCCCCTCAGGACCGCCA  
>tdbD00004571 *Wolbachia endosymbiont of Drosophila melanogaster* 163164 Asp GTC  
-GGGGGTGTAGCTCAGT--GGTT-AGAGCGCATGCCTGTCACGCATGAG-----GTCGTGAGTTCAGTCTCATCACTCCCGCCA  
>tdbD00004488 *Xanthomonas axonopodis* pv. *citri* str. 306 190486 Asp GTC  
-GGAGCGGTAGTTCAGT--GGTT-AGAATGCTGGCCTGTCACGGCGGAG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004557 *Yersinia pestis* biovar *Microtus* str. 91001 229193 Asp GTC  
-GGAGCGGTAGTTCAGT--GGTT-AGAATACCTGCCTGTCACGCAGGAG-----GTCGCGGGTTCGAGCCCCGTCCGTTCCGCCA  
>tdbD00001349 *Acholeplasma laidlawii* 2148 Lys TTT  
-GTCCCCTTAGCTCAGGT--GGT--AGAGCACTTGACTTTTAAATCAAGGT-----GTCGATGGTTCGAGTCCATCAGGGACACCA  
>tdbD00006378 *Acinetobacter* sp. ADP1 62977 Lys TTT

-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGCGGACTTTTAAATCCGTTG-----GTCCCGCGTTTCGAGTCGCGGACGACCCACCA  
>tdbD00006146 Agrobacterium tumefaciens\_str.\_C58 176299 Lys TTT  
-GAGAGCGTAGCTCAGCC-GGT--AGAGCAACTGACTTTTAAATCAGTAG-----GTCCAGGGTTTCGAATCCCTGCGCTCTCACCA  
>tdbD00006115 Aquifex aeolicus VF5 224324 Lys TTT  
-GAGCCGTTAGCTCAGTT-GGT--AGAGCAACCGCCTTTTAAAGCCGTGG-----GTCGCGGGTTTCGAGTCCCGCCCGGCTCACCA  
>tdbD00001360 Azospirillum lipoferum 193 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCGAAGGTTTCGAGTCCCTTCATGGCTCACCA  
>tdbD00006325 Bacillus anthracis\_str.\_Ames 198094 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCGAAGGTTTCGAGTCCCTTCATGGCTCA---  
>tdbD00006322 Bacteroides thetaiotaomicron VPI-5482 226186 Lys TTT  
-GATTCAGTAGCTCAGCA-GGT--AGAGCACAACACTTTTAAATGTTGGG-----GTCCTGGGTTTCGAGCCCCAGCTGGATCA---  
>tdbD00006326 Bartonella henselae\_str.\_Houston-1 283166 Lys TTT  
-GAGCGCGTAGCTCAGCT-GGT--AGAGCAACTGACTTTTAAATCAGTAG-----GTCCAGGGTTTCGAATCCCTGCGCGCTCACCA  
>tdbD00006385 Bartonella quintana\_str.\_Toulouse 283165 Lys TTT  
-GAGCGCGTAGCTCAGCT-GGT--AGAGCAACTGACTTTTAAATCAGTAG-----GTCCAGGGTTTCGAATCCCTGCGCGCTCACCA  
>tdbD00006328 Bdellovibrio bacteriovorus HD100 264462 Lys TTT  
-GGTTCGTTAGCTCAGTT-GGT--AGAGCACTTCACTTTTAAATGAAGGG-----GTCGATGGTTTCGAATCCATCGCGAGCCACCA  
>tdbD00006232 Bifidobacterium longum NCC2705 206672 Lys TTT  
-GCCCTTTAGCTCAAC--GGTT-AGAGCAGCGCTCCTTTTAAAGTCGTGG-----GTTGTGGGTTTCGAATCCACAGGGGGCA---  
>tdbD00001352 Borrelia burgdorferi 139 Lys TTT  
-GGGTCATAGCTCAGGT-GGT--AGAGCAGCGCCCTTTTAAAGCGGTTTAAAG--GCG-----TTTGTGCTAGGTTTCGAGTCCCTACTGAGCTCA---  
>tdbD00006093 Borrelia burgdorferi\_B31 224326 Lys TTT  
-GGGTCATAGCTCAGGT-GGT--AGAGCAGCGCCCTTTTAAAGCGGTTT-----GTCGTAGGTTTCGAGTCCCTACTGAGCTCA---  
>tdbD00006280 Bradyrhizobium japonicum\_USDA\_110 224911 Lys TTT  
-GAGCGCGTAGCTCAGCC-GGT--AGAGCAGCTGACTTTTAAATCAGCGG-----GTCCTGGGTTTCGAGCCCCAGCGCGCTCACCA  
>tdbD00006131 Brucella melitensis\_16M 224914 Lys TTT  
-GAGCGCGTAGCTCAGCC-GGT--AGAGCAACTGACTTTTAAATCAGTAG-----GTCCAGGGTTTCGAATCCCTGCGCGCTCACCA  
>tdbD00006070 Buchnera aphidicola\_str.\_APS (Acyrtosiphon pisum) 107806 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAAATCAATTG-----GTCGCGAGTTTCGAATCCCTGCACGACCCCA---  
>tdbD00006232 Buchnera aphidicola\_str.\_Sg (Schizaphis graminum) 198804 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAAATCAATTG-----GTCGCGAGTTTCGAATCCCTGCACGACCCCA---  
>tdbD00006094 Campylobacter jejuni\_subsp.\_jejuni\_NCTC\_11168 192222 Lys TTT  
-GTCTCGTTAGCTCAGCC-GGT--AGAGCATCTCCCTTTTAAAGGAGGGG-----GCCGTTGGTTTCGAATCCCAACACGGGACACCA  
>tdbD00006387 Candidatus Blochmannia floridanus 203907 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAAATCAATTG-----GTCGCGAGTTTCGAATCCCTGCACGACCCCA---  
>tdbD00006334 Candidatus Protochlamydia amoebophila\_UWE25 264201 Lys TTT  
-GAGTCTTTAGCTCAGTT-GGT--AGAGCACCTCACTTTTAAATGAGGGG-----GTCGATGGTTTCGAGTCCATCAAGACTCA---  
>tdbD00006096 Caulobacter crescentus\_CB15 190650 Lys TTT  
-GGGCCGTTAGCTCAGT-GGT--AGAGCATTGCGACTTTTAAATCGAATG-----GTCCTGGGTTTCGAGTCCCAGCCGGCCTACCA  
>tdbD00006122 Chlamydia muridarum\_Nigg 243161 Lys TTT  
-GGGTCGTTAGCTCAGC--GGTT-AGAGCATCTCACTTTTAAATGAGAGG-----GTCGCGAGTTTCGAATCCCTTCAAGACCCCA---  
>tdbD00006067 Chlamydia trachomatis\_D/UW-3/CX 272561 Lys TTT  
-GGGTCGTTAGCTCAGC--GGTT-AGAGCATCTCACTTTTAAATGAGAGG-----GTCGAAGGTTTCGAATCCCTTCAAGACCCCA---  
>tdbD00006065 Chlamydia pneumoniae\_AR39 115711 Lys TTT  
-GGGTCGTTAGCTCAGC--GGTT-AGAGCACCTCACTTTTAAATGAGGGG-----GTCGAAGGTTTCGAATCCCTTCAAGACCCCA---  
>tdbD00006226 Chlorobium tepidum\_TLS 194439 Lys TTT  
-GAGAATATAGCTCAGTC-GGT--AGAGCAACTGCCTTTTAAATCGAGTGG-----GTCGAAGGTTTCGAGTCCCTTCTATTCTCA---  
>tdbD00006127 Clostridium acetobutylicum\_ATCC\_824 272562 Lys TTT  
-GGTTTATTAGCTCAGTT-GGT--AGAGCACATGACTTTTAAATCATGTT-----GTCCGGGGTTTCGACTCCCAGGATAAGCCCA---  
>tdbD00006120 Clostridium perfringens\_str.\_13 195102 Lys TTT  
-GATTTGCTAGCTCAGTC-GGT--AGAGCAGCTGACTTTTAAATCAGCGT-----GTCCAGGGTTTCGATTCCCTGGCAGATCACCA  
>tdbD00006282 Clostridium tetani\_E88 212717 Lys TTT  
-GATCCACTAGCTCAGTC-GGT--AGAGCACATGACTTTTAAATCATGTT-----GTCCGGGGTTTCGATTCCCGGTTGGATCACCA  
>tdbD00006330 Corynebacterium diphtheriae\_NCTC\_13129 257309 Lys TTT  
-GGGCCCTTAGCTCAGTC-GGT--AGAGCTACGGACTTTTAAATCCGCAG-----GTCCCGGGTTTCGAGCCCCGAGGGGCCCA---  
>tdbD00006265 Corynebacterium efficiens\_YS-314 196164 Lys TTT  
-GGGCCCTTAGCTCAGTT-GGT--AGAGCTACGGACTTTTAAATCCGCAG-----GTCCCGGGTTTCGAGCCCCGAGGGGCCCA---  
>tdbD00006236 Corynebacterium glutamicum\_ATCC\_13032 196627 Lys TTT  
-GGGCCATAGCTCAGTC-GGT--AGAGCTACGGACTTTTAAATCCGCAG-----GTCTTGGGTTTCGAGTCCCAATGGGGCCA---  
>tdbD00006304 Coxiella burnetii\_RSA\_493 227377 Lys TTT  
-GGGTCGTTAGCTCAGCT-GGT--AGAGCAGCGGACTTTTAAATCCGTTG-----GTCATAGGTTTCGAATCCCTATACGACCCACCA  
>tdbD00006098 Deinococcus radiodurans\_R1 243230 Lys TTT  
-GGGTTGTTAGCTCAAT--GGT--AGAGCAGCTGACTTTTAAATCAGCGG-----GTTCTCGGTTTCGAGTCCGAGGCGACCCACCA  
>tdbD00006365 Desulfovibrio vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough 882 Lys TTT  
-GGGTCGTTACTCAGTC-GGT--AGAGTACCTGCCTTTTAAAGCAGAGA-----GTCGCGAGTTTCGAATCCCTGCACGACCCACCA  
>tdbD00006284 Enterococcus faecalis\_V583 226185 Lys TTT  
-GAGCCGTTAGCTCAGTC-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCACAGGTTTCGAGCCCTGTACGGCTCA---  
>tdbD00006286 Enterococcus faecalis\_V583 226185 Lys TTT  
-AGACGTGTTAGCTCAATA-GGT--AGAGCAATTGATTTTAAATCAATGGTGCG---TGAT---TGCTTGTGCAGGTTTCGACTCCTGTACGTCAA---  
>tdbD00001359 Escherichia coli 562 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAAATCAATTG-----GTCGCGAGTTTCGAATCCCTGCACGACCCACCA  
>tdbD00006228 Fusobacterium nucleatum\_subsp.\_nucleatum\_ATCC\_25586 190304 Lys TTT  
-GCGTCATTAGCTCAGTT-GGT--AGAGCACAGACTTTTAAATCGTGT-----GTCACAAGTTTCGAATCCCTGTATGACGCACCA  
>tdbD00006346 Geobacter sulfurreducens\_PCA 243231 Lys TTT  
-GAGCCGTTAGCTCAGAT-GGT--AGAGCACCTGACTTTTAAATCAGGTG-----GTCGTTGGTTTCGATCCCAACCGGCTCACCA



>tdbD00001361 Haemophilus influenzae 727 Lys TTT  
-GGGTCGTTAGCTCAGAC-GGT--AGAGCAGCGGACTTTTAAATCCGTTG-----GTCGAAGGTTTCAATCCTTCACGACCCACCA  
>tdbD00001362 Haemophilus influenzae 727 Lys TTT  
-GGGTCGTTAGCTCAGTC-GGT--AGAGCAGCGGACTTTTAAATCCGTTG-----GTCGAAGGTTTCAATCCTTCACGACCCACCA  
>tdbD00001356 Helicobacter pylori 210 Lys TTT  
-GACCCGTTAGCTCAGCT-GGT--AGAGCAATTCCTTTTAAAGGAATGG-----GCCGTTGGTTCAAATCCAACACGGGTCACCA  
>tdbD00006348 Lactobacillus johnsonii\_NCC\_533\_257314 Lys TTT  
-GAGTCGTTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCGGCAGTTTCGAGCCTGCCACGACTCA---  
>tdbD00006287 Lactobacillus plantarum WCFS1\_220668 Lys TTT  
-GAGCCGTTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCGACAGTTTCGAGACTGTCACGGCTCA---  
>tdbD00006350 Leifsonia xyli\_subsp.\_xyli\_str.\_CTCB07\_281090 Lys TTT  
-GGGCTCTAGCTCAGTC-GGT--AGAGCATCGGACTTTTAAATCCGCGG-----GTCGTGGGTTTCGAGCCCCACGGGGCCCA---  
>tdbD00006266 Leptospira interrogans serovar\_Lai\_str.\_56601\_189518 Lys TTT  
-GAGTCGTTAGCTCAGCT-GGT--AGAGCAATTCCTTTTAAAGGAATGG-----GTCGGGGTTTCAATCCCCGACGACTCA---  
>tdbD00006117 Listeria innocua Clipl1262\_272626 Lys TTT  
-GAGCCGTTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCGCTGGTTTCAACCCAGCAGCGGCTCA---  
>tdbD00006370 Mesoplasma florum L1\_265311 Lys TTT  
-GACTCGTAGCTCAGTC-GGT--AGAGCAACTGGCTTTTAAATCAGAGG-----GTCGGGAGTTTCGAGCCTCCGGCGAGTCACCA  
>tdbD00006132 Mesorhizobium loti MAFF303099\_266835 Lys TTT  
-GAGCGCTAGCTCAGCC-GGT--AGAGCAACTGACTTTTAAATCAGTAG-----GTCATGGGTTTCAATCCCATCGCGCTCACCA  
>tdbD00006299 Mycobacterium bovis AF2122/97\_233413 Lys TTT  
-GCCCTATAGCTCAGTT-GGT--AGAGTACGCGACTTTTAAATCCGCGAG-----GTCCAGGTTTCGAGTCTCTGGTGGGGCA---  
>tdbD00006081 Mycobacterium leprae TN\_272631 Lys TTT  
-GCCCTATAGCTCAGTT-GGT--AGAGTACGCGACTTTTAAATCCGCGAG-----GTCCTAGGTTTCGAGTCTCTAGTGGGGCA---  
>tdbD00001341 Mycoplasma capricolum 2095 Lys TTT  
-GACTCGTTAGCTCAGCC-GGT--AGAGCAACTGGCTTTTAAATCAGAGG-----GTCGGGGTTTCAATCCCCGACGAGTCACCA  
>tdbD00006297 Mycoplasma gallisepticum R\_233150 Lys TTT  
-GACTCACTAGCTCAGC--GGT--AGAGCATTGACTTTTAAATCAAAGG-----GTCCGGGTTTCGATCCCCGGGTGGGTCACCA  
>tdbD00001343 Mycoplasma genitalium 2097 Lys TTT  
-GACTCACTAGCTCAGC--GGT--AGAGCATTGACTTTTAAATCAAAGG-----GTCCGGGTTTCGATCCTCGGGTGGGTCACCA  
>tdbD00006100 Mycoplasma genitalium G37\_243273 Lys TTT  
-GACTCACTAGCTCAGC--GGT--AGAGCATTGACTTTTAAATCAAAGG-----GTCCGGGTTTCGATCCTCGGGTGGGTCACCA  
>tdbD00001345 Mycoplasma pneumoniae 2104 Lys TTT  
-GACTCACTAGCTCAGC--GGT--AGAGCATTGACTTTTAAATCAAAGG-----GTCCGGGTTTCGATCCTCGGGTGGGTCACCA  
>tdbD00006144 Mycoplasma pulmonis UAB CTIP\_272635 Lys TTT  
-GCGCCTTAGCTCAGCA-GGT--AGAGCAAATGGCTTTTAAATCAAAGG-----GTCAGAGGTTTCAATCCTCTAAGGCGTACCA  
>tdbD00006073 Neisseria meningitidis MC58\_122586 Lys TTT  
-GGTTCGTTAGCTCAGTC-GGT--AGAGCAGCGGACTTTTAAATCCGTTG-----GTCGAGCGTTTCAATCGCTCAGACCCACCA  
>tdbD00006074 Neisseria meningitidis MC58\_122586 Lys TTT  
-GGTTCGTTAGCTCAGTC-GGT--AGAGCAGCGGACTTTTAAATCCGTTG-----GTCGAGCGTTTCAATCGCTCAGACCCACCA  
>tdbD00006320 Nitrosomonas europaea ATCC\_19718\_228410 Lys TTT  
-GGTTCGTTAGCTCAGTC-GGT--AGAGCAGCGGACTTTTAAATCCGTTG-----GTCGAGCGTTTCAATCGCTCAGACCCACCA  
>tdbD00006141 Nostoc sp.\_PCC\_7120\_103690 Lys TTT  
-GGGGTATTGGCATAGC--GGCA-AGTGCATCGGACTTTTAAATCCGACT-----TAGACAGGTTTCGACTCCTGTATACCCACCA  
>tdbD00006142 Nostoc sp.\_PCC\_7120\_103690 Lys TTT  
-GGGTCGTAACCAAC--GGT--AGAGTACTCGGCTTTTAAATCCGACT-----GTTCCGGGTTTCAATCCCCGGCGACCCA---  
>tdbD00006267 Oceanobacillus iheyensis HTE831\_221109 Lys TTT  
-GAGCCATTAGCTCAGTC-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCGAAGGTTTCAATCCTTCATGGCTCACCA  
>tdbD00006268 Oceanobacillus iheyensis HTE831\_221109 Lys TTT  
-GAGCCATTAGCTCAGTC-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCGAAGGTTTCAATCCTTCATGGCTCACCA  
>tdbD00006331 Onion yellows phytoplasma OY-M\_262768 Lys TTT  
-GTCCCGTTAGCTCAGCT-GGT--AGAGCACTGACTTTTAAATCAAAGG-----GTCGAAGGTTTCGACTCCTTCACGGGATACCA  
>tdbD00006335 Photobacterium luminescens subsp.\_laumondii\_TTO1\_243265 Lys TTT  
-GGTTCGTTAGCTCAGTC-GGT--AGAGCAGTTGACTTTTAAATCAAAGG-----GTCGAGGTTTCAATCCTTCATGGCTCACCA  
>tdbD00006351 Porphyromonas gingivalis W83\_242619 Lys TTT  
-GAATCGTAGCTCAGCA-GGT--AGAGCACATCCCTTTTAAAGGATGGG-----GTCCTGGGTTTCAATCCCCAGCGGATTC---  
>tdbD00006372 Propionibacterium acnes KPA171202\_267747 Lys TTT  
-GCCCCGTTAGCTCAGAT-GGTT-AGAGCAGCGGACTTTTAAATCCGCGG-----GTCCTGGGTTTCGAGTCCCAGTGGGGCA---  
>tdbD00006106 Pseudomonas aeruginosa PAO1\_208964 Lys TTT  
-GGGTCGTTAGCTCAGTC-GGT--AGAGCAGTTGGCTTTTAAATCAAAGG-----GTCGTTAGGTTTCAATCCTACACGACCCACCA  
>tdbD00006323 Pseudomonas syringae pv.\_tomato\_str.\_DC3000\_223283 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGGCTTTTAAATCAAAGG-----GTCGTTAGGTTTCAATCCTACACGACCCACCA  
>tdbD00006139 Ralstonia solanacearum GMI1000\_267608 Lys TTT  
-GGGTCGTTAGCTCAGTC-GGT--AGAGCAGCGGACTTTTAAATCCGTTG-----GTCGCGTGTTCGAGTACGCACGACCCACCA  
>tdbD00006317 Rhodopirellula baltica SH\_1\_243090 Lys TTT  
-GAGAGTGTAGCTCAGTT-GGC--AGAGCATTGACTTTTAAATCAAAGG-----GTCCTGGGTTTCGAGTCCCAGCACTCTCA---  
>tdbD00006318 Rhodopirellula baltica SH\_1\_243090 Lys TTT  
-GGGGTGTGGTGTAACT-GGC--AGCATGACGGACTTTTAAATCCGTTG-----GGTGAGGTTTCAATCCTTCGGCCCCA---  
>tdbD00006338 Rhodopseudomonas palustris CGA009\_258594 Lys TTT  
-GAGCGCTAGCTCAGCC-GGT--AGAGCACGTGACTTTTAAATCAAAGG-----GTCGAGGTTTCGAGTCCCCTCCGGCTCACCA  
>tdbD00006129 Rickettsia conorii\_str.\_Malish\_7\_272944 Lys TTT  
-GAGCTCGTAGCTCAGTC-GGT--AGAGCATTGACTTTTAAATCAAAGG-----GTCCGGGTTTCAATCCCCGCGAGCTCACCA  
>tdbD00006233 Rickettsia prowazekii\_str.\_Madrid\_E\_272947 Lys TTT  
-GAGCTCGTAGCTCAGTT-GGT--AGAGCATTGACTTTTAAATCAAAGG-----GTCCGGGTTTCAATCCCCGCGAGCTCACCA  
>tdbD00006353 Rickettsia typhi\_str.\_Wilmington\_257363 Lys TTT

-GAGCTCGTAGCTCAGTT-GGT--AGAGCATTGACTTTTAAATCAAAGG-----GTCCCGGGTTCAAATCCCGGCGAGCTCACCA  
>tdbD00006147 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341\_Lys\_TTT  
-GGTCTGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAAATCAATTG-----GTCGAGGTTTCAATCCTGCACGACCCA---  
>tdbD00006315 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261\_Lys\_TTT  
-GGTCTGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAAATCAATTG-----GTCGAGGTTTCAATCCTGCACGACCCA---  
>tdbD00006272 Shewanella\_oneidensis\_MR-1\_211586\_Lys\_TTT  
-GGTCTGTTAGCTCAGTC-GGT--AGAGCAGTTGGCTTTTAAACCAATTG-----GTCGAGGTTTCAATCCTGCACGACCCA---  
>tdbD00001355 Staphylococcus\_aureus\_1280\_Lys\_TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCAGAGGTTTCAATCCTCTATGGCTCACCA  
>tdbD00006339 Staphylococcus\_aureus\_subsp.\_aureus\_MRSA252\_282458\_Lys\_TTT  
-GAGCCATTAGCTCAGCT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCAGAGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006341 Staphylococcus\_aureus\_subsp.\_aureus\_MRSA252\_282458\_Lys\_TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCAGAGGTTTCAATCCTCTATGGCTCAC--  
>tdbD00006239 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620\_Lys\_TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCAGAGGTTTCAATCCTCTATGGCTCACTA  
>tdbD00006078 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879\_Lys\_TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCAGAGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006273 Streptococcus\_agalactiae\_2603V/R\_208435\_Lys\_TTT  
-GACTCGTTAGCTCAGTT-GGT--AGAGCAATTGACTTTTAAATCAATGG-----GTCAGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006277 Streptococcus\_mutans\_UA159\_210007\_Lys\_TTT  
-GACTCGTTAGCTCAGTT-GGT--AGAGCATTGACTTTTAAATCAAAGG-----GTCAGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006302 Streptococcus\_pyogenes\_SSI-1\_193567\_Lys\_TTT  
-GGTCTGTTAGCTCAGTT-GGT--AGAGCAATTGACTTTTAAATCAATGG-----GTCAGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006311 Streptomyces\_avermitilis\_MA-4680\_227882\_Lys\_TTT  
-GGACCTTAGCTCAATT-GGC--AGAGCAGTGGACTTTTAAATCCATTG-----GTTGTGGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006269 Streptomyces\_coelicolor\_A3(2)\_100226\_Lys\_TTT  
-GGGCCCTTAGCTCAATT-GGC--AGAGCAGTGGACTTTTAAATCCATTG-----GTTGTGGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006355 Symbiobacterium\_thermophilum\_IAM\_14863\_292459\_Lys\_TTT  
-GGGCCATTAGCTCAGT--GGC--AGAGCATCCGCCTTTTAAAGCGGGT-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00001364 Synechocystis\_sp.\_1143\_Lys\_TTT  
-GGTCTGTTAGCTCAGC--GGT--AGAGCACTCGGCTTTTAAACCGATTG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006248 Thermoanaerobacter\_tengcongensis\_MB4\_273068\_Lys\_TTT  
-GACCCATTAGCTCAGGA-GGT--AGAGCACCTGCCTTTTAAAGCAGGGT-----GTCGCGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006249 Thermoanaerobacter\_tengcongensis\_MB4\_273068\_Lys\_TTT  
-GACCCATTAGCTCAGGA-GGT--AGAGCACCTGCCTTTTAAAGCAGGGT-----GTCGCGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006109 Thermotoga\_maritima\_MSB8\_243274\_Lys\_TTT  
-GACCCGGTAGCTCAGCA-GGC--AGAGCACCTGACTTTTAAATCAGGGG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006374 Thermus\_thermophilus\_HB27\_262724\_Lys\_TTT  
TGGGCCGTTAGCTCAGT-GGC--AGAGCAACCGACTTTTAAATCGGTAG-----GTCGAGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006375 Treponema\_denticola\_ATCC\_35405\_243275\_Lys\_TTT  
-GGGCTATTAGCTCAGTA-GGT--AGAGCAACGCCCTTTTAAAGCGGTGG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00001351 Treponema\_pallidum\_160\_Lys\_TTT  
-GGGCTATTAGCTCAGT-GGT--AGAGCAACGCCCTTTTAAAGCGGTGG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006291 Tropheryma\_whipplei\_str.\_Twist\_203267\_Lys\_TTT  
-GGGCTATTAGCTCAGT-GGT--AGAGCAACGCCCTTTTAAAGCGGTGG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006083 Ureaplasma\_parvum\_serovar\_3\_38504\_Lys\_TTT  
-GCCTCATTAGCTCAGT--GGT--AGAGCATTGACTTTTAAATGAAGGG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006076 Vibrio\_cholerae\_O1\_biovar\_El\_Tor\_str.\_N16961\_243277\_Lys\_TTT  
-GGGCTATTAGCTCAGT-GGT--AGAGCAGTTGGCTTTTAAACCAATTG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006377 Wolbachia\_endosymbiont\_of\_Drosophila\_melanogaster\_163164\_Lys\_TTT  
-GATCCGTTAGCTCAGCC-GGT--AGAGCAACTGACTTTTAAATCAGTGG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006253 Xanthomonas\_axonopodis\_pv.\_citri\_str.\_306\_190486\_Lys\_TTT  
-GGGCCGTTAGCTCAGTC-GGT--AGAGCAGAAGACTTTTAAATCTTTTG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006111 Xylella\_fastidiosa\_9a5c\_160492\_Lys\_TTT  
-GGGCCGTTAGCTCAGTC-GGT--AGAGCATCGGACTTTTAAATCAGTGG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006112 Xylella\_fastidiosa\_9a5c\_160492\_Lys\_TTT  
-ATAGCGTTTTTAGTCTCGGT--AGAGCATCGGACTTTTAAATCAGTGG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00006356 Yersinia\_pestis\_biovar\_Microtus\_str.\_91001\_229193\_Lys\_TTT  
-GGTCTGTTAGCTCAGT-GGT--AGAGCAGTTGACTTTTAAATCAATTG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00001939 Acholeplasma\_laidlawii\_2148\_Asn\_GTT  
-GCCTACTTAGCTCAGTT-GGTT-AGAGCACCTGACTGTTAATCAGGGG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00008021 Acinetobacter\_sp.\_ADP1\_62977\_Asn\_GTT  
-TCTCCAATAGCTCAGTC-GGT--AGAGCGACGGACTGTTAATCCGCAG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00008022 Acinetobacter\_sp.\_ADP1\_62977\_Asn\_GTT  
-TCTCCAATAGCTCAGTC-GGT--AGAGCGACGGACTGTTAATCCGCAG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00007859 Agrobacterium\_tumefaciens\_str.\_C58\_176299\_Asn\_GTT  
-TCCCTGTTAGCTCAGC--GGT--AGAGCATTCGACTGTTAATCAGCAG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00007833 Aquifex\_aeolicus\_VF5\_224324\_Asn\_GTT  
-TCCGGGTTAGCTCAATC-GGC--AGAGCGGTTGGCTGTTAACCACCTG-----GTTGGGGTTTCAATCCTCTATGGCTCA---  
>tdbD00008024 Bacillus\_anthraxis\_str.\_A2012\_191218\_Asn\_GTT  
-TCCGAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAATCCGATCG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00008025 Bacillus\_anthraxis\_str.\_A2012\_191218\_Asn\_GTT  
-TCCGAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAATCCGATCG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---  
>tdbD00007983 Bacillus\_anthraxis\_str.\_Ames\_198094\_Asn\_GTT  
-TCCGAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAATCCGATCG-----GTCGTTGGTTTCAATCCTCTATGGCTCA---

>tdbD00007984 *Bacillus anthracis*\_str.\_Ames 198094 Asn GTT  
-TCCGAGTAGCTCAGC--GGT--AGAGCTATCGGCTGTAAACCGATCG-----GTCGTAGGTTTCGATTCTACCTGCGGAGCCA  
>tdbD00007951 *Bacillus halodurans*\_C-125 272558 Asn GTT  
-TCCACAGTAGCTCAGT--GGT--AGAGCAATCGGCTGTAAACCGATCG-----GTCGTAGGTTTCGAGTCTACCTGTGGAGCCA  
>tdbD00007952 *Bacillus halodurans*\_C-125 272558 Asn GTT  
-TCCGAGTAGCTCAGT--GGT--AGAGCAATCGGCTGTAAACCGATCG-----GTCGTAGGTTTCGAGTCTACCTGCGGAGCCA  
>tdbD00001949 *Bacillus*\_sp.\_PS3 2334 Asn GTT  
-TCCGAGTAGCTCAGT--GGT--AGAGCAATCGGCTGTAAACCGATCG-----GTCGAGGTTTCGAATCCTGCCTGCGGAGCCA  
>tdbD00001947 *Bacillus subtilis* 1423 Asn GTT  
-TCCACAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTAAACCGATCG-----GTCGAGGTTTCGAATCCTGCCTGTGGAGCCA  
>tdbD00001948 *Bacillus subtilis* 1423 Asn GTT  
-TCCGAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTAAACCGATCG-----GTCGTAGGTTTCGAATCCTACCTGCGGAG---  
>tdbD00007801 *Bacillus subtilis*\_subsp.\_subtilis\_str.\_168 224308 Asn GTT  
-TCCGAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTAAACCGATCG-----GTCGTAGGTTTCGAATCCTACCTGCGGAGCCA  
>tdbD00007981 *Bacteroides thetaiotaomicron*\_VPI-5482 226186 Asn GTT  
-TCTTCTTAGCTCAGTC--GGT--AGAGCATCTGACTGTAAATCAGAGG-----GTCCTTGGTTCAAGTCCAAGAGGAAGAG---  
>tdbD00007985 *Bartonella henselae*\_str.\_Houston-1 283166 Asn GTT  
-TCCCGGTAGCTCAGT--GGT--AGAGCAACCGGCTGTAAACCGGTTG-----GTCGCTGGTTTCGAATCCGCGCCCGGGAGCCA  
>tdbD00007986 *Bdellovibrio bacteriovorus*\_HD100 264462 Asn GTT  
-TCAGAGTAGCTCAGTC--GGT--AGAGCAACCGGCTGTAAACCGGTTG-----GTCGCGGTTTCGAGTCCCTCCTTCTGAGCCA  
>tdbD00007936 *Bifidobacterium longum*\_NCC2705 206672 Asn GTT  
-TCCTCGGTAGCTCAGT--GGC--AGAGCATCCGACTGTAAATCCGAGC-----GTCGCTGGTTTCAGCCAGCCGCGAGGAG---  
>tdbD00007937 *Bifidobacterium longum*\_NCC2705 206672 Asn GTT  
-TCCTCGGTAGCTCAGT--GGC--AGAGCATCCGACTGTAAATCCGAGC-----GTCGCTGGTTTCAGCCAGCCGCGAGGAG---  
>tdbD00007938 *Bifidobacterium longum*\_NCC2705 206672 Asn GTT  
-TCCTCGGTAGCTCAGT--GGC--AGAGCATCCGACTGTAAATCCGAGC-----GTCGCTGGTTTCAGCCAGCCGCGAGGAG---  
>tdbD00001941 *Borrelia burgdorferi* 139 Asn GTT  
-TCCCTATAGCTCAGT--GGT--AGAGCGGTTGGCTGTAAACCACTAG-----GTCGAGGTTTCAGTCTTCTGGGGGAG---  
>tdbD00007953 *Bradyrhizobium japonicum*\_USDA 110 224911 Asn GTT  
-TCCCGGTAGCTCAGC--GGT--AGAGCATCCGACTGTAAATCCGATG-----GTCGCTGGTTTCGAATCCAGCCCGGGAGCCA  
>tdbD00007849 *Brucella melitensis*\_16M 224914 Asn GTT  
-TCCCGGTAGCTCAGC--GGT--AGAGCAACCGGCTGTAAACCGGTTG-----GTCGCTGGTTTCGAATCCGCGCCCGGGAGCCA  
>tdbD00007802 *Buchnera aphidicola*\_str.\_APS (Acyrtosiphon\_pisum) 107806 Asn GTT  
-TCCTCTGTAGTTTTCAGT--GGT--AGAACGGCGGACTGTAAATCCGAT-----GTCGCTGGTTTCGAATCCAGTCCGAGGAG---  
>tdbD00007973 *Buchnera aphidicola*\_str.\_Bp (Baizongia\_pistaciae) 224915 Asn GTT  
-TCCTCTGTAGTTTTCAGT--GGT--AGAACGGCGGACTGTAAATCCGAT-----GTCGCTGGTTTCGAATCCAGTCCGAGGAG---  
>tdbD00007918 *Buchnera aphidicola*\_str.\_Sg (Schizaphis\_graminum) 198804 Asn GTT  
-TCCTCTGTAGTTTTCAGT--GGT--AGAACGGCGGACTGTAAATCCGAT-----GTCGCTGGTTTCGAGCCAGTCCAGGGGAG---  
>tdbD00007822 *Campylobacter jejuni*\_subsp.\_jejuni\_NCTC 11168 192222 Asn GTT  
-TCCGATTAGCTCAGC--GGT--AGAGTAGTCCGCTGTAAACCGATTG-----GTCGTAGGTTTCGAATCCTACATCCGGAGCCA  
>tdbD00008030 *Candidatus Blochmannia floridanus* 203907 Asn GTT  
-TCCTCTGTAGTTTTCAGT--GGT--AGAACGGCGGACTGTAAATCCGAT-----GTCGCTGGTTTCGAATCCAGTCCAGGGGAGCCA  
>tdbD00007990 *Candidatus Protochlamydia amoebophila*\_UWE25 264201 Asn GTT  
-TCCGATTAGCTCAGC--GGT--AGAGCAGTGGACTGTAAATCCATTG-----GTCGCTAGTTTCGAATCTAGCATCCGGAG---  
>tdbD00007823 *Caulobacter crescentus*\_CB15 190650 Asn GTT  
-TCCCGGTAGCTCAGT--GGT--AGAGCAGCCGCTGTAAACCGGCTG-----GTCGTAGGTTTCGAATCCTACCCGCGGAGCCA  
>tdbD00007842 *Chlamydia muridarum*\_Nigg 243161 Asn GTT  
-TCCGAGTAGCTCAGC--GGT--AGAGCAGTGGACTGTAAATCCATTG-----GTCGTTGGTTTCGAACCCATCCTCCGGAG---  
>tdbD00007915 *Chlorobium tepidum*\_TLS 194439 Asn GTT  
-TCCGCGATAGCTCAAT--GGT--AGAGCATTCCGCTGTAAACCGAAGG-----GTTGTAGGTTTCGAATCCTACTCAGGAG---  
>tdbD00007846 *Clostridium acetobutylicum*\_ATCC 824 272562 Asn GTT  
-TCCGCGATAGCTCAAC--GGT--GGAGCACTCGGCTGTAAACCGATAG-----GTTGAAGGTTTCGAATCCTTTTCGCGGAGCCA  
>tdbD00007847 *Clostridium acetobutylicum*\_ATCC 824 272562 Asn GTT  
-TCCGTGATAGCTCAAC--GGT--GGAGCACTCGGCTGTAAACCGATAG-----GTTGAAGGTTTCGAATCCTTTTCAGGAGCCA  
>tdbD00007839 *Clostridium perfringens*\_str.\_13 195102 Asn GTT  
-TCCTCGGTAGCTCAAT--GGT--GGAGCACTCGGCTGTAAACCGATAG-----GTTGGAGGTTTCGAGTCTCTCCGAGGAGCCA  
>tdbD00007840 *Clostridium perfringens*\_str.\_13 195102 Asn GTT  
-TCCTCGATAGCTCAAT--GGT--GGAGCACTCGGCTGTAAACCGATAG-----GTTGGAGGTTTCGAGTCTCTCTCCGAGGAGCCA  
>tdbD00007955 *Clostridium tetani*\_E88 212717 Asn GTT  
-TCCGTGGTAGCTCAAT--GGT--GGAGCATTCCGCTGTAAACCGAAGG-----GTTGAAGGTTTCGAATCCTTTCCAGGAGCCA  
>tdbD00007987 *Corynebacterium diphtheriae*\_NCTC 13129 257309 Asn GTT  
-TCCCCATAGCTCAATT--GGC--AGAGCATTCCGACTGTAAATCGAAGG-----GTTACTGGTTTCGAGTCCAGTTGGGGGAG---  
>tdbD00007940 *Corynebacterium efficiens*\_YS-314 196164 Asn GTT  
-TCCTCCATAGCTCAGTT--GGC--AGAGCATTCCGACTGTAAATCGAAGG-----GTCGCTGGTTTCGAGCCAGTTCGAGGAG---  
>tdbD00007920 *Corynebacterium glutamicum*\_ATCC 13032 196627 Asn GTT  
-TCTCCATAGCTCAGTT--GGC--AGAGCATTCCGACTGTAAATCGAAGG-----GTCGCTGGTTTCGAGCCAGTTCGAGGAG---  
>tdbD00007970 *Coxiella burnetii*\_RSA 493 227377 Asn GTT  
-TCCTCGGTAGCTCAGTC--GGT--AGAGCAGGTGACTGTAAATCACTTG-----GTCGCGGTTTCAGTCCCTCCGAGGAGCCA  
>tdbD00007824 *Deinococcus radiodurans*\_R1 243230 Asn GTT  
-TCGGCAGTAGCTCAGT--GGC--AGAGCATCCGACTGTAAATCCGAGC-----GTCGTTGGTTTCGACCCCACTGCGGAGCCA  
>tdbD00008013 *Desulfovibrio vulgaris*\_subsp.\_vulgaris\_str.\_Hildenborough 882 Asn GTT  
-TCCCGGTGGCTCAATC--GGC--AGAGCGGTTGACTGTAAATCACTAG-----GTTGGCGGTTTCAGTCCGTTCCCGGGAGCCA  
>tdbD00007956 *Enterococcus faecalis*\_V583 226185 Asn GTT  
-TCCGCGATAGCTCAGTT--GGT--GTAGCGCATGACTGTAAATCATGAT-----GTCGTAGGTTTCGAGTCTACTGCGGAG---  
>tdbD00001950 *Escherichia coli* 562 Asn GTT

-TCCTCTGTAGTTCAGTC-GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTCAGAGGAGCCA  
>tdbD00007815 Escherichia coli\_O157H7\_EDL933 155864 Asn GTT:  
-TCCTCTGTAGTTCAGTC-GGT--AGAASGGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTCAGAGGAGCCA  
>tdbD00007916 Fusobacterium nucleatum subsp. nucleatum ATCC\_25586 190304 Asn GTT  
-GCTTCCTTAGCTCAGTC-GGT--AGAGCATGCGGCTGTTAACCAGCAGC-----GTCAATGGTTCGAGTCCATTAGGAAGCGCCA  
>tdbD00007998 Geobacter\_sulfurreducens\_PCA 243231 Asn GTT  
-TCCCCAATAGCTCAGTC-GGT--AGAGCGGGTGGCTGTTAACCACCAT-----GTCCCTGGTTCGAGTCCGGGTTGGGGAGCCA  
>tdbD00001953 Haemophilus influenzae 727 Asn GTT  
-TCCTCCTTAGTTCAGTC-GGT--AGAACGGTGGACTGTTAATCCATAT-----GTCGCGAGTTCGAGTCCCGCAGGAGGAGCCA  
>tdbD00001954 Haemophilus influenzae 727 Asn GTT  
-TCCTCCTTAGTTCAGTC-GGT--AGAACGGTGGACTGTTAATCCATAT-----GTCGCTGGTTCGAGTCCAGCAGGAGGAGCCA  
>tdbD00007966 Helicobacter hepaticus ATCC\_51449 235279 Asn GTT  
-TCCGGATTAGCTCAGC--GGT--AGAGTAGGTGGCTGTTAACCACCTG-----GTCGCGAGTTCGAGTCCGATCCCGAGGAGCCA  
>tdbD00007817 Helicobacter pylori\_26695 85962 Asn GTT  
-TCCAGATTAGCTCAGC--GGT--AGAGTAGGCGGCTGTTAACCAGCTG-----GTCGCTAGGTTGAGTCCATCTGAGGAGGAGCCA  
>tdbD00001945 Lactobacillus delbrueckii subsp. bulgaricus 1585 Asn GTT  
-TCCGCCTTAGCTCAGTT-GGT--AGAGCGCTTGACTGTTAATCAGGAT-----GTCGTCAGTTCGAGTCTGACAGCGGGAG---  
>tdbD00007999 Lactobacillus\_johnsonii\_NCC 533 257314 Asn GTT  
-TCCGGCTTAGCTCAGTT-GGT--AGAGCACCTGACTGTTAATCAGGTT-----GTCGTCAGTTCGAGTCTGACAGCCGGAG---  
>tdbD00008000 Lactobacillus\_johnsonii\_NCC 533 257314 Asn GTT  
-TCCGGCTTAGCTCAGTT-GGT--AGAGCACCTGACTGTTAATCAGGTT-----GTCGTCAGTTCGAGTCTGACAGCCGGAGCCA  
>tdbD00007957 Lactobacillus plantarum\_WCFs1 220668 Asn GTT  
-TCCGACATAGCTCAGTT-GGT--AGAGCGCTTGACTGTTAATCAAGAT-----GTCGCGAGTTCGAGTCCCGCTGTCGGAG---  
>tdbD00007958 Lactobacillus plantarum\_WCFs1 220668 Asn GTT  
-GTGGCCTTAGCTCAGTT-GGT--AGAGCACCTGACTGTTAATCAGGTT-----GTCGCTGGTTCGAGTCCAGCAGGCTACG---  
>tdbD00007959 Lactobacillus plantarum\_WCFs1 220668 Asn GTT  
-TGCCCGGTAGTTCAGC--GGT--AGAATAATTGACTGTTAATCAAGAG-----GTCGCTGGTTCGATCCAGCCCGGGCAG---  
>tdbD00001946 Lactococcus lactis 1358 Asn GTT  
-TGCCGATTAGCTCAGTT-GGTA-GTAGCGCATGACTGTTAATCATGAT-----GTCGTCAGTTCGAGTCTGACATCCGCAG---  
>tdbD00007941 Leptospira\_interrogans\_serovar\_Lai\_str.\_56601 189518 Asn GTT  
-TCCCTTTTAGCTCAGTC-GGT--AGAGCAAGTACTGTTAATCACTGG-----GTCGCTGGTTCGAGCCAGCAGGGGGAGCCA  
>tdbD00007834 Listeria\_innocua\_Clip11262 272626 Asn GTT  
-TCCACAGTAGCTCAGTT-GGT--AGAGCAATCGGCTGTTAACCAGATCG-----GTCGCGAGTTCGAGTCCCTGCCTGTGGAG---  
>tdbD00007835 Listeria\_innocua\_Clip11262 272626 Asn GTT  
-TCCACAGTAGCTCAGTT-GGT--AGAGCAATCGGCTGTTAACCAGATCG-----GTCGCGAGTTCGAGTCCCTGCCTGTGGAGCCA  
>tdbD00007836 Listeria\_innocua\_Clip11262 272626 Asn GTT  
-TCCACAGTAGCTCAGTT-GGT--AGAGCAATCGGCTGTTAACCAGATCG-----GTCGCGAGTTCGAGTCCCTGCCTGTGGAGCC-  
>tdbD00008016 Mesoplasma\_florum\_L1 265311 Asn GTT  
-GGCTTTTTAGCTCAGTT-GGT--AGAGCAACCGGCTGTTAACCAGGTT-----GTCACAGTTCGAGTCCCTGTAAAAGCCGCCA  
>tdbD00007967 Mycobacterium\_bovis\_AF2122/97 233413 Asn GTT  
-TCCCTGTAGCTCAATT-GGC--AGAGCGTTCGGCTGTTAACCAGGAG-----GTTGGAGGTTTCGAGTCCCTCCCGGGGGAG---  
>tdbD00007810 Mycobacterium\_leprae\_TN 272631 Asn GTT  
-TCCCTGTAGCTCAATT-GGC--AGAGCATTGGCTGTTAACCAGGAG-----GTTGGAGGTTTCGAGTCCCTCCCGGGGGAG---  
>tdbD00001935 Mycoplasma\_capricolum 2095 Asn GTT  
-GGCTTTTTAGCTCAGCA-GGT--AGAGCAACCGGCTGTTAACCAGGTT-----GTCACAGTTCGAGCCCTGTAAAAGCCGCCA  
>tdbD00007965 Mycoplasma\_gallisepticum\_R 233150 Asn GTT  
-GGCCACATAGCTCAGC--GGT--AGAGCAACCGGCTGTTAACCAGGTT-----GTCACAGTTCGAAATCCTGTGTGGCCGCCA  
>tdbD00001936 Mycoplasma\_genitalium 2097 Asn GTT  
-CTCAGCGTAGCTCAGC--GGT--AGAGCAACCGGCTGTTAACCAGGTT-----GTCACAGTTCGATCCCTGTGTGGCCGCCA  
>tdbD00007825 Mycoplasma\_genitalium\_G37 243273 Asn GTT  
-GGCCACATAGCTCAGC--GGT--AGAGCAACCGGCTGTTAACCAGGTT-----GTCACAGTTCGATCCCTGTGTGTGGCCGCCA  
>tdbD00007858 Mycoplasma\_pulmonis\_UAB\_CTIP 272635 Asn GTT  
-GCCGATTTAGCTCAGT--GGT--AGAGCAGCTGGCTGTTAACCAGTTG-----GTCACAAGTTCGAAATCTGTAAATCGGGGCCA  
>tdbD00007804 Neisseria\_meningitidis\_MC58 122586 Asn GTT  
-TCCCGATAGCTCAGTC-GGT--AGAGCGACGGACTGTTAATCCGCAG-----GTCCCTGGTTCGAGCCAGGTCGGGGAGCCA  
>tdbD00007980 Nitrosomonas\_europaea\_ATCC\_19718 228410 Asn GTT  
-TCCCGATAGCTCAGTC-GGT--AGAGCGACGGACTGTTAATCCGCAG-----GTCCCGAGTTCGAGCCCTGGTCGGGGAGCCA  
>tdbD00007855 Nostoc\_sp.\_PCC\_7120 103690 Asn GTT  
-TGCCCATAGCTCAAT--GGC--AGAGCAAGCGGCTGTTAACCAGGAG-----GTTGTAAAGTTCGACTCTTACTGGGGAGGAGCCA  
>tdbD00007857 Nostoc\_sp.\_PCC\_7120 103690 Asn GTT  
-TCCTCAGTAGCTCAGT--GGT--AGAGCGATCGACTGTTAATCGATTG-----GTCACTGGTTCGAAATCCAGTCTGGGGAG---  
>tdbD00007942 Oceanobacillus\_ihayensis\_HTE831 221109 Asn GTT  
-TCCACAGTAGCTCAGT--GGT--AGAGCAATCGGCTGTTAACCAGTCCG-----GTCGCTAGGTTGAGTCCATCTGAGGAGGAGCCA  
>tdbD00007988 Onion\_yellows\_phytoplasma\_OY-M 262768 Asn GTT  
-GCCTACGTAGCTCAGTT-GGTT-AGAGCATCTGACTGTTAATCAGAGG-----GTCCTAGGTTTCGAGTCCCTAGCGTGGGGGCCA  
>tdbD00007827 Pasteurella\_multocida\_subsp.\_multocida\_str.\_Pm70 272843 Asn GTT  
-TCCTCCTTAGTTCAGTC-GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCGCTGGTTCGAGTCCAGCAGGAGGAGCCA  
>tdbD00007991 Photorhabdus\_luminescens\_subsp.\_laumondii\_TTO1 243265 Asn GTT  
-TCCTCCATAGTTCAGTC-GGT--AGAACAGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTTCGGGGAGGAGCCA  
>tdbD00007992 Photorhabdus\_luminescens\_subsp.\_laumondii\_TTO1 243265 Asn GTT  
-TCCTCCATAGTTCAGTC-GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTTCGGAGGAGGAGCCA  
>tdbD00008002 Porphyromonas\_gingivalis\_W83 242619 Asn GTT  
-TCTTCTTAGCTCAGTT-GGTT-AGAGCATCTGACTGTTAATCAGAGG-----GTCCTTGGTTCGAGTCCAGGAGGAGGAG---  
>tdbD00008003 Porphyromonas\_gingivalis\_W83 242619 Asn GTT  
-GCTTCTTAGCTCAGTC-GGTT-AGAGCATCTGACTGTTAATCAGAGG-----GTCCTTGGTTCGAGCCCAAGAGAAAGCG---

>tdbD00008017 *Propionibacterium acnes*\_KPA171202\_267747\_Asn\_GTT  
-TCCCCTGTAGCTCAATT-GGC--AGAGCATCTGACTGTTAATCAGAGG-----GTTACTGGTTCGAGTCCAGTCCGGGGGAG---  
>tdbD00007829 *Pseudomonas aeruginosa*\_PAO1\_208964\_Asn\_GTT  
-TCCCGGATAGCTCAGTC-GGT--AGAGCAAATGACTGTTAATCATTGG-----GTCCCTGGTTCGAGTCCAGTCCGGGGAGCCA  
>tdbD00007982 *Pseudomonas syringae*\_pv.\_tomato\_str.\_DC3000\_223283\_Asn\_GTT  
-TCCCGGATAGCTCAGTT-GGT--AGAGCAAGTACTGTTAATCAGTGG-----GTCCCTGGTTCGAGTCCAGTCCGGGGAGCCA  
>tdbD00007854 *Ralstonia solanacearum*\_GMI1000\_267608\_Asn\_GTT  
-TCCCCGATAGCTCAGTC-GGT--AGAGCGCCGGACTGTTAATCCGTAG-----GTCCCTGGTTCGAGCCCAGTCCGGGGAGCCA  
>tdbD00007977 *Rhodopirellula baltica*\_SH\_1\_243090\_Asn\_GTT  
-TCCGGTGTGCCCAAT--GGT--AAGGCGGCTCCCTGTTAAGGAGACG-----AGTGATGGTTCGAGTCCATCCGCCGGAG---  
>tdbD00007978 *Rhodopirellula baltica*\_SH\_1\_243090\_Asn\_GTT  
-TCCCCTGTAGCTCAGTT-GGT--AGAGCAGCGGGCTGTTAACCGCCTT-----GTCACAGGTTTCGAGTCCGTTCGGGGGAG---  
>tdbD00007993 *Rhodopseudomonas palustris*\_CGA009\_258594\_Asn\_GTT  
-TCCCTGTAGCTCAGTC-GGT--AGAGCAAACCGGCTGTTAACCGTTCG-----GTCGCTGGTTCGAATCCGGCCCCGGGGAGCCA  
>tdbD00007848 *Rickettsia conorii*\_str.\_Malish\_7\_272944\_Asn\_GTT  
-TCCTCGGTAGCTTAGT--GGT--AGAGCAAACCGGCTGTTAACCGTTCG-----GTCGCTGGTTCGAGTCCGGCCCCGGGGAGCCA  
>tdbD00007919 *Rickettsia prowazekii*\_str.\_Madrid\_E\_272947\_Asn\_GTT  
-TCCCTGTAGCTCAGTC-GGT--AGAGCAAACCGGCTGTTAACCGTTCG-----GTCGCTGGTTCGAGTCCGGCCCCGGGGAGCCA  
>tdbD00007945 *Shewanella oneidensis*\_MR-1\_211586\_Asn\_GTT  
-TCCCCTGTAGTTCAGTC-GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCAGTGGTTCAGTCCAGTCCAGTCCGGGGAGCCA  
>tdbD00007946 *Shigella flexneri*\_2a\_str.\_301\_198214\_Asn\_GTT  
-TCCTGTAGTTCAGTC-GGT--AGAAGCGGGGACTGTTAACCGTTCG-----GTCAGTGGTTCGAGTCCAGTCCAGTCCGGGGAGCCA  
>tdbD00007861 *Sinorhizobium meliloti*\_1021\_266834\_Asn\_GTT  
-TCCCTGGTAGCTCAGC--GGT--AGAGCACTCGACTGTTAATCGATAG-----GTCGCGGGTTCGAATCCGGCCCCGGGGAGCCA  
>tdbD00007994 *Staphylococcus aureus*\_subsp.\_aureus\_MRSA252\_282458\_Asn\_GTT  
-TCCACAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAACCGTTCG-----GTCGCTAGGTTTCGAGTCCCTACCTGTGGAGCCA  
>tdbD00007961 *Staphylococcus epidermidis*\_ATCC\_12228\_176280\_Asn\_GTT  
-TCCACAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAACCGTTCG-----GTCGCTAGGTTTCGAATCCCTACCTGTGGAGCCA  
>tdbD00007948 *Streptococcus agalactiae*\_2603V/R\_208435\_Asn\_GTT  
-TCCGGCATAGCTCAGTT-GGTA-GTAGCGCATGACTGTTAATCATGAT-----GTCGCGAGGTTTCGAGTCCGTTCGCTGCCGGAG---  
>tdbD00007949 *Streptococcus agalactiae*\_2603V/R\_208435\_Asn\_GTT  
-TCCGGCATAGCTCAGTT-GGTA-GTAGCGCATGACTGTTAATCATGAT-----GTCGCTAGGTTTCGAGTCCCTACTGCGGGAG---  
>tdbD00007975 *Streptomyces avermitilis*\_MA-4680\_227882\_Asn\_GTT  
-TCCTCCGTAGCTCAATT-GGC--AGAGCAGCCGGCTGTTAACCGGCAG-----GTTACTGGTTCGAGTCCAGTCCGGGGGAG---  
>tdbD00007944 *Streptomyces coelicolor*\_A3(2)\_100226\_Asn\_GTT  
-TCCTCGGTAGCTCAATT-GGC--AGAGCAGCCGGCTGTTAACCGGCAG-----GTTACTGGTTCGAGTCCAGTCCGGGGGAG---  
>tdbD00008005 *Symbiobacterium thermophilum*\_IAM\_14863\_292459\_Asn\_GTT  
-TCCGGGTAGCTCAGC--GGT--AGAGCGTCCGGCTGTTAACCGGAGG-----GTCGCTAGGTTTCGAATCCCTACCGCCGGAGCCA  
>tdbD00001955 *Synechocystis*\_sp.\_1143\_Asn\_GTT  
-TCCTCGGTAGCTCAGT--GGT--AGAGCGGTCCGGCTGTTAACCGATTG-----GTCGCTAGGTTTCGAATCCCTACCGGGGAG---  
>tdbD00007928 *Thermoanaerobacter tengcongensis*\_MB4\_273068\_Asn\_GTT  
-TCCTCAGTAGCTCAAG--GGT--AGAGCAAACCGGCTGTTAACCGGTAG-----GTTGTAGGTTTCGAATCCCTACCTGAGGAGCCA  
>tdbD00007929 *Thermoanaerobacter tengcongensis*\_MB4\_273068\_Asn\_GTT  
-TCCTCAGTAGCTCAAG--GGT--AGAGCAGCCGGCTGTTAACCGGCAG-----GTTGTAGGTTTCGAATCCCTACCTGAGGAGCCA  
>tdbD00007926 *Thermosynechococcus elongatus*\_BP-1\_197221\_Asn\_GTT  
-TCCTCAGTAGCTCAGC--GGT--AGAGCGGTCCGGCTGTTAACCGATTG-----GTCGCTGGTTCGAATCCAGCTCCGGGGAG---  
>tdbD00007831 *Thermotoga maritima*\_MSB8\_243274\_Asn\_GTT  
-TCCGGGTAGCTCAACC-GGT--AGAGCGCTGGCTGTTAACCGAGTG-----GTTGCAGGTTTCGAGTCCGTGCCCGGGAGCCA  
>tdbD00008018 *Thermus thermophilus*\_HB27\_262724\_Asn\_GTT  
--CCGGGTAGCTCAGCA-GGT--AGAGCAGCCGGCTGTTAACCGGTAG-----GTCGCGAGGTTTCGAGTCCGTGCCCGGGAGCCA  
>tdbD00008019 *Treponema denticola*\_ATCC\_35405\_243275\_Asn\_GTT  
-TCCCCTGTAGCTCAGTA-GGC--AGAGCAAGTGGCTGTTAACCACTGG-----GTCCGTGGTTCGAACCCCGCGGGGGAG---  
>tdbD00001940 *Treponema pallidum*\_160\_Asn\_GTT  
-TCCCCTGTAGCTCAGTT-GGT--AGAGCAAATGGCTGTTAACCATTTGG-----GTCCGTGGTTCGAGCCCAGCGGGGGAG---  
>tdbD00007962 *Tropheryma whippelii*\_str.\_Twist\_203267\_Asn\_GTT  
-TCCTCGATAGCTCAATT-GGC--AGAGCAGCCGGCTGTTAACCGGCAG-----GTTCTTGGTTCGAGTCCAGTCCGGGGAG---  
>tdbD00007811 *Ureaplasma parvum*\_serovar\_3\_38504\_Asn\_GTT  
-GGTACATAGCTCAGC--GGT--AGAGCAAACCGGCTGTTAACCGGTTG-----GTCGCTAGGTTTCGATCCCTACTGTAGCCGCCA  
>tdbD00007806 *Vibrio cholerae*\_O1\_biovar\_El\_Tor\_str.\_N16961\_243277\_Asn\_GTT  
-TCCTCCTTAGTTCAGTC-GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCGCGAGGTTTCGAGTCCCGCAGGAGGAGCCA  
>tdbD00007807 *Vibrio cholerae*\_O1\_biovar\_El\_Tor\_str.\_N16961\_243277\_Asn\_GTT  
-TCCTCCTTAGTTCAGTC-GGT--AGAGCGACGGACTGTTAATCCGCAG-----GTCGCTGGTTCGAGCCCAGCAGGAGGAGCCA  
>tdbD00007808 *Vibrio cholerae*\_O1\_biovar\_El\_Tor\_str.\_N16961\_243277\_Asn\_GTT  
-TCCTCCTTAGTTCAGTC-GGT--AGAGCGACGGACTGTTAATCCGCAG-----GTCGCTGGTTCAGTCCAGCAGGAGGAGCCA  
>tdbD00008020 *Wolbachia endosymbiont of Drosophila melanogaster*\_163164\_Asn\_GTT  
-TCCTCGGTAGCTCAGT--GGT--AGAGCAGTGGCTGTTAACCAATTG-----GTCGCTGGTTCGAATCCGGCCCCGGGGAG---  
>tdbD00007931 *Xanthomonas axonopodis*\_pv.\_citri\_str.\_306\_190486\_Asn\_GTT  
-GCCCGAATAGCTCAGCC-GGTT-AGAGCACTTACTGTTAATCAGGGG-----GTCGTTGGTTCGAGTCCAACTTCGGGGCCCA  
>tdbD00004924 *Buchnera aphidicola*\_str.\_APS\_(Acyrtosiphon\_pisum)\_107806\_Phe\_GAA  
-GCCCGGATAGCTCAGTT-GGT--AGAGCAGGGGACTGAAATCCCCGT-----GTCGCTGGTTCATTCGCCCTCCGGGCA---  
>tdbD00005017 *Buchnera aphidicola*\_str.\_Sg\_(Schizaphis\_graminum)\_198804\_Phe\_GAA  
-GCCCGGATAGCTCAGTC-GGT--AGAGCAGGGGACTGAAATCCCCGT-----GTCGCTGGTTCATTCGCCCTCCGGGCA---  
>tdbD00005098 *Desulfovibrio vulgaris*\_subsp.\_vulgaris\_str.\_Hildenborough\_882\_Phe\_GAA  
-GCCGAGGTAGCTCAGTT-GGT--AGAGCAGGGGACTGAAATCCCCGT-----GTCGGGAGTTCATTCCTCTCCCTCCGGCACCA  
>tdbD00000686 *Escherichia coli*\_562\_Phe\_GAA

-GCCCCGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTTGGTTTCGATTCCGAGTCCGGGCACCA  
>tdbD00004935 Escherichia coli\_O157H7 83334 Phe GAA:  
-GCCCCGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTTGGTTCAATTCCGAGTCCGGGCACCA  
>tdbD00005015 Fusobacterium nucleatum subsp. nucleatum\_ATCC\_25586 190304 Phe GAA  
-GCCCAGATAGCTCAGTC-GGT--AGAGCAGGGGACTGAAAATCCCCGT-----GTCGGTGGTTTCGATTCCGCCTCTGGGCACCA  
>tdbD00000687 Haemophilus influenzae 727 Phe GAA  
-CCCTCGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCGGTGGTTTCGATTCCGCCTCGAGGCACCA  
>tdbD00000688 Haemophilus influenzae 727 Phe GAA  
-GCCTCGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCGGTGGTTTCGATTCCGCCTCGAGGCACCA  
>tdbD00004951 Pseudomonas aeruginosa PAO1 208964 Phe GAA  
-GCCCAGGTAGCTCAGTT-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCGGCGGTTTCGATTCCGCTCCCTGGGCACCA  
>tdbD00005066 Pseudomonas syringae pv. tomato\_str. DC3000 223283 Phe GAA  
-GCCCAGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCGGCGGTTTCGATTCCGCTCTCTGGGCACCA  
>tdbD00005028 Xanthomonas axonopodis pv. citri\_str. 306 190486 Phe GAA  
-GGCCGAGTAGCTCAGTT-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCGGCGGTTTCGATTCCGCTCTCGGCCACCA  
>tdbD00004954 Xylella fastidiosa\_9a5c 160492 Phe GAA  
-GGCCGGTAGCTCAGTT-GGT--AGAGCAGGGGACTGAAAATCCCCGT-----GTCGGGGGTTTCGATTCCCTCCCCGGCCACCA  
>tdbD00005052 Xylella fastidiosa Temecula 183190 Phe GAA  
-GGCCGGTAGCTCAGTC-GGT--AGAGCAGGGGACTGAAAATCCCCGT-----GTCGGGGGTTTCGATTCCCTCCCCGGCCACCA  
>tdbD00000029 Acetobacter aceti 435 Ala TGC  
-GGGGGCATAGCTCAGCT-GGG--AGAGCACCTGCTTTCGCAAGCAGGGG-----GTCGTGCGGTTTCGAAACCCGCTGCTCCACCA  
>tdbD00000036 Acholeplasma laidlawii 2148 Ala TGC  
-GGGGCTTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGAT-CCGCTAAGCTCCACCA  
>tdbD00000037 Acholeplasma laidlawii 2148 Ala TGC  
-GGGGCCTTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGAT-CCGCTAGGCTCCACCA  
>tdbD00000036 Acidithiobacillus ferrooxidans 920 Ala TGC  
-GGGGCTGTAGCTCAGTT-GGG--AGAGCACCTGCTTTCGCAAGCAGGGG-----GTCATCGGTTTCGAGACCCGGTCAGCTCCACCA  
>tdbD00000071 Aeromonas hydrophila 644 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCCTGCTTTCGCAAGCAGGAG-----GTCGTGCGGTTTCGATCCCGCATAGCTCCACCA  
>tdbD00003788 Agrobacterium tumefaciens\_str. C58 176299 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCACCA  
>tdbD00003787 Agrobacterium tumefaciens\_str. C58 176299 Ala TGC  
-GGGGCTGTAGCTCAGCT-GGG--AGAGCACCTGCTTTCGCAAGCAGGGG-----GTCAGCGGTTTCGATCCCGCTCAGCTCCACCA  
>tdbD00003754 Aquifex aeolicus VF5 224324 Ala GGC  
-GGGGCGGTAGCTCAGCT-GGG--AGAGCGCCGATATGGCATGTCGGAG-----GTCGGGGGTTTCGAGTCCCTCCGCTCCACCA  
>tdbD00004011 Bacillus anthracis\_str. Ames 198094 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00004012 Bacillus anthracis\_str. Ames 198094 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00003960 Bacillus halodurans\_C-125 272558 Ala GGC  
-GGGGCATTAGCTCAGCT-GGG--AGAGCGCTTCGCTGGCAGCGAAGAG-----GTCAGCGGTTTCGAGCCCCGCTATGCTCCACCA  
>tdbD00003961 Bacillus halodurans\_C-125 272558 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCTTTCGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00000056 Bacillus subtilis 1423 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCTTTCGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00003691 Bacillus subtilis\_subsp. subtilis\_str. 168 224308 Ala GGC  
-GGGGCATTAGCTCAGCT-GGG--AGAGCGCTACGCTGGCAGCGTAGAG-----GTCAGGGGTTTCGAGCCCCCTTGGCTCCA---  
>tdbD00000025 Bartonella elizabethae 807 Ala TGC  
-GGGGCCTAGCTCAGCT-GGG--AGAGCACCTGCTTTCGCAAGCAGGGG-----GTCGTGCGGTTTCGATCCCGCTCCGCTCCACCA  
>tdbD00004084 Bartonella quintana\_str. Toulouse 283165 Ala GGC  
-GGGGCTATAGCTCAGTT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCACCA  
>tdbD00004015 Bdellovibrio bacteriovorus\_HD100 264462 Ala GGC  
-GGGGCCTAGCTCAGCT-GGG--AGAGCGCAACGCTGGCAGTGTGAG-----GTCGTGCGGTTTCGATCCCGATCGGCTCCACCA  
>tdbD00004016 Bdellovibrio bacteriovorus\_HD100 264462 Ala TGC  
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>tdbD00003962 Bradyrhizobium japonicum\_USDA\_110 224911 Ala CGC  
-GGGGCATTAGCTCAGCT-GGG--AGAGCGCGTTCGCTGCAATGACGAG-----GTCGGCGGTTTCGATCCCGCTGGCTCCACCA  
>tdbD00003963 Bradyrhizobium japonicum\_USDA\_110 224911 Ala GGC  
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>tdbD00003964 Bradyrhizobium japonicum\_USDA\_110 224911 Ala TGC  
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>tdbD00003769 Brucella melitensis\_16M 224914 Ala CGC  
-GGGGCTGTAGCTCAGCT-GGG--AGAGCGCGTTCGCTGCAATGACGAG-----GTCAGGGGTTTCGATCCCGCTCAGCTCCACCA  
>tdbD00003941 Brucella suis\_1330 204722 Ala GGC  
-GGGGCATTAGCTCAGCT-GGG--AGAGCGCCTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCGCTGGCTCCACCA  
>tdbD00003695 Buchnera aphidicola\_str. APS\_ (Acyrtosiphon pisum) 107806 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTCAATCCCGCTTAGCTCCA---  
>tdbD00003991 Buchnera aphidicola\_str. Bp\_ (Baizongia pistaciae) 224915 Ala TGC  
-GGGGTATTAGCTCAGCT-GGG--AGAGCGCTTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTTAAGTCCA---  
>tdbD00000045 Burkholderia cepacia 292 Ala TGC  
-GGGGCATTAGCTCAGCT-GGG--AGAGCACCTGCTTTCGCAAGCAGGGG-----T-CGTGCGGTTTCGATCCCGCTGCTCCACCA  
>tdbD00000078 Campylobacter jejuni 197 Ala TGC  
-GGGGCATTAGCTCAGCT-GGG--AGAGCGCCTGCTTTCGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTATTCTCCACCA  
>tdbD00003728 Campylobacter jejuni\_subsp. jejuni\_NCTC\_11168 192222 Ala GGC  
-GGGGCATTAGCTCAGCT-GGG--AGAGCACACGCTGGCAGCGTTGGG-----GTCAGCGGTTTCGAAACCCGCTATGCTCCACCA

>tdbD00003729 *Campylobacter\_jejuni\_subsp.\_jejuni\_NCTC\_11168\_192222* Ala TGC  
-GGGGAATTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTATTCTCCACCA  
>tdbD00004086 *Candidatus\_Blochmannia\_floridanus\_203907* Ala TGC  
-GGGGTATAGCTCAATT-GGG--AGAGCATCTGTTTTGCACACAGAAG-----GTTAGCGGTTTCGATCCCGCTTAGCTCCA---  
>tdbD00003766 *Clostridium\_acetobutylicum\_ATCC\_824\_272562* Ala TGC  
-GGGGGATTAGCTCAGCT-GGG--AGAGCACCTGCCTTGCACGCAGGGG-----GTCAAGAGTTTCAATCTCTTATTCTCCACCA  
>tdbD00003761 *Clostridium\_perfringens\_str.\_13\_195102* Ala TGC  
-GGGGTATAGCTCAGTT-GGG--AGAGCACCTGCCTTGCACGCAGGGG-----GTCAGGAGTTTCAATCTCTTACCTCCACCA  
>tdbD00003965 *Clostridium\_tetani\_E88\_212717* Ala TGC  
-GGGGTATAGCTCAGCT-GGG--AGAGCACCTGCCTTGCACGCAGGGG-----GTCAAGAGTTTCAATCTCTTATTCTCCACCA  
>tdbD00003966 *Clostridium\_tetani\_E88\_212717* Ala TGC  
-GGGGTATAGCTCAGTT-GGG--AGAGCACCTGCCTTGCACGCAGGGG-----GTCAGGAGTTTCAATCTCTTATTCTCCACCA  
>tdbD00000046 *Coxiella\_burnetii\_777* Ala TGC  
-GGGGCATAGCTCAGCT-GGG--AGAGCATCTGCCTTGCACGCAGAGG-----GTCGGCGGTTTCGACTCCGCCTGGCTCCACCA  
>tdbD00003986 *Coxiella\_burnetii\_RSA\_493\_227377* Ala GGC  
-GGGGTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCA---  
>tdbD00003733 *Deinococcus\_radiodurans\_R1\_243230* Ala CGC  
-GGGTCGTAGCTCAGCT-GGG--AGAGCGCTGCCTTGCACGCAGGGG-----GTCAGGGGTTTCGATCCCGCTTCGACTCCACCA  
>tdbD00003734 *Deinococcus\_radiodurans\_R1\_243230* Ala GGC  
-GGGGTGTGGCGCAGTT-GGG--AGCGCGTCTGAATGGCATTCAAGAG-----GTCAGGGGTTTCGATCCCGCTCAGCTCCACCA  
>tdbD00003735 *Deinococcus\_radiodurans\_R1\_243230* Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCATCCGCTTGCACGCAGGAG-----GTCTAGGGTTTCAATCCCTAAGCCTCCACCA  
>tdbD00004063 *Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882* Ala CGC  
-GGGGATGTAGCTCAGCT-GGG--AGAGCGCAGCTTGCACGCAGGAG-----GTCAGGGGTTTCAATCCCGCTCATCTCCACCA  
>tdbD00004061 *Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882* Ala GGC  
-GGGGCTGTAGCTCAGTT-GGG--AGAGCGCTTGAATGGCATTCAAGAG-----GTCAGGAGTTTCAATCTCTCAGCTCCACCA  
>tdbD00004062 *Desulfovibrio\_vulgaris\_subsp.\_vulgaris\_str.\_Hildenborough\_882* Ala TGC  
-GGGGCGTAGCTCAGCT-GGG--AGAGCACCTGCCTTGCACGCAGGGG-----GTCAACGGTTTCAATCCCGTTTCGCTCCACCA  
>tdbD00003898 *Fusobacterium\_nucleatum\_subsp.\_nucleatum\_ATCC\_25586\_190304* Ala TGC  
-GGGGATATAGCTCAGCT-GGG--AGAGCGCAGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTTATTCTCCACCA  
>tdbD00004034 *Geobacter\_sulfurreducens\_PCA\_243231* Ala CGC  
-GGGGAGTAGCTCAGCT-GGG--AGAGCGATGCGTTTCGCAACGCATAG-----GTCGAGGGTTTCGATCCCGCTTCGTCTCCACCA  
>tdbD00004036 *Geobacter\_sulfurreducens\_PCA\_243231* Ala GGC  
-GGGGCTGTAGCTCAGTT-GGG--AGAGCGCTTGAATGGCATTCAAGAG-----GTCGTTCGATTCGATCCTGATCAGCTCCACCA  
>tdbD00004035 *Geobacter\_sulfurreducens\_PCA\_243231* Ala TGC  
-GGGGTGTAGCTCAGCT-GGG--AGAGCGCTGCCTTGCACGCAGGAG-----GTCATCGGTTTCGACCCGTTTACCTCCACCA  
>tdbD00000030 *Gluconacetobacter\_europaeus\_33995* Ala TGC  
-GGGGCGTAGCTCAGCT-GGG--AGAGCACCTGCCTTGCACGCAGGGG-----GTCGTTCGATTCGATCCCGCTCCCGCTCCACCA  
>tdbD00000034 *Gluconacetobacter\_liquefaciens\_89584* Ala TGC  
-GGGGCGTAGCTCAGCT-GGG--AGAGCACCTGCCTTGCACGCAGGGG-----GTCGTTCGATTCGACCCGTTCCGCTCCACCA  
>tdbD00000035 *Gluconacetobacter\_liquefaciens\_89584* Ala TGC  
-GGGGCGTAGCTCAGCT-GGG--AGAGCACCTGCCTTGCACGCAGGGG-----GTCGTTCGATTCGACCCGTTCCGCTCCACCA  
>tdbD00000088 *Haemophilus\_influenzae\_727* Ala GGC  
-GGGGATATAGCTCAGTT-GGG--AGAGCGCTTGAATGGCATTCAAGAG-----GTCGTTCGATTCGATCCCGATTATTCTCCACCA  
>tdbD00000089 *Haemophilus\_influenzae\_727* Ala TGC  
-GGGGATATAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----T-CAGCGGTTTCGATCCCGCTTATTCTCCACCA  
>tdbD00003726 *Haemophilus\_influenzae\_Rd\_KW20\_71421* Ala TGC  
-GGGGATATAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTTATTCTCCACCA  
>tdbD00003981 *Helicobacter\_hepaticus\_ATCC\_51449\_235279* Ala GGC  
-GGGGTGTAGCTCAGTT-GGG--AGAGCGCAACGCTGGCAGCGTTGAG-----GTCAGGGGTTTCGACCCCTTACACTCCACCA  
>tdbD00000051 *Helicobacter\_pylori\_210* Ala GGC  
-GGGGTGTAGCTCAGCT-GGG--AGAGCGCAACGCTGGCAGCGTTGAG-----GTCAGGGGTTTCGACCCCTTACACTCCACCA  
>tdbD00000052 *Helicobacter\_pylori\_210* Ala TGC  
-GGGGAATTAGCTCAGCT-GGG--AGAGCACCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTTATTCTCCACCA  
>tdbD00000059 *Lactobacillus\_acidophilus\_1579* Ala TGC  
-GGGGCTTAGCTCAGTT-GGG--AGAGCACCTGCCTTGCACGCAGGAG-----GTCATCGGTTTCGACCCGTTAGCTCCA---  
>tdbD00000060 *Lactobacillus\_casei\_1582* Ala TGC  
-GGGGATTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCATCGGTTTCGATCCCGTTATTCTCCCA---  
>tdbD00000050 *Lactobacillus\_delbrueckii\_subsp.\_bulgaricus\_1585* Ala TGC  
-GGGGCATAGCTCAGCT-GGG--AGAGCACCTGCCTTGCACGCAGGAG-----GTCATCGGTTTCGATCCCGTTTGCCTCCA---  
>tdbD00004037 *Lactobacillus\_johnsonii\_NCC\_533\_257314* Ala TGC  
-GGGGCTTAGCTCAGAT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCATCGGTTTCGATCCCGTTAGCTCCA---  
>tdbD00003968 *Lactobacillus\_plantarum\_WCF51\_220668* Ala TGC  
-GGGGAATTAGCTCAGCT-GGG--AGAGCACCTGCCTTGCACGCAGGGG-----GTCAGCGGTTTCGATCCCGCTATTCTCCA---  
>tdbD00000053 *Lactococcus\_lactis\_1358* Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCA---  
>tdbD00003944 *Leptospira\_interrogans\_serovar\_Lai\_str.\_56601\_189518* Ala GGC  
-GGGGACGTAGCTCAGTT-GGG--AGAGCATTTGAATGGCATTCAAAAG-----GTCGGGGGTTTCGATCCCGCTCGCTCCA---  
>tdbD00003945 *Leptospira\_interrogans\_serovar\_Lai\_str.\_56601\_189518* Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCATCTGATTTGCATTCAAGAG-----GTCGTTCGATTCGATCCCGACAAGCTCCA---  
>tdbD00003772 *Mesorhizobium\_loti\_MAFF303099\_266835* Ala CGC  
-GGGGTGTAGCTCAGCT-GGG--AGAGCGCATCGTTTCGCAATGATGAG-----GTCAGGGGTTTCGATCCCGCTCAGCTCCACCA  
>tdbD00003773 *Mesorhizobium\_loti\_MAFF303099\_266835* Ala GGC  
-GGGGCATAGCTCAGTT-GGG--AGAGCGCTTGAATGGCATTCAAGAG-----GTCGTTCGATTCGATTCGATTGGCTCCACCA  
>tdbD00003771 *Mesorhizobium\_loti\_MAFF303099\_266835* Ala TGC

-GGGGCCGTAGCTCAGCT-GGG--AGAGCGCCTGCTTTGCAAGCAGGAT-----GTCGTCGGTTTCGATCCCCGTCGGCTCCACCA  
>tdbD00004006 Nitrosomonas europaea ATCC 19718 228410 Ala GGC  
-GGGGGTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCGTTATCTCCACCA  
>tdbD00004005 Nitrosomonas europaea ATCC 19718 228410 Ala TGC  
-GGGGGTGTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCATCGGTTTCGATCCCCGTTCACTCCACCA  
>tdbD00003948 Oceanobacillus iheyensis HTE831 221109 Ala GGC  
-GGGGCATTAGCTCAGCT-GGG--AGAGCGCTTCACTGGCAGTGAAGAG-----GTCAGCGGTTTCGAGCCCCTATGCTCCA---  
>tdbD00003738 Pasteurella multocida subsp. multocida str. Pm70 272843 Ala GGC  
-GGGGATATAGCTCAGTT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCGTCGGTTTCGATCCCCGATTATCTCCACCA  
>tdbD00004024 Photorhabdus luminescens subsp. laumondii TTO1 243265 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCCGTTAGCTCCACCA  
>tdbD00000074 Pseudomonas aeruginosa 287 Ala TGC  
-GGGGCCATAGCTCAGCT-GGG--AGAGCGCCTGCTTTGCACGCAGGAG-----GTCAGGAGTTTCGATCCTCCTTGCTCCACCA  
>tdbD00003743 Pseudomonas aeruginosa PAO1 208964 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCGACGGTTTCGATCCCCGTTAGCTCCACCA  
>tdbD00000076 Pseudomonas fluorescens 294 Ala TGC  
-GGGGCCATAGCTCAGCTGGGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAACGGTTTCGATCCCCGTTTGCTCCACCA  
>tdbD00000079 Pseudomonas mendocina 300 Ala TGC  
-CGGGCCATAGCTCAGCT-GGG--AGAGCGCCTGCTTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCCGTTTGCTCCACCA  
>tdbD00004010 Pseudomonas syringae pv. tomato str. DC3000 223283 Ala GGC  
-GGGGCTTTAGCTCAGCT-GGG--AGAGCGCCTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCGTTAAGCTCCACCA  
>tdbD00004001 Pseudomonas syringae pv. tomato str. DC3000 223283 Ala TGC  
-GGGGCCATAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCCGTTTGCTCCACCA  
>tdbD00000086 Ralstonia pickettii 329 Ala TGC  
-GGGGGATTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----T-CGTCGGTTTCGATCCCCGTCATCTCCACCA  
>tdbD00003781 Ralstonia solanacearum GMI1000 267608 Ala CGC  
-GGGGCGGTAGCTCAGCT-GGG--AGAGCGTCGCGTTCGCAATGCGAAG-----GTCGGGAGTTTCGATCCTCCTCCGCTCCACCA  
>tdbD00003779 Ralstonia solanacearum GMI1000 267608 Ala TGC  
-GGGGGATTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCGTCGGTTTCGATCCCCGTCATCTCCACCA  
>tdbD00004001 Rhodopirellula baltica SH\_1 243090 Ala GGC  
-GGGGGATTAGCTCAGTT-GGG--AGAGCGACGCGCTGGCAGCGCGTAG-----GTCATCGGTTCAAGTCCGTTATCTCCCA---  
>tdbD00004000 Rhodopirellula baltica SH\_1 243090 Ala TGC  
-GGGGCGCTCGTCCAAC--GGG--AAGACGTCTGTTTTGCACGCAGAAA-----A-TCGGGGTTTCGATTCCCCGGTGCTCCA---  
>tdbD00004002 Rhodopirellula baltica SH\_1 243090 Ala TGC  
-GGGGGTATAGCTCAGTT-GGG--AGAGCGTCTGCTTTGCAAGCAGAAT-----GTCGTCGGTTTCGAGTCCGTCTACCTCCA---  
>tdbD00004003 Rhodopirellula baltica SH\_1 243090 Ala TGC  
-GGGGCGCTCGTCCAAC--GGG--AAGACATCTGTTTTGCACGCAGAAA-----A-TCGGGGTTTCGATTCCCCGGTGCTCCA---  
>tdbD00004027 Rhodopseudomonas palustris CGA009 258594 Ala CGC  
-GGGGCCATAGCTCAGCT-GGG--AGAGCGCATCGTTGCGAATGATGAG-----GTCGGCGGTTTCGATCCCCGCTGGCTCCACCA  
>tdbD00003955 Shewanella oneidensis MR-1 211586 Ala GGC  
-GGGGGTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCGACGGTTTCGATCCCCGTTAGCTCCACCA  
>tdbD00003953 Shewanella oneidensis MR-1 211586 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCTCGGTTTCGATCCCCGATAGCTCCACCA  
>tdbD00003793 Sinorhizobium meliloti 1021 266834 Ala CGC  
-GGGGTCGTAGCTCAGTT-GGG--AGAGCGCGCAATCGCACTGCGGAG-----GTCGAGGGTTTCGACTCCCTTCGGCTCCACCA  
>tdbD00000049 Staphylococcus aureus 1280 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCCTGCTTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCCGTTAGTCTCCACCA  
>tdbD00000090 Stenotrophomonas maltophilia 40324 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----T-CGTCGGTTTCGATCCCCGACAGGCTCCACCA  
>tdbD00000095 Streptococcus salivarius 1304 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCCTGCTTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCCGTTAGGCTCCA---  
>tdbD00004047 Symbiobacterium thermophilum IAM 14863 292459 Ala CGC  
-GGGGCTATAGCTCAGTT-GGG--AGAGCGCGTGAATCGCACTCAGGAG-----GTCAGGGGTTTCGAATCCCCTTAGCTCCACCA  
>tdbD00004050 Symbiobacterium thermophilum IAM 14863 292459 Ala CGC  
-GGGGCTATAGCTCAGTT-GGG--AGAGCGCGTGAATCGCACTCAGGAG-----GTCGGGGGTTTCGAGTCCCCTTAGCTCCACCA  
>tdbD00004046 Symbiobacterium thermophilum IAM 14863 292459 Ala GGC  
-GGGGCTATAGCTCAGTT-GGG--AGAGCGCTTGAATGGCATTCAAGAG-----GTCAGGGGTTTCGAATCCCCTTAGCTCCACCA  
>tdbD00004048 Symbiobacterium thermophilum IAM 14863 292459 Ala GGC  
-GGGGCTATAGCTCAGTT-GGG--AGAGCGCTTGAATGGCATTCAAGAG-----GTCAGGGGTTTCGACTCCCCTTAGCTCCACCA  
>tdbD00004049 Symbiobacterium thermophilum IAM 14863 292459 Ala GGC  
-GGGGCTGTAGCTCAGAT-GGG--AGAGCGCTTGAATGGCATTCAAGAG-----GTCAGGGGTTTCGATTCCCCTTAGCTCCACCA  
>tdbD00004051 Symbiobacterium thermophilum IAM 14863 292459 Ala TGC  
-GGGGCTGTAGCTCAGCT-GGG--AGAGCGCGCCTTGCACGCAGGAG-----GTCGAGGGTTTCGAGTCCCCTTAGCTCCACCA  
>tdbD00003918 Thermoanaerobacter tengcongensis MB4 273068 Ala GGC  
-GGGGCTGTAGCTCAGTT-GGG--AGAGCGCCACAATGGCATTGTGGAG-----GCCGTGGGTTCAAGTCCCATCAGCTCCACCA  
>tdbD00003919 Thermoanaerobacter tengcongensis MB4 273068 Ala TGC  
-GGGACGTAGCTCAGTT-GGG--AGAGCACCTGCCTTGCACGCAGGGG-----GTCGGGAGTTTCGAATCTCCTCGTCTCCACCA  
>tdbD00003920 Thermoanaerobacter tengcongensis MB4 273068 Ala TGC  
-GGGGGTGTAGCTCAGTT-GGG--AGAGCACCTGCCTTGCACGCAGGGG-----GTCAGGAGTTTCGAATCTCCTCATCTCCACCA  
>tdbD00003748 Thermotoga maritima MSB8 243274 Ala CGC  
-GGGGCGTAGCTCAGCT-GGG--AGAGCGCTACCTTCGCACGGTAGAG-----GTCGTTGGTTCAAGTCCCATCGGCTCCACCA  
>tdbD00003749 Thermotoga maritima MSB8 243274 Ala GGC  
-GGGGCGTAGCTCAGCT-GGG--AGAGCGCTACCTTCGCACGGTAGAG-----GTCGTTGGTTCAAGTCCCATCGGCTCCACCA  
>tdbD00003750 Thermotoga maritima MSB8 243274 Ala TGC  
-GGGACGTAGCTCAGCT-GGG--AGAGCGCCTGCTTTGCAAGCAGGAG-----GTCAGGGGTTTCGAATCCCCTCGTCTCCACCA



>tdbD00004072 *Thermus\_thermophilus*\_HB27\_262724 Ala CGC  
-GGGGCCGTGGCGCAGTT-GGG--AGCGCGCCTGAATCGCACTCAGGAG-----GTCAGGGGTTTCAATCCCCTCGGCTCCACCA  
>tdbD00004071 *Thermus\_thermophilus*\_HB27\_262724 Ala GGC  
TGGGGCCGTGGCGCAGTT-GGG--AGCGCGCCTCAATGGCATGAGGAG-----GTCAGGGGTTTCAATCCCCTCGGCTCCACCA  
>tdbD00003705 *Vibrio\_cholerae*\_O1\_biovar\_El\_Tor\_str.\_N16961\_243277 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCTGCGGTTTCGATCCCGCATAGCTCCACCA  
>tdbD00003707 *Vibrio\_cholerae*\_O1\_biovar\_El\_Tor\_str.\_N16961\_243277 Ala TGC  
-GGGGTTATAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCTGCGGTTTCGATCCCGCATAACTCCACCA  
>tdbD00003925 *Xanthomonas\_axonopodis*\_pv.\_citri\_str.\_306\_190486 Ala CGC  
-GGGGCGGTAGCTCAGCT-GGG--AGAGCGTCGCGTTTCGCATCGCGAAG-----GTCGAGGGTTTCGATCCCCTTCCGCTCCACCA  
>tdbD00003924 *Xanthomonas\_axonopodis*\_pv.\_citri\_str.\_306\_190486 Ala GGC  
-GGGGCCATAGCTCAGCT-GGG--AGAGCGCCTGCATGGCATGCAGGAG-----GTCGCGGTTTCGATCCCGCCTGGCTCCACCA  
>tdbD00003926 *Xanthomonas\_axonopodis*\_pv.\_citri\_str.\_306\_190486 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCGTGCGTTTCGATCCCGACAGGCTCCACCA

**Bacteria - siblings**

>tdbD00011134 *Escherichia coli* CFT073 199310 Val GAC  
-GCGTTCATAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCAATTGAACGCACCA  
>tdbD00011135 *Escherichia coli* CFT073 199310 Val GAC  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCACTCGGACGCACCA  
>tdbD00011133 *Escherichia coli* CFT073 199310 Val TAC  
-GGGTGATTAGCTCAGCT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GTCGGCGGTTTCGATCCCCTCATCACCACCA  
>tdbD00010859 *Escherichia coli* K12 83333 Val GAC  
-GCGTTCATAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCAATTGAACGCACCA  
>tdbD00010860 *Escherichia coli* K12 83333 Val GAC  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCACTCGGACGCACCA  
>tdbD00010861 *Escherichia coli* K12 83333 Val TAC  
-GGGTGATTAGCTCAGCT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GTCGGCGGTTTCGATCCCCTCATCACCACCA  
>tdbD00010862 *Escherichia coli* O157H7 83334 Val GAC:  
-GCGTTCATAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCAATTGAACGCACCA  
>tdbD00010863 *Escherichia coli* O157H7 83334 Val GAC:  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCACTCGGACGCACCA  
>tdbD00010865 *Escherichia coli* O157H7 83334 Val TAC:  
-GGGTGATTAGCTCAGCT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GTCGGCGGTTTCGATCCCCTCATCACCACCA  
>tdbD00010866 *Escherichia coli* O157H7 EDL933 155864 Val GAC:  
-GCGTTCATAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCAATTGAACGCACCA  
>tdbD00010867 *Escherichia coli* O157H7 EDL933 155864 Val GAC:  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCACTCGGACGCACCA  
>tdbD00010868 *Escherichia coli* O157H7 EDL933 155864 Val TAC:  
-GGGTGATTAGCTCAGCT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GGCGGCGGTTTCGATCCCCTCATCACCACCA  
>tdbD00010869 *Escherichia coli* O157H7 EDL933 155864 Val TAC:  
-GGGTGATTAGCTCAGCT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GTCGGCGGTTTCGATCCCCTCATCACCACCA  
>tdbD00010848 *Neisseria meningitidis* Z2491 122587 Val TAC  
-GGGTGATTAGCTCAGTT-GGT--AGAGCGTCTGCCTTACAAGCAGAAT-----GTCGGCGGTTTCGACTCCGTCATCACCACCA  
>tdbD00011174 *Photobacterium luminescens* subsp. *laumondii* T101 243265 Val GAC  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCACTCGGACGCACCA  
>tdbD00010942 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. CT18 220341 Val GAC  
-GCGTTCATAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCAATTGAACGCACCA  
>tdbD00010945 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. CT18 220341 Val TAC  
-GGGTGATTAGCTCAGCT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GTCGGCGGTTTCGATCCCCTCATCACCACCA  
>tdbD00011144 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. Ty2 209261 Val GAC  
-GCGTCTGTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGATGGTTCGAGTCCATTCAGACGCACCA  
>tdbD00011145 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. Ty2 209261 Val GAC  
-GCGTTCATAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCAATTGAACGCACCA  
>tdbD00011143 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. Ty2 209261 Val TAC  
-GGGTGATTAGCTCAGCT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GTCGGCGGTTTCGATCCCCTCATCACCACCA  
>tdbD00010931 *Salmonella typhimurium* LT2 99287 Val TAC  
-GGGTGATTAGCTCAGCT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GTCGGCGGTTTCGATCCCCTCATCACCACCA  
>tdbD00010932 *Salmonella typhimurium* LT2 99287 Val TAC  
-GGGTGATTAGCTCAGCT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GTCGGCGGTTTCGATCCCCTCATCACCACCA  
>tdbD00011095 *Shigella flexneri* 2a str. 301 198214 Val TAC  
-GGGTGATTAGCTCAGCT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GTCGGCGGTTTCGATCCCCTCATCACCACCA  
>tdbD00010850 *Vibrio cholerae* O1 biovar *El Tor* str. N16961 243277 Val GAC  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCACTCGGACGCACCA  
>tdbD00011058 *Xanthomonas campestris* pv. *campestris* str. ATCC 33913 190485 Val TAC  
-GGGTGCTTAGCTCAGC--GGT--AGAGCGTCTCCCTTACACGGAGAGG-----GTCGGGGGTTTCGAAACCCTCAGCACCACCA  
>tdbD00010902 *Xylella fastidiosa* 9a5c 160492 Val GAC  
-GCGTTCATAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCAATTGAACGCACCA  
>tdbD00010903 *Xylella fastidiosa* 9a5c 160492 Val GAC  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGTTGGTTCGAGTCCACTCGGACGCACCA  
>tdbD00010904 *Xylella fastidiosa* 9a5c 160492 Val TAC  
-GGGTGATTAGCTCAGCT-GGG--AGAGCACCTCCCTTACAAGGAGGGG-----GTCGGCGGTTTCGATCCCCTCATCACCACCA  
>tdbD00010928 *Yersinia pestis* CO92 214092 Val GAC  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGATGGTTCGAGTCCATTTCGGACGCACCA  
>tdbD00010929 *Yersinia pestis* CO92 214092 Val GAC  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGATGGTTCGAGTCCATTTCGGACGCACCA  
>tdbD00011068 *Yersinia pestis* KIM 187410 Val GAC  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGATGGTTCGAGTCCATTTCGGACGCACCA  
>tdbD00011069 *Yersinia pestis* KIM 187410 Val GAC  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGATGGTTCGAGTCCATTTCGGACGCACCA  
>tdbD00011200 *Yersinia pseudotuberculosis* IP 32953 273123 Val GAC  
-GCGTCCGTAGCTCAGTT-GGTT-AGAGCACCACCTTGACATGGTGGGG-----GTCGATGGTTCGAGTCCATTTCGGACGCACCA  
>tdbD00006009 *Bacillus anthracis* str. Sterne 260799 Ile GAT  
-GGGCCTATAGCTCAGCT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTTAGGCCACCA  
>tdbD00006025 *Bacillus cereus* ATCC 10987 222523 Ile GAT  
-GGGCCTATAGCTCAGCT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTTAGGCCACCA  
>tdbD00006026 *Bacillus cereus* ATCC 10987 222523 Ile GAT  
-GGGCCTATAGCTCAGCT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTTAGGCCACCA  
>tdbD00005988 *Bacillus cereus* ATCC 14579 226900 Ile GAT

-GGGCCTATAGCTCAGCT-GGTT-AGAGCGCACGCCTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTTAGGCCACCA  
>tdbD00001154 Bacillus subtilis 1423 Ile GAT  
-GGGCCTGTAGCTCAGCT-GGTT-AGAGCGCACGCCTGATAAGCGTGAG-----GTCGGTGGTTCGAGTCCACTCAGGCCACCA  
>tdbD00005845 Bacillus subtilis subsp. subtilis str. 168 224308 Ile GAT  
-GGGCCTGTAGCTCAGCT-GGTT-AGAGCGCACGCCTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTCAGGCCACCA  
>tdbD00005846 Bacillus subtilis subsp. subtilis str. 168 224308 Ile GAT  
-GGGCCTGTAGCTCAGCT-GGTT-AGAGCGCACGCCTGATAAGCGTGAG-----GTCGGTGGTTCGAGTCCACTCAGGCCACCA  
>tdbD00006035 Bacillus thuringiensis serovar konkukian\_str. 97-27 281309 Ile GAT  
-GGGCCTATAGCTCAGCT-GGTT-AGAGCGCACGCCTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTTAGGCCACCA  
>tdbD00001125 Bartonella elizabethae 807 Ile GAT  
-GGGCTTGTAGCTCAGTT-GGTT-AGAGCGCGCCTTGATAAGCGTGAG-----GTCGGAGGTTCAAGTCTCCAGGCCACCA  
>tdbD00006001 Bartonella henselae\_str. Houston-1 283166 Ile GAT  
-GGGCTTGTAGCTCAGTT-GGTT-AGAGCGCGCCTTGATAAGCGTGAG-----GTCGGAGGTTCAAGTCTCCAGGCCACCA  
>tdbD00006038 Bartonella quintana\_str. Toulouse 283165 Ile GAT  
-GGGCTTGTAGCTCAGCT-GGTT-AGAGCGCGCCTTGATAAGCGTGAG-----GTCGGAGGTTCAAGTCTCCAGGCCACCA  
>tdbD00001181 Brucella melitensis 29459 Ile GAT  
-GGGCTTGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCTCCAGGCCACCA  
>tdbD00005858 Brucella melitensis\_16M 224914 Ile GAT  
-GGGCTTGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCTCCAGGCCACCA  
>tdbD00005886 Brucella melitensis\_16M 224914 Ile GAT  
-GGGCTTGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCTCCAGGCCACCA  
>tdbD00001180 Brucella suis 29461 Ile GAT  
-GGGCTTGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCTCCAGGCCACCA  
>tdbD00005963 Brucella suis\_1330 204722 Ile GAT  
-GGGCTTGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCTCCAGGCCACCA  
>tdbD00005865 Campylobacter jejuni\_subsp. jejuni\_NCTC\_11168 192222 Ile GAT  
-GGGCCTATAGCTCAGCT-GGTT-AGAGTGCACCCCTGATAAGGGTGAG-----GTCACAAGTTCAGTCTTGTTAGGCCACCA  
>tdbD00005990 Escherichia coli\_CFT073 199310 Ile GAT  
-AGGCTTGTAGCTCAGGT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCAGTCCACTCAGGCCTACCA  
>tdbD00005858 Escherichia coli\_K12 83333 Ile GAT  
-AGGCTTGTAGCTCAGGT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCAGTCCACTCAGGCCTACCA  
>tdbD00005859 Escherichia coli\_O157H7 83334 Ile GAT:  
-AGGCTTGTAGCTCAGGT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCAGTCCACTCAGGCCTACCA  
>tdbD00005860 Escherichia coli\_O157H7\_EDL933 155864 Ile GAT:  
-AGGCTTGTAGCTCAGGT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCAGTCCACTCAGGCCTACCA  
>tdbD00001135 Gluconacetobacter hansenii 436 Ile GAT  
-GGGCTAGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCTCCCTGGGCCACCA  
>tdbD00001138 Gluconacetobacter liquefaciens 89584 Ile GAT  
-GGGCTAGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCTCCCTGGGCCACCA  
>tdbD00001149 Gluconobacter oxydans 442 Ile GAT  
-GGGCTAGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCTCCCTGGGCCACCA  
>tdbD00005861 Helicobacter pylori\_26695 85962 Ile GAT  
-GGGCTTATAGCTCAGGT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGAGGTTCAACTCCTCCTAAGGCCACCA  
>tdbD00005862 Helicobacter pylori\_J99 85963 Ile GAT  
-GGGCTTATAGCTCAGGT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGAGGTTCAACTCCTCCTAAGGCCACCA  
>tdbD00005977 Lactobacillus plantarum\_WCF51 220668 Ile GAT  
-GGGCCTATAGCTCAGCT-GGTTTAGAGCGCACGCCTGATAAGCGTGAG-----GTCGATGGTTCAGTCCATTTAGGCCCA---  
>tdbD00005877 Listeria innocua\_Clip11262 272626 Ile GAT  
-GGGCCTATAGCTCAGCT-GGTT-AGAGCGCACGCCTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTTAGGCCCA---  
>tdbD00005878 Listeria monocytogenes\_EGD-e 169963 Ile GAT  
-GGGCCTATAGCTCAGCT-GGTT-AGAGCGCACGCCTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTTAGGCCCA---  
>tdbD00006028 Listeria monocytogenes\_str. 4b\_F2365 265669 Ile GAT  
-GGGCCTATAGCTCAGCT-GGTT-AGAGCGCACGCCTGATAAGCGTGAG-----GTCGATGGTTCGAGTCCATTTAGGCCCA---  
>tdbD00005888 Mesorhizobium loti\_MAFF303099 266835 Ile GAT  
-GGGCTTGTAGCTCAGTT-GGTT-AGAGCGCGCCTTGATAAGCGTGAG-----GTCGGAGGTTCAAGTCTCCAGGCCACCA  
>tdbD00001134 Mycoplasma mycoides 2102 Ile CAT  
-GGACCTTATAGCTCAGTT-GGTT-AGAGCATCCGGCTCATAACCGGACG-----GTCATTTGGTTCAGTCCAATAAGGTCCACCA  
>tdbD00005966 Oceanobacillus\_ihayensis\_HTE831 221109 Ile GAT  
-GGGCCTGTAGCTCAGCT-GGTT-AGAGCGCACGCCTGATAAGCGTGAG-----GTCGGTGGTTCGAGTCCACTCAGGCCACCA  
>tdbD00001185 Ochrobactrum anthropi 529 Ile GAT  
-GGGCTTGTAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGGG-----GTCGGAGGTTCAAGTCTCCAGGCCACCA  
>tdbD00006006 Photorhabdus luminescens\_subsp. laumondii\_TTO1 243265 Ile GAT  
-AGGCTTGTAGCTCAGGT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCAGTCCACTCAGGCCTACCA  
>tdbD00001168 Phytoplasma\_sp. 2155 Ile GAT  
-GGGCCTATAGCTCAGTT-GGTT-AGAGCACACGCTTGATAAGCGTGAG-----GTCGGTGGTTCAGTCCATTTAGGCCACCA  
>tdbD00001170 Prevotella ruminicola 839 Ile GAT  
-AGGCTTGTAGCTCAGGT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCAGTCCACTCAGGCCTACCA  
>tdbD00006007 Rhodopseudomonas palustris\_CGA009 258594 Ile GAT  
-GGGCTTGTAGCTCAGTT-GGTT-AGAGCGCGCCTTGATAAGCGTGAG-----GTCGGAAGTTCAGTCTCCAGGCCACCA  
>tdbD00005897 Salmonella enterica\_subsp. enterica\_serovar\_Typhi\_str. CT18 220341 Ile GAT  
-AGGCTTGTAGCTCAGGT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCAGTCCACTCAGGCCTACCA  
>tdbD00005992 Salmonella enterica\_subsp. enterica\_serovar\_Typhi\_str. Ty2 209261 Ile GAT  
-AGGCTTGTAGCTCAGGT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCAGTCCACTCAGGCCTACCA  
>tdbD00001190 Salmonella enteritidis 592 Ile GAT  
-AGGCTTGTAGCTCAGGT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCGGTGGTTCAGTCCACTCAGGCCTACCA

>tdbD00005890 Salmonella\_typhimurium\_LT2\_99287\_Ile\_GAT  
-AGGCTGTAGCTCAGGT-GGTT-AGAGCGACCCCTGATAAGGGTGAG-----GTCGGTGGTTCAAGTCCACTCAGGCCTACCA  
>tdbD00005969 Shigella\_flexneri\_2a\_str.\_301\_198214\_Ile\_GAT  
-AGGCTGTAGCTCAGGT-GGTT-AGAGCGACCCCTGATAAGGGTGAG-----GTCGGTGGTTCAAGTCCACTCAGGCCTACCA  
>tdbD00005950 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620\_Ile\_GAT  
-GGGCCTATAGCTCAGCT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGTGGTTTCGAGTCCACTTAGGCCACCA  
>tdbD00005854 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879\_Ile\_GAT  
-GGGCCTATAGCTCAGCT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGTGGTTTCGAGTCCACTTAGGCCACCA  
>tdbD00005980 Staphylococcus\_epidermidis\_ATCC\_12228\_176280\_Ile\_GAT  
-GGGCCTATAGCTCAGCT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGTGGTTTCGAGTCCACTTAGGCCACCA  
>tdbD00005951 Streptococcus\_agalactiae\_NEM316\_211110\_Ile\_GAT  
-GGGCGGTAGCTCAGGT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGTGGTTTCGAGTCCACTCGTGCCCA---  
>tdbD00005883 Streptococcus\_pneumoniae\_TIGR4\_170187\_Ile\_GAT  
-GGGCGGTAGCTCAGGT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGTGGTTTCGAGTCCACTCGTGCCCA---  
>tdbD00005881 Streptococcus\_pyogenes\_M1\_GAS\_160490\_Ile\_GAT  
-GGGCGGTAGCTCAGGT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGTGGTTTCGAGTCCACTCGTGCCCA---  
>tdbD00005952 Streptococcus\_pyogenes\_MGAS315\_198466\_Ile\_GAT  
-GGGCGGTAGCTCAGGT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGTGGTTTCGAGTCCACTCGTGCCCA---  
>tdbD00005986 Streptococcus\_pyogenes\_SSI-1\_193567\_Ile\_GAT  
-GGGCGGTAGCTCAGGT-GGTT-AGAGCGCAGCCTGATAAGCGTGAG-----GTCGGTGGTTTCGAGTCCACTCGTGCCCA---  
>tdbD00005873 Synechocystis\_sp.\_PCC\_6803\_1148\_Ile\_GAT  
-GGCTATTAGCTCAGGT-GGTT-AGAGCGACCCCTGATAAGGGTGAG-----GTCTCTGGTTCAAGTCCAGAAATGGCCCA---  
>tdbD00005953 Thermosynechococcus\_elongatus\_BP-1\_197221\_Ile\_GAT  
-GGCTATTAGCTCAGGT-GGTT-AGAGCGACCCCTGATAAGGGTGAG-----GTCCCTGGTTTCGAGTCCAGGATGGCCCA---  
>tdbD00007117 Bacillus\_anthraxis\_str.\_Sterne\_260799\_Leu\_CAA  
-GCCGATGTGGCGGAATT-GGCA-GACGCGCAGACTCAAAATCGTGTTC-----TTCG-----GGAGTGTGGTTTCGACCCCGACCATCGGTA---  
>tdbD00007116 Bacillus\_anthraxis\_str.\_Sterne\_260799\_Leu\_GAG  
-GCGGTGTGGCGGAAC--GGCA-GACGCGCTAGGTTGAGGGCCTAGTGGGGG---AAA---CCCCG-TGGAGGTTCAAGTCTCTCGGCCGA---  
>tdbD00007119 Bacillus\_anthraxis\_str.\_Sterne\_260799\_Leu\_TAA  
-GCCGGGTGGCGGAACA-GGCA-GACGCACAGGACTTAAAATCCTGCGGTGG---GTGA---CCACCGTGGGGTTTCGACCCCGCCCTCGGCACCA  
>tdbD00007118 Bacillus\_anthraxis\_str.\_Sterne\_260799\_Leu\_TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCACTAGACTTAGGATCTAGCGCC-----TTT-----GGCGTGGGGTTTCGACTCCCTTCACCCGCA---  
>tdbD00007120 Bacillus\_anthraxis\_str.\_Sterne\_260799\_Leu\_TAG  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGACTTAGGATCTGCGCC-----TTT-----GGCGTGGGGTTTCGACTCCCTTCACCCGCA---  
>tdbD00007171 Bacillus\_cereus\_ATCC\_10987\_222523\_Leu\_CAA  
-GCCGATGTGGCGGAATT-GGCA-GACGCGCAGACTCAAAATCGTGTTC-----TTCG-----GGAGTGTGGTTTCGACCCCGACCATCGGTA---  
>tdbD00007170 Bacillus\_cereus\_ATCC\_10987\_222523\_Leu\_GAG  
-GCGGTGTGGCGGAAC--GGCA-GACGCGCTAGGTTGAGGGCCTAGTGGGGG---AAA---CCCCG-TGGAGGTTCAAGTCTCTCGGCCGA---  
>tdbD00007173 Bacillus\_cereus\_ATCC\_10987\_222523\_Leu\_TAA  
-GCCGGGTGGCGGAACA-GGCA-GACGCACAGGACTTAAAATCCTGCGGTGG---GTGA---CCACCGTGGGGTTTCGACCCCGCCCTCGGCACCA  
>tdbD00007174 Bacillus\_cereus\_ATCC\_10987\_222523\_Leu\_TAA  
-GCCGGGTGGCGGAACA-GGCA-GACGCACAGGACTTAAAATCCTGCGGTGG---GTGA---CCACCGTGGGGTTTCGACCCCGCCCTCGGCACCA  
>tdbD00007172 Bacillus\_cereus\_ATCC\_10987\_222523\_Leu\_TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCACTAGACTTAGGATCTAGCGCC-----TTT-----GGCGTGGGGTTTCGACTCCCTTCACCCGCA---  
>tdbD00007175 Bacillus\_cereus\_ATCC\_10987\_222523\_Leu\_TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCACAGACTTAGGATCTGCGCC-----TTT-----GGCGTGGGGTTTCGACTCCCTTCACCCGCA---  
>tdbD00007018 Bacillus\_cereus\_ATCC\_14579\_226900\_Leu\_CAA  
-GCCGATGTGGCGGAATT-GGCA-GACGCGCAGACTCAAAATCGTGTTC-----TTCG-----GGAGTGTGGTTTCGACCCCGACCATCGGTA---  
>tdbD00007017 Bacillus\_cereus\_ATCC\_14579\_226900\_Leu\_GAG  
-GCGGTGTGGCGGAAC--GGCA-GACGCGCTAGGTTGAGGGCCTAGTGGGGG---AAA---CCCCG-TGGAGGTTCAAGTCTCTCGGCCGA---  
>tdbD00007016 Bacillus\_cereus\_ATCC\_14579\_226900\_Leu\_TAA  
-GCCGGGTGGCGGAACA-GGCA-GACGCACAGGACTTAAAATCCTGCGGTGG---GTGA---CCACCGTGGGGTTTCGACCCCGCCCTCGGCACCA  
>tdbD00007015 Bacillus\_cereus\_ATCC\_14579\_226900\_Leu\_TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCACTAGACTTAGGATCTAGCGCC-----TTT-----GGCGTGGGGTTTCGACTCCCTTCACCCGCA---  
>tdbD00007019 Bacillus\_cereus\_ATCC\_14579\_226900\_Leu\_TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCACAGACTTAGGATCTGCGCC-----TTT-----GGCGTGGGGTTTCGACTCCCTTCACCCGCA---  
>tdbD00001529 Bacillus\_subtilis\_1423\_Leu\_TAA  
-GCCGGGTGGTGAATT-GGCA-GACACACAGGACTTAAAATCCTGCGGTAG---GTGA---CTACCGTGCCGGTTCAAGTCCGGCCCTCGGCACCA  
>tdbD00006448 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308\_Leu\_CAG  
-GCGGATGTGGCGGAATT-GGCA-GACGCGCTAGAATCAGGCTCTAGTGTCT-----TTAC---AGACGTGGGGTTCAAGTCCCTTCATCCGACCA  
>tdbD00006450 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308\_Leu\_TAA  
-GCCGGGTGGTGAATT-GGCA-GACACACAGGACTTAAAATCCTGCGGTAG---GTGA---CTACCGTGCCGGTTCAAGTCCGGCCCTCGGCACCA  
>tdbD00006451 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308\_Leu\_TAA  
-GCCGGGTGGTGAATT-GGCA-GACACACAGGACTTAAAATCCTGCGGTAG---GTGA---CTACCGTGCCGGTTCAAGTCCGGCCCTCGGCACCA  
>tdbD00006452 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308\_Leu\_TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCGCTAGACTTAGGATCTAGTGTCT-----TTA---TGACGTGGGGTTCAAGTCCCTTCACCCGCA---  
>tdbD00007214 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27\_281309\_Leu\_CAA  
-GCCGATGTGGCGGAATT-GGCA-GACGCGCAGACTCAAAATCGTGTTC-----TTCG-----GGAGTGTGGTTTCGACCCCGACCATCGGTACCA  
>tdbD00007216 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27\_281309\_Leu\_TAA  
-GCCGGGTGGCGGAACA-GGCA-GACGCACAGGACTTAAAATCCTGCGGTGG---GTGA---CCACCGTGGGGTTTCGACCCCGCCCTCGGCACCA  
>tdbD00007217 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27\_281309\_Leu\_TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCACTAGACTTAGGATCTAGCGCC-----TTT-----GGCGTGGGGTTTCGACTCCCTTCACCCGCA---  
>tdbD00007218 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27\_281309\_Leu\_TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCACAGACTTAGGATCTGCGCC-----TTT-----GGCGTGGGGTTTCGACTCCCTTCACCCGCA---  
>tdbD00007224 Bartonella\_quintana\_str.\_Toulouse\_283165\_Leu\_CAA

-GCGGGTGTGGTGGAACT-GGTA-GACGCGCCAGACTCAAAATCTGGTTCC-----GAGA-----GGAGTGTGCGGTTTCGAGTCCGACCACCCGCACCA  
>tdbD00006525 Borrelia\_burgdorferi\_B31\_224326\_Leu\_CAA  
-GCGGTATGGCGGAATT-GGTA-GACGCGCCAGACTCAAAATCTGGTGAGG----GCAA-----CTTCATGTGCGGTTTCGACTCCGACTACCGGTA---  
>tdbD00006526 Borrelia\_burgdorferi\_B31\_224326\_Leu\_GAG  
-GCTGTGGTGGTGGAACT-GGTA-GACACGCTAGCTTGAGGGGCTAGTGGGC----GCAA-----GCCCGTGTGCGGTTCAAGTCCAGTTCACAGCA---  
>tdbD00006527 Borrelia\_burgdorferi\_B31\_224326\_Leu\_TAA  
-GCCGAAGTGGTGGAACT-GGTA-GACACACAGGACTTAAATCTGAGGAG----GAAG-----CTCG-TACCGGTTCAAGTCCGGTCTTCGGTA---  
>tdbD00006528 Borrelia\_burgdorferi\_B31\_224326\_Leu\_TAG  
-CCAGGAGTGGTGGAACT-GGCA-GACACGCTAGACTTAGGATCTAGTGCC-----TTT-----GGCGTGTGGGTTTCGACTCCCACCTTCTGTA---  
>tdbD00006624 Brucella\_melitensis\_16M\_224914\_Leu\_TAG  
-GCGGATGTGGCGAAATT-GGTA-GACGCACCAGATTTAGGTTCTGGCGGG-----AGA-----CCG-TGGGGGTTTCGAGTCCCTCCATCCGCACCA  
>tdbD00006910 Brucella\_suis\_1330\_204722\_Leu\_CAA  
-GCGGGTGTGGTGGAACT-GGTA-GACGCGCCGACTCAAAATCCGGTTCC-----GAAA-----GGAGTGTGCGGTTTCGATTCCGACCACCCGCACCA  
>tdbD00006908 Brucella\_suis\_1330\_204722\_Leu\_CAG  
-GCCAGATGGCGGAATT-GGTA-GACGCACCAGCTTCAGGTGCTGGCGCTC----GCAA-----GGCGTGGAGGTTTCGAGTCCCTCTTCTGGGCACCA  
>tdbD00006911 Brucella\_suis\_1330\_204722\_Leu\_TAA  
-GCGGTCGTGGCGAAATT-GGTA-TACGCAACGGACTTAAATCCGTCGTCT----TTA-----AGACTTGGCGGTTTCGAGTCCCGCCGACCGCACCA  
>tdbD00006909 Brucella\_suis\_1330\_204722\_Leu\_TAG  
-GCGGATGTGGCGAAATT-GGTA-GACGCACCAGATTTAGGTTCTGGCGGG-----AGA-----CCG-TGGGGGTTTCGAGTCCCTCCATCCGCACCA  
>tdbD00006535 Caulobacter\_crescentus\_CB15\_190650\_Leu\_GAG  
-GCGGTCGTGGCGGAATT-GGTA-GACGCGCAGCGTTGAGGTGCTGTGGGG-----CAA-----CCCG-TGGAAGTTCGAGTCTTCTCGACCGCACCA  
>tdbD00006437 Chlamydia\_trachomatis\_D/UW-3/CX\_272561\_Leu\_CAA  
-GCCGCGTGGCGGAAT--GGTA-GACGCGGTAGACTCAAAATCTACTCTTA----GCAG-----TAAGGTGTGGTTCGAGTCCAATCGCCGGCA---  
>tdbD00006438 Chlamydia\_trachomatis\_D/UW-3/CX\_272561\_Leu\_CAG  
-GCAGTATGGCGGAACC-GGTA-GACGCGCTAGATTCAGGTTCTAGTGAGC----TTTT-----GTCATGGAAGTTCGAGTCTTCTTAGCTGCA---  
>tdbD00006439 Chlamydia\_trachomatis\_D/UW-3/CX\_272561\_Leu\_GAG  
-GCGGAAGTGGCGGAATT-GGTA-TACGCGCTATCTTGAGGTGGTAGTGA-----GCTT-----TCCTTAGGGGTTTCGAGTCCCTCTTTTCGCA---  
>tdbD00006440 Chlamydia\_trachomatis\_D/UW-3/CX\_272561\_Leu\_TAA  
-GCTCAGATGGTGGAAAT--GGTA-GACACTAGGACTTAAATCCCTTGGGC-----TTTG-----GCCCGTGCAAGTTCGAGTCTTGTCTGAGCA---  
>tdbD00006429 Chlamydomytila\_pneumoniae\_AR39\_115711\_Leu\_GAG  
-GCGGAAGTGGCGGAATT-GGTA-TACGCGCTATCTTGAGGTGGTAGTGA-----GCTT-----TCCTTAGGGGTTTCGAGTCCCTCTTTTCGCA---  
>tdbD00006432 Chlamydomytila\_pneumoniae\_CWL029\_115713\_Leu\_CAA  
-GCCGTCGTGGCGGAAT--GGTA-GACGCGGTAGACTCAAAATCTACTCTTA----GCAA-----TAAGGTGTGGTTCGAGTCCGATCACCGGCA---  
>tdbD00006433 Chlamydomytila\_pneumoniae\_CWL029\_115713\_Leu\_CAG  
-GCAGTATGGCGGAATC-GGTA-GACGCGCTAGATTCAGGTTCTAGTGAGC----TTAT-----GTCATGGAAGTTCGAGTCTTCTTAGCTGCA---  
>tdbD00006434 Chlamydomytila\_pneumoniae\_CWL029\_115713\_Leu\_GAG  
-GCGGAAGTGGCGGAATT-GGTA-TACGCGCTATCTTGAGGTGGTAGTGA-----GCTT-----TCCTTAGGGGTTTCGAGTCCCTCTTTTCGCA---  
>tdbD00006435 Chlamydomytila\_pneumoniae\_CWL029\_115713\_Leu\_TAA  
-GCTCAGATGGTGGAAAT--GGTA-GACACTAGGACTTAAATCCCTTGGGC-----GTAG-----GCCCGTGCAAGTTCGAGTCTTGTCTGAGCA---  
>tdbD00006436 Chlamydomytila\_pneumoniae\_CWL029\_115713\_Leu\_TAG  
-GCCAGGTGGTGGAAAT--GGTA-GACACGCTGGATTTAGGATCCAGTGCT----TTTC-----GGCATGTAGGTTTCGAGTCCATCCTGGGCA---  
>tdbD00006492 Chlamydomytila\_pneumoniae\_J138\_138677\_Leu\_CAA  
-GCCGTCGTGGCGGAAT--GGTA-GACGCGGTAGACTCAAAATCTACTCTTA----GCAA-----TAAGGTGTGGTTCGAGTCCGATCACCGGCA---  
>tdbD00006493 Chlamydomytila\_pneumoniae\_J138\_138677\_Leu\_CAG  
-GCAGTATGGCGGAATC-GGTA-GACGCGCTAGATTCAGGTTCTAGTGAGC----TTAT-----GTCATGGAAGTTCGAGTCTTCTTAGCTGCA---  
>tdbD00006494 Chlamydomytila\_pneumoniae\_J138\_138677\_Leu\_GAG  
-GCGGAAGTGGCGGAATT-GGTA-TACGCGCTATCTTGAGGTGGTAGTGA-----GCTT-----TCCTTAGGGGTTTCGAGTCCCTCTTTTCGCA---  
>tdbD00006495 Chlamydomytila\_pneumoniae\_J138\_138677\_Leu\_TAA  
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>tdbD00006496 Chlamydomytila\_pneumoniae\_J138\_138677\_Leu\_TAG  
-GCCAGGTGGTGGAAAT--GGTA-GACACGCTGGATTTAGGATCCAGTGCT----TTTC-----GGCATGTAGGTTTCGAGTCCATCCTGGGCA---  
>tdbD00006597 Clostridium\_perfringens\_str.\_13\_195102\_Leu\_TAG  
-GCAGTGTGGCGGAATT-GGCA-GACGCACTAGACTTAGGATCTAGCGCC-----TAC-----GGCGTGGGGGTTTCGACTCCCTTCCACTGCACCA  
>tdbD00006848 Corynebacterium\_glutamicum\_ATCC\_13032\_196627\_Leu\_GAG  
-GCCCGGTGGCGGAAT--GGCA-GACGCGCTAGCTTGAGGTGCTAGTGCTTA---TTA---ACGGACGTGGGGGTTTCGAGTCCCGCCCGGGCA---  
>tdbD00007027 Escherichia\_coli\_CFT073\_199310\_Leu\_CAA  
-GCCGAAGTGGCGGAATC-GGTA-GACGCGCTGATTCAAAATCAACCGTA-----GAAA-----TACGTGCCGGTTCGAGTCCGGCCTTCGGCACCA  
>tdbD00007026 Escherichia\_coli\_CFT073\_199310\_Leu\_CAG  
-GCGAAGGTGGCGGAATT-GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTC-----TTAC-----GGAGTGGGGGTTTCGAGTCCCGCCCGGGCACCA  
>tdbD00007025 Escherichia\_coli\_CFT073\_199310\_Leu\_GAG  
-GCCGAGGTGGTGGAAATT-GGTA-GACACGCTACCTTGAGGTGGTAGTGCC-----AATA-----GGGCTTACGGGTTTCGAGTCCCGTCCCGGTACCA  
>tdbD00007024 Escherichia\_coli\_CFT073\_199310\_Leu\_TAA  
-GCCCGGATGGTGGAAATC-GGTA-GACACAAGGGATTTAAATCCCTCGGGC-----TTTC-----CGCTGTGCGGGTTTCGAGTCCCGTCCCGGTACCA  
>tdbD00007023 Escherichia\_coli\_CFT073\_199310\_Leu\_TAG  
-GCGGAGTGGCGGAATT-GGTA-GACGCACCAGATTTAGGTTCTGGCGCC-----GCAA-----GGTGTGCGAGTTTCGAGTCTCGCCTCCCGCACCA  
>tdbD00006497 Escherichia\_coli\_K12\_83333\_Leu\_CAA  
-GCCGAAGTGGCGGAATC-GGTA-GACGCGTGGATTCAAAATCAACCGTA-----GAAA-----TACGTGCCGGTTCGAGTCCCGCCTTCGGCACCA  
>tdbD00006498 Escherichia\_coli\_K12\_83333\_Leu\_CAG  
-GCGAAGGTGGCGGAATT-GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTC-----TTAC-----GGAGTGGGGGTTTCGAGTCCCGCCCGGGCACCA  
>tdbD00006499 Escherichia\_coli\_K12\_83333\_Leu\_GAG  
-GCGAAGGTGGCGGAATT-GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTC-----TTAC-----GGAGTGGGGGTTTCGAGTCCCGCCCGGGCACCA  
>tdbD00006500 Escherichia\_coli\_K12\_83333\_Leu\_GAG  
-GCCGAGGTGGTGGAAATT-GGTA-GACACGCTACCTTGAGGTGGTAGTGCC-----AATA-----GGGCTTACGGGTTTCGAGTCCCGTCCCGGTACCA  
>tdbD00006501 Escherichia\_coli\_K12\_83333\_Leu\_TAA  
-GCCCGGATGGTGGAAATC-GGTA-GACACAAGGGATTTAAATCCCTCGGGC-----TTTC-----CGCTGTGCGGGTTTCGAGTCCCGTCCCGGTACCA

>tdbD00006502 Escherichia\_coli\_K12\_83333\_Leu\_TAG  
-GCGGAGTGGCGAAAATT-GGTA-GACGCACCAGATTAGGTTCTGGCGCC-----GCAA-----GGTGTGCGAGTTCAAGTCTCGCCTCCCGCACCA  
>tdbD00006503 Escherichia\_coli\_O157H7\_83334\_Leu\_CAA:  
-GCCGAAGTGGCGAAAATC-GGTA-GACGCAGTTGATTCAAAATCAACCGTA-----GAAA-----TACGTGCCGGTTCGAGTCCGGCCTTCGGCACCA  
>tdbD00006504 Escherichia\_coli\_O157H7\_83334\_Leu\_CAG:  
-GCCAAGGTGGCGGAATT-GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC-----TTAC-----GGACGTGGGGGTTCAAGTCCCCCCTCGCACCA  
>tdbD00006505 Escherichia\_coli\_O157H7\_83334\_Leu\_GAG:  
-GCCGAGGTGGTGAATT-GGTA-GACACGCTACCTTGAGGTGGTAGTGCCT-----AATA-----GGGCTTACGGGTTCAAGTCCCGTCTCGGTACCA  
>tdbD00006506 Escherichia\_coli\_O157H7\_83334\_Leu\_TAA:  
-GCCCAGGTGGTGAATT-GGTA-GACACAAGGGATTAAATCCCTCGGCC-----TTCG-----CGCTGTGCGGGTTCAAGTCCCGTCCGGGTACCA  
>tdbD00006507 Escherichia\_coli\_O157H7\_83334\_Leu\_TAG:  
-GCGGAGTGGCGAAAATT-GGTA-GACGCACCAGATTAGGTTCTGGCGCC-----GCAA-----GGTGTGCGAGTTCAAGTCTCGCCTCCCGCACCA  
>tdbD00006508 Escherichia\_coli\_O157H7\_EDL933\_155864\_Leu\_CAA:  
-GCCGAAGTGGCGAAAATC-GGTA-GACGCAGTTGATTCAAAATCAACCGTA-----GAAA-----TACGTGCCGGTTCGAGTCCGGCCTTCGGCACCA  
>tdbD00006509 Escherichia\_coli\_O157H7\_EDL933\_155864\_Leu\_CAG:  
-GCCAAGGTGGCGGAATT-GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC-----TTAC-----GGACGTGGGGGTTCAAGTCCCCCCTCGCACCA  
>tdbD00006510 Escherichia\_coli\_O157H7\_EDL933\_155864\_Leu\_GAG:  
-GCCGAGGTGGTGAATT-GGTA-GACACGCTACCTTGAGGTGGTAGTGCCT-----AATA-----GGGCTTACGGGTTCAAGTCCCGTCTCGGTACCA  
>tdbD00006511 Escherichia\_coli\_O157H7\_EDL933\_155864\_Leu\_TAA:  
-GCCCAGGTGGTGAATT-GGTA-GACACAAGGGATTAAATCCCTCGGCC-----TTCG-----CGCTGTGCGGGTTCAAGTCCCGTCCGGGTACCA  
>tdbD00006512 Escherichia\_coli\_O157H7\_EDL933\_155864\_Leu\_TAG:  
-GCGGAGTGGCGAAAATT-GGTA-GACGCACCAGATTAGGTTCTGGCGCC-----GCAA-----GGTGTGCGAGTTCAAGTCTCGCCTCCCGCACCA  
>tdbD00006521 Haemophilus\_influenzae\_Rd\_KW20\_71421\_Leu\_CAA  
-GCCTGGGTGGCGAAAATT-GGTA-GACGCAGCGGATTCAAAAATCCCGCGTTG-----AAT-----AAACGTGTGCGTTCGAGTCCGACCTTAGGCACCA  
>tdbD00006523 Haemophilus\_influenzae\_Rd\_KW20\_71421\_Leu\_TAA  
-GCCCAGGTGGTGAATT-GGTA-GACACAAGGGATTAAATCCCTCGGCC-----TTCG-----AGCGGTGCCAGTTCAAGTCTGGCTTCGGGCACCA  
>tdbD00006513 Helicobacter\_pylori\_26695\_85962\_Leu\_CAA  
-GCCGAAGTGGTGAATT-GGTA-GACACGCTAGACTCAAAAATCTGGTGGGA-----GCAA-----TCCCGTGTGCGTTCGAGTCCGACCTTCGGCACCA  
>tdbD00006514 Helicobacter\_pylori\_26695\_85962\_Leu\_GAG  
-GCCTGGTGGTGAATT-GGTA-GACACGCCATCTTGAGGGGGTGGTGGGA-----GCAA-----TCTCGTGGAGTTTCGAGTCTCGCCAGTGCACCA  
>tdbD00006515 Helicobacter\_pylori\_26695\_85962\_Leu\_TAA  
-GCCCAGGTGGTGAATT-GGTA-GACACAAGGGACTTAAATCCCTCGGTA-----GCAA-----TACCGTCCGGTTCGAGTCCGGCTTGGGCACCA  
>tdbD00006516 Helicobacter\_pylori\_26695\_85962\_Leu\_TAG  
-GCCGAAGTGGCGAAAATT-GGTA-GACGCCTAGACTTAGGATCTAGCGCC-----GCAA-----GGCATGAAGTTTCGATTCCTTTCTTCGGCACCA  
>tdbD00006517 Helicobacter\_pylori\_J99\_85963\_Leu\_CAA  
-GCCGAAGTGGTGAATT-GGTA-GACACGCTAGACTCAAAAATCTGGTGGGA-----GCAA-----TCCCGTGTGCGTTCGAGTCCGACCTTCGGCACCA  
>tdbD00006518 Helicobacter\_pylori\_J99\_85963\_Leu\_GAG  
-GCCTGGTGGTGAATT-GGTA-GACACGCCATCTTGAGGGGGTGGTGGGA-----GCAA-----TCTCGTGGAGTTTCGAGTCTCGCCAGTGCACCA  
>tdbD00006519 Helicobacter\_pylori\_J99\_85963\_Leu\_TAA  
-GCCCAGGTGGTGAATT-GGTA-GACACAAGGGACTTAAATCCCTCGGTA-----GCAA-----TACCGTCCGGTTCGAGTCCGGCTTGGGCACCA  
>tdbD00006520 Helicobacter\_pylori\_J99\_85963\_Leu\_TAG  
-GCCGAAGTGGCGAAAATT-GGTA-GACGCCTAGACTTAGGATCTAGCGCC-----GCAA-----GGCATGAAGTTTCGATTCCTTTCTTCGGCACCA  
>tdbD00006592 Listeria\_monocytogenes\_EGD-e\_169963\_Leu\_CAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCGCTGGACTCAAAAATCCTGTGCC-----GCAA-----GGCGGTGCCGGTTCGACCCCGCCGCGCGTA---  
>tdbD00006590 Listeria\_monocytogenes\_EGD-e\_169963\_Leu\_TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGGACTTAAATCCTGCGGATA-----GTGA---TATCCGTACCGGTTTCGATTCGGTCTTCGGCA---  
>tdbD00006589 Listeria\_monocytogenes\_EGD-e\_169963\_Leu\_TAG  
-GCGGGTGGCGGAATT-GGCA-GACGCACCAGATTAGGATCTGGCGCC-----GCGA-----GGCGTGGGGTTCAAGTCCCTTCACCCGCA---  
>tdbD00007185 Listeria\_monocytogenes\_str\_4b\_F2365\_265669\_Leu\_CAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCGCTGGACTCAAAAATCCTGTGCC-----GCAA-----GGCGGTGCCGGTTCGACCCCGCCGCGCGTA---  
>tdbD00007184 Listeria\_monocytogenes\_str\_4b\_F2365\_265669\_Leu\_GAG  
-GCGGTGTTGGCGGAATC-GGCA-GACGCGCTAGGTTGAGGGCCTAGTGGGGT---AAA---ACCG-TGGAGTTCAAGTCTCTCGGCCGCA---  
>tdbD00007183 Listeria\_monocytogenes\_str\_4b\_F2365\_265669\_Leu\_TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGGACTTAAATCCTGCGGATA-----GTGA---TATCCGTACCGGTTTCGATTCGGTCTTCGGCA---  
>tdbD00007182 Listeria\_monocytogenes\_str\_4b\_F2365\_265669\_Leu\_TAG  
-GCGGGTGGCGGAATT-GGCA-GACGCACCAGATTAGGATCTGGCGCC-----GCGA-----GGCGTGGGGTTCAAGTCCCTTCACCCGCA---  
>tdbD00006628 Mesorhizobium\_loti\_MAFF303099\_266835\_Leu\_GAG  
-GCGGTGTTGGCGGAATT-GGTA-GACGCGCAGCGTTGAGGTGCTGTGGGG-----CAA-----CCCG-TGGAAGTTTCGAGTCTCTCGACCGCACCA  
>tdbD00006485 Mycobacterium\_leprae\_TN\_272631\_Leu\_CAG  
-GGCGAGTGGCGGAAT--GGCA-GACGCGCTGGCTTCAGGTGCCAGTGTCC-----CTCG-----GGACGTGGGGGTTCAAGTCCCCCTTCGCCA---  
>tdbD00006487 Mycobacterium\_leprae\_TN\_272631\_Leu\_TAA  
-GCCCCATAGCCCAATT-GGCA-GAGGCAGCGGACTTAAATCCGTCA-----AGTGTGCGTTCGAGTCCGACTGGGGGCA---  
>tdbD00006457 Mycobacterium\_tuberculosis\_CDC1511\_83331\_Leu\_CAA  
-GCCCTCGTATCCCAACT-GGCA-GAGGAAACGGACTCAAAACCCGTCC-----AGTGTGGGTTTCGAATCCCACCGAGGGCACCA  
>tdbD00006458 Mycobacterium\_tuberculosis\_CDC1511\_83331\_Leu\_CAG  
-GGCGAGTGGCGGAAT--GGCA-GACGCGCTGGCTTCAGGTGCCAGTGTCC-----TTCG-----GGACGTGGGGGTTCAAGTCCCCCTTCGCCA---  
>tdbD00006459 Mycobacterium\_tuberculosis\_CDC1511\_83331\_Leu\_GAG  
-GTCCGAGTGGCGGAAT--GGCA-GACGCGCTAGCTTCAGGTGCTAGTGCCTA---CTAA---TGGGCG-TGGGGTTCAAGTCCCCCTTCGGACA---  
>tdbD00006460 Mycobacterium\_tuberculosis\_CDC1511\_83331\_Leu\_TAA  
-GCCCCATAGCCCAATT-GGCA-GAGGCAGCGGACTTAAATCCGTCA-----AGTGTGCGTTCGAGTCCGACTGGGGGCA---  
>tdbD00006461 Mycobacterium\_tuberculosis\_CDC1511\_83331\_Leu\_TAG  
-GCGGGCTGATGAAATT-GGCA-AACATGCCGGTTTTAGGTGCCGGTGTCT---GAAA---GAGTTTGGGGTTTCGAGTCCCTTCGCCGCA---  
>tdbD00007092 Mycobacterium\_tuberculosis\_H37Rv\_83332\_Leu\_CAA  
-GCCCTCGTATCCCAACT-GGCA-GAGGAAACGGACTCAAAACCCGTCC-----AGTGTGGGTTTCGAATCCCACCGAGGGCACCA  
>tdbD00007089 Mycobacterium\_tuberculosis\_H37Rv\_83332\_Leu\_CAG

-GGCGGAGTGGCGGAAT--GGCA-GACGCGCTGGCTTCAGGTGCCAGTGTCC----TTCG---GGACGTGGGGGTTCAAGTCCCCCTTCGCCCA---  
>tdbD00007093 Mycobacterium\_tuberculosis\_H37Rv\_83332\_Leu\_GAG  
-GTCCGAGTGGCGGAAT--GGCA-GACGCGCTAGCTTGAGGTGCTAGTGCCCTA---CTAA---TGGGCG-TGGGGGTTCAAGTCCCCCTCGGACA---  
>tdbD00007090 Mycobacterium\_tuberculosis\_H37Rv\_83332\_Leu\_TAA  
-GCCCCATAGCCCAATT-GGCA-GAGGCAGCGGACTTAAAATCCGTCA-----AGTGTGCGGTTTCAGTCCGACTGGGGGCA---  
>tdbD00007091 Mycobacterium\_tuberculosis\_H37Rv\_83332\_Leu\_TAG  
-GCGGGCGTGTGAAATT-GGCA-AACATGCCGGTTTTAGGTGCCGGTGTCT----GAAA---GAGTTTGGAGGTTTCAGTCCCTCCGCCGCA---  
>tdbD00006544 Mycoplasma\_genitalium\_G37\_243273\_Leu\_GAG  
-GTCGGAGTGGTGAAT--GGTA-GACACGCAAGCTTGAGGTGCTTGTGGTCG---TTAA---AGACTGTGCCAGTTCAAGTCTGGTCTCCGACACCA  
>tdbD00006545 Mycoplasma\_genitalium\_G37\_243273\_Leu\_TAA  
-GCCCAAGTGGCGGAAT--GGTA-GACGCATGGGATTTAAGATCCCACGCCA----GTAA---TGGTGTGCCGGTTCAAGTCCGGCTTTGGGCACCA  
>tdbD00006546 Mycoplasma\_genitalium\_G37\_243273\_Leu\_TAG  
-GCACTCGTGGCGGAAT--GGTA-GACGCGCTAGACTTAGGATCTAGTTTCA----TCT----AGAAGTGGGGGTTCAAGTCCCTTCGGGTGCACCA  
>tdbD00006547 Mycoplasma\_pneumoniae\_M129\_272634\_Leu\_CAA  
-CCTGGAGTGGCGGAAT--GGTA-GACGCGGTGGACTCAAAACCCACTAGG-----AAA-----CTG-TAGGAGTTCAAGTCTCCTCTCCAGGACCA  
>tdbD00006549 Mycoplasma\_pneumoniae\_M129\_272634\_Leu\_TAA  
-GCCCAAGTGGCGGAAT--GGTA-GACGCATGGGATTTAAGATCCCACGCTA----GCAA---TAGCGTGCCGGTTCAAGTCCGGCTTTGGGCACCA  
>tdbD00006550 Mycoplasma\_pneumoniae\_M129\_272634\_Leu\_TAG  
-GCACTCGTGGCGGAAT--GGTA-GACGCGCTAGACTTAGGATCTAGTTTCA----TTG----TGAGTGGGGGTTCAAGTCCCTTCGAGTGCACCA  
>tdbD00006467 Neisseria\_meningitidis\_Z2491\_122587\_Leu\_CAG  
-GCCCGGTTGGCGGAAT--GGTA-GACGCGCTAGCTTCAGGTGCTAGTATCC----TCAC---GGGTGTGGAAGTTCGAGTCTTCTCCCGGGCACCA  
>tdbD00006470 Neisseria\_meningitidis\_Z2491\_122587\_Leu\_TAA  
-GCCCGGTTGGTGAATA-GGTA-GACACAACGACTTAAAATCCGTGGGACT---AAA---CATCCCGTGCCGGTTTCGATTCGGCTCCGGGCACCA  
>tdbD00006471 Neisseria\_meningitidis\_Z2491\_122587\_Leu\_TAG  
-GCGGACGTGGCGAAAT--GGTA-GACGCACAGATTTAGGTCTTGCGCC-----GAGA---GGTGTGAGAGTTCGAGTCTTCTCCGTCCGCACCA  
>tdbD00006926 Oceanobacillus\_ihayensis\_HTE831\_221109\_Leu\_CAA  
-GCCGGTGTGGCGGAAT--GGCA-GACGCGCAGACTCAAAATCGTGTTC-----TTCT----GGAGTGTGCGGTTTCGACCCCGACACCGGTA---  
>tdbD00007099 Photobacterium\_luminescens\_subsp.\_laumondii\_TT01\_243265\_Leu\_TAG  
-GCGGGAGTGGCGAAAT--GGTA-GACGCACAGATTTAGGTCTTGCGCC-----GCAA---GGTGTGCGAGTTCAAGTCTCGCTCCCGCACCA  
>tdbD00006842 Rickettsia\_prowazekii\_str.\_Madrid\_E\_272947\_Leu\_TAA  
-GCCCGCTGTGGAATA-GGTA-GACATAACGACTTAAAATCCGTGGAGC----GTAA---GCTCTTGCCGGTTCAAGTCCGGCCGCGGTACCA  
>tdbD00007145 Rickettsia\_typhi\_str.\_Wilmington\_257363\_Leu\_GAG  
-GCGGTCTGTGGCGAAAT--GGTA-GACGCGCAGCATTGAGGTGCTGTTCTG---TAAA---AGGATTGGAAGTTCAAATCTTCTCGACCCACCA  
>tdbD00007147 Rickettsia\_typhi\_str.\_Wilmington\_257363\_Leu\_TAG  
-GCGGATGTGATGGAAT--GGTA-GACATGCAAGATTTAGGTCTTGTGTCT----GTGA---GGCGTGGGGGTTCAAGTCCCTTCATCCGTACCA  
>tdbD00006667 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341\_Leu\_CAA  
-GCCGAAGTGGCGAAATC--GGTA-GACGCAGTTGATTCAAAATCAACCGTA----GAAA---TACGTGCCGGTTTCGAGTCCGGCTTCGGCACCA  
>tdbD00006666 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341\_Leu\_CAG  
-GCCAAGTGGCGGAAT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC----TTAC---GGACGTGGGGGTTCAAGTCCCCCCTCGCACCA  
>tdbD00006668 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341\_Leu\_CAG  
-GCCAAGTGGCGGAAT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTTC----TTAC---GGACGTGGGGGTTCAAGTCCCCCCTCGCACCA  
>tdbD00006664 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341\_Leu\_TAA  
-GCCCGATGTGGAATC--GGTA-GACACAAGGGATTTAAAATCCCTCGGCG----TTCG---CGTGTGCGGGTTCAAGTCCCGTCCGGGTACCA  
>tdbD00006663 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341\_Leu\_TAG  
-GCGGGAGTGGCGAAAT--GGTA-GACGCACAGATTTAGGTCTTGCGCC-----GCAA---GGTGTGCGAGTTCAAGTCTCGCTCCCGCACCA  
>tdbD00007038 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261\_Leu\_CAA  
-GCCGAAGTGGCGAAATC--GGTA-GACGCAGTTGATTCAAAATCAACCGTA----GAAA---TACGTGCCGGTTTCGAGTCCGGCTTCGGCACCA  
>tdbD00007037 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261\_Leu\_CAG  
-GCCAAGTGGCGGAAT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC----TTAC---GGACGTGGGGGTTCAAGTCCCCCCTCGCACCA  
>tdbD00007039 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261\_Leu\_CAG  
-GCCAAGTGGCGGAAT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTTC----TTAC---GGACGTGGGGGTTCAAGTCCCCCCTCGCACCA  
>tdbD00007036 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261\_Leu\_GAG  
-GCCGAGTGGTGAAT--GGTA-GACACGCTACCTTGAGGTGGTAGTGCCT----AATA---GGGCTTACGGGTTCAAGTCCCGTCCCGGTACCA  
>tdbD00007034 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261\_Leu\_TAA  
-GCCCGATGTGGAATC--GGTA-GACACAAGGGATTTAAAATCCCTCGGCG----TTCG---CGTGTGCGGGTTCAAGTCCCGTCCGGGTACCA  
>tdbD00007035 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261\_Leu\_TAG  
-GCGGGAGTGGCGAAAT--GGTA-GACGCACAGATTTAGGTCTTGCGCC-----GCAA---GGTGTGCGAGTTCAAGTCTCGCTCCCGCACCA  
>tdbD00001538 Salmonella\_typhimurium\_602\_Leu\_CAG  
-GCCAAGTGGCGGAAT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC----TTAC---GGACGTGGGGGTTCAAGTCCCCCCTCGCACCA  
>tdbD00006640 Salmonella\_typhimurium\_LT2\_99287\_Leu\_CAG  
-GCCAAGTGGCGGAAT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC----TTAC---GGACGTGGGGGTTCAAGTCCCCCCTCGCACCA  
>tdbD00006639 Salmonella\_typhimurium\_LT2\_99287\_Leu\_GAG  
-GCCGAGTGGTGAAT--GGTA-GACACGCTACCTTGAGGTGGTAGTGCCT----AATA---GGGCTTACGGGTTCAAGTCCCGTCCCGGTACCA  
>tdbD00006638 Salmonella\_typhimurium\_LT2\_99287\_Leu\_TAA  
-GCCCGATGTGGAATC--GGTA-GACACAAGGGATTTAAAATCCCTCGGCG----TTCG---CGTGTGCGGGTTCAAGTCCCGTCCCGGTACCA  
>tdbD00006637 Salmonella\_typhimurium\_LT2\_99287\_Leu\_TAG  
-GCGGAGTGGCGAAAT--GGTA-GACGCACAGATTTAGGTCTTGCGCC-----GCAA---GGTGTGCGAGTTCAAGTCTCGCTCCCGCACCA  
>tdbD00006940 Shigella\_flexneri\_2a\_str.\_301\_198214\_Leu\_CAA  
-GCCGAAGTGGCGAAATC--GGTA-GACGCAGTTGATTCAAAATCAACCGTA----GAAA---TACGTGCCGGTTTCGAGTCCGGCTTCGGCACCA  
>tdbD00006942 Shigella\_flexneri\_2a\_str.\_301\_198214\_Leu\_CAG  
-GCCAAGTGGCGGAAT--GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTCC----TTAC---GGACGTGGGGGTTCAAGTCCCCCCTCGCACCA  
>tdbD00006941 Shigella\_flexneri\_2a\_str.\_301\_198214\_Leu\_GAG  
-GCCGAGTGGTGAAT--GGTA-GACACGCTACCTTGAGGTGGTAGTGCCT----AATA---GGGCTTACGGGTTCAAGTCCCGTCCCGGTACCA  
>tdbD00006944 Shigella\_flexneri\_2a\_str.\_301\_198214\_Leu\_TAA  
-GCCCGATGTGGAATC--GGTA-GACACAAGGGATTTAAAATCCCTCGGCG----TTCG---CGTGTGCGGGTTCAAGTCCCGTCCGGGTACCA

>tdbD00006943 *Shigella flexneri*\_2a\_str.\_301 198214 Leu TAG  
-GCGGAGTGGCGAAATT-GGTA-GACGCACAGATTAGGTTCTGCGGCC-----GCAA-----GGTGTGCGAGTTCAAGTCTCGCCTCCCGCACCA  
>tdbD00001542 *Sinorhizobium meliloti* 382 Leu CAG  
-GCCAGATGGCGGAATT-GGTA-GACGCGCCAGCTTCAGGTGCTGTACTC-----GAAA-----GGGTGTGGAGGTTTCAGTCTCTTCTGGGCACCA  
>tdbD00006669 *Sinorhizobium meliloti*\_1021 266834 Leu CAG  
-GCCAGATGGCGGAATT-GGTA-GACGCGCCAGCTTCAGGTGCTGTACTC-----GAAA-----GGGTGTGGAGGTTTCAGTCTCTTCTGGGCACCA  
>tdbD00006670 *Sinorhizobium meliloti*\_1021 266834 Leu GAG  
-GCGGTCTGGCGGAATT-GGTA-GACGCGCAGCGTTGAGGTGCTGTGGGG-----CAA-----CCCG-TGGAAGTTTCAGTCTTCTCGACCGCACCA  
>tdbD00007113 *Staphylococcus aureus* subsp. *aureus* MRSA252 282458 Leu TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGACTTAAAAATCCTGCGGTGA-----GTGA---TCACCGTACCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006851 *Staphylococcus aureus* subsp. *aureus* MW2 196620 Leu CAA  
-GCCGTGTGGCGGAATT-GGCA-GACGCGCGGACTCAAAAATCCTGTTCCA-----CTTG---TGAGTGTTCAGTCTCGACCCCGACCCGGTA---  
>tdbD00006850 *Staphylococcus aureus* subsp. *aureus* MW2 196620 Leu TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGACTTAAAAATCCTGCGGTGA-----GAGA---TCACCGTACCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006852 *Staphylococcus aureus* subsp. *aureus* MW2 196620 Leu TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGACTTAAAAATCCTGCGGTGA-----GTGA---TCACCGTACCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006853 *Staphylococcus aureus* subsp. *aureus* MW2 196620 Leu TAG  
-GCCGGTGTGGCGGAATT-GGCA-GACGCACTAGACTTAGGATCTAGCGCC-----TTAC---GGCGTGGGGGTTTCAGTCTCCCTTACCCCGCA---  
>tdbD00006479 *Staphylococcus aureus* subsp. *aureus* N315 158879 Leu CAA  
-GCCGTGTGGCGGAATT-GGCA-GACGCGCGGACTCAAAAATCCTGTTCCA-----CTTG---TGAGTGTTCAGTCTCGACCCCGACCCGGTA---  
>tdbD00006480 *Staphylococcus aureus* subsp. *aureus* N315 158879 Leu GAG  
-GCGGTCTGGCGGAATT-GGCA-GACGCGCTAGGTTGAGGGCTAGTGGGA-----GAGA---TCACCGTACCGGTTTCAGTCTCTCGGCCGCA---  
>tdbD00006481 *Staphylococcus aureus* subsp. *aureus* N315 158879 Leu TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGACTTAAAAATCCTGCGGTGA-----GAGA---TCACCGTACCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006482 *Staphylococcus aureus* subsp. *aureus* N315 158879 Leu TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGACTTAAAAATCCTGCGGTGA-----GAGA---TCACCGTACCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006483 *Staphylococcus aureus* subsp. *aureus* N315 158879 Leu TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCACTAGACTTAGGATCTAGCGCC-----TTAC---GGCGTGGGGGTTTCAGTCTCCCTTACCCCGCA---  
>tdbD00006980 *Staphylococcus epidermidis* ATCC 12228 176280 Leu TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGACTTAAAAATCCTGCGGTGA-----GAGA---TCACCGTACCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006981 *Staphylococcus epidermidis* ATCC 12228 176280 Leu TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCACTAGACTTAGGATCTAGCGCC-----TTA---CGCGTGGGGGTTTCAGTCTCCCTTACCCCGCA---  
>tdbD00006858 *Streptococcus agalactiae* NEM316 211110 Leu AAG  
-GCGGGATGGCGGAATT-GGCA-GACGCGCAAGACTAAGGATCTGTGACCG-----CTTT---TGTCGTGAGGGTTTCAGTCTCCCTTCTCCGCA---  
>tdbD00006857 *Streptococcus agalactiae* NEM316 211110 Leu CAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCGCTGGACTCAAAAATCCAGTGTCC-----TCAC---GGAGTGTCCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006856 *Streptococcus agalactiae* NEM316 211110 Leu TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGACTTAAAAATCCTGCGATGG-----TAA---ACATCGTACCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006855 *Streptococcus agalactiae* NEM316 211110 Leu TAG  
-GCGGTGTGGCGGAATT-GGCA-GACGCACAGACTTAAAAATCCTGCGGTGA-----TAA---ACATCGTACCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006949 *Streptococcus mutans* UA159 210007 Leu AAG  
-GCGGGATGGCGGAATT-GGCA-GACGCGCAAGACTAAGGATCTGTGACCG-----CTTT---TGTCGTGAGGGTTTCAGTCTCCCTTCTCCGCA---  
>tdbD00006611 *Streptococcus pneumoniae* TIGR4 170187 Leu CAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCGCTGGACTCAAAAATCCAGTGTCC-----GCAA---GGAGTGTCCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006606 *Streptococcus pyogenes* M1 GAS 160490 Leu CAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCGCTGGACTCAAAAATCCAGTGTCC-----GCAA---GGAGTGTCCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006604 *Streptococcus pyogenes* M1 GAS 160490 Leu TAG  
-GCGGGTTGGCGGAATT-GGCA-GACGCACAGACTTAAAAATCCTGCGGTGA-----TAA---ACATCGTACCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006861 *Streptococcus pyogenes* MGAS315 198466 Leu AAG  
-GCGGGATGGCGGAATT-GGCA-GACGCGCAGGACTAAGGATCCTGTGACCG-----CTTT---AGTTCGTGTGGGTTTCAGTCTCCACTCTCCGCA---  
>tdbD00006860 *Streptococcus pyogenes* MGAS315 198466 Leu CAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCGCTGGACTCAAAAATCCAGTGTCC-----GCAA---GGAGTGTCCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006859 *Streptococcus pyogenes* MGAS315 198466 Leu TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGACTTAAAAATCCTGCGATGG-----TTT---ACATCGTACCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006862 *Streptococcus pyogenes* MGAS315 198466 Leu TAG  
-GCGGGTTGGCGGAATT-GGCA-GACGCACAGACTTAAAAATCCTGCGGTGA-----TAA---ACATCGTACCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00007009 *Streptococcus pyogenes* SSI-1 193567 Leu AAG  
-GCGGGATGGCGGAATT-GGCA-GACGCGCAGGACTAAGGATCCTGTGACCG-----CTTT---AGTTCGTGTGGGTTTCAGTCTCCACTCTCCGCA---  
>tdbD00007008 *Streptococcus pyogenes* SSI-1 193567 Leu CAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCGCTGGACTCAAAAATCCAGTGTCC-----GCAA---GGAGTGTCCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00007007 *Streptococcus pyogenes* SSI-1 193567 Leu TAA  
-GCCGGGTGGCGGAATT-GGCA-GACGCACAGACTTAAAAATCCTGCGATGG-----TTT---ACATCGTACCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00007006 *Streptococcus pyogenes* SSI-1 193567 Leu TAG  
-GCGGGTTGGCGGAATT-GGCA-GACGCACAGACTTAAAAATCCTGCGGTGA-----TAA---ACATCGTACCGGTTTCAGTCTCCGGTCTCGGCACCA  
>tdbD00006930 *Streptomyces coelicolor* A3(2) 100226 Leu GAG  
-GTCCGGGTGGCGGAATT-GGCA-GACGCGCTAGCTTGGAGTGTAGTGCCT-----TTAT---CGGGCGTGGGGGTTTCAGTCTCCCTTCCGACACCA  
>tdbD00006565 *Synechocystis*\_sp.\_PCC 6803 1148 Leu CAA  
-GGGCGGTGGCGGAATT-GGTA-GACGCACACACTCAAAAATGTGGCGAC-----TTCG-----GTCGTGAGAGTTTCAGTCTCTCGTGCCTCA---  
>tdbD00006566 *Synechocystis*\_sp.\_PCC 6803 1148 Leu CAG  
-GCGGAATGGCGGAATT-GGTA-GACGCGCTAGATTTCAGTCTTAGTGTTC-----GTAA---GGACTTCCGGGTTTCAGTCTCCGGGTTCCGCA---  
>tdbD00006567 *Synechocystis*\_sp.\_PCC 6803 1148 Leu GAG  
-GCGGATGTGGCGGAATT-GGTA-TACGCGCACGTTTGGAGGGCGTGTGGC-----TTT-----GCCTTGCAGTTTCAGTCTCGCATCCGCA---  
>tdbD00006569 *Synechocystis*\_sp.\_PCC 6803 1148 Leu TAG  
-GCGGAGTGGCGGAATT-GGTA-GACGCGCTAGATTTCAGTCTTAGTGTTC-----TTT-----GGCGTGGGAGTTTCAGTCTCCCGTCCGCA---  
>tdbD00006864 *Thermosynechococcus elongatus*\_BP-1 197221 Leu GAG



-GCCGATGTGGCGGAATT-GGTA-TACGCGCACGTTTGAGGGGGCGTGTGGC-----TTT-----GCCTTGCAGAGTTCGAGTCTCGCCATCCGCA---  
>tdbD00006554 Treponema pallidum subsp. pallidum str. Nichols 243276 Leu CAA  
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>tdbD00006555 Treponema pallidum subsp. pallidum str. Nichols 243276 Leu CAG  
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>tdbD00006556 Treponema pallidum subsp. pallidum str. Nichols 243276 Leu GAG  
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>tdbD00006557 Treponema pallidum subsp. pallidum str. Nichols 243276 Leu TAA  
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>tdbD00006558 Treponema pallidum subsp. pallidum str. Nichols 243276 Leu TAG  
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>tdbD00006989 Tropheryma whipplei TW08/27 218496 Leu CAA  
-GCCGCGTGGCGGAATC-GGCA-GACGCGGAGCACTCAAAATGCTTTGCC-----TCAT-----GGGCGTGTGGGTTCAAATCCCTCCCGCGCA---  
>tdbD00006991 Tropheryma whipplei TW08/27 218496 Leu CAG  
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>tdbD00006988 Tropheryma whipplei TW08/27 218496 Leu GAG  
-GCGGCGTGGCGGAATC-GGTA-GACGCGCTAGCTTCAGGTGCTAGTGCCTAAAT---TTG---AAAGGCGTAGGGGTTCAAGTCCCTCCTCGCA---  
>tdbD00006992 Tropheryma whipplei TW08/27 218496 Leu TAA  
-GCCCTCGTAGCCCAATC-GGCA-GAGGCAGACACTTAAAATCGTCCC-----AGTGTGGGTTTCAGTCCACCGAGGGCA---  
>tdbD00006990 Tropheryma whipplei TW08/27 218496 Leu TAG  
-GCGGAGTGGTGAATT-GGCA-GACACGACGATTTAGGTTCCTGTGCC-----TTT-----GGCGTGGGGTTCAAGTCCCTCCCTCGCA---  
>tdbD00006881 Xanthomonas campestris pv. campestris str. ATCC 33913 190485 Leu CAA  
-GCCGAAGTGGCGGAATC-GGTA-GACGCGAGCGACTCAAAATCCGCCGCT-----TAA-----AAGCG-TGTGGGTTTCAGTCCACCTTCGGCACCA  
>tdbD00006878 Xanthomonas campestris pv. campestris str. ATCC 33913 190485 Leu CAG  
-GCCAGGTGGCGGAATT-GGTA-GACGCACTAGCTTCAGGTGCTAGCGGGGG-----CAA-----CTTCG-TGGAGGTTTCAGTCCCTCCTCGCACCA  
>tdbD00006879 Xanthomonas campestris pv. campestris str. ATCC 33913 190485 Leu GAG  
-GCCAGGTGGCGGAATT-GGTA-GACGCACTAGCTTCAGGTGCTAGCGGGGG-----CAA-----CTTCG-TGGAGGTTTCAGTCCCTCCTCGCACCA  
>tdbD00006882 Xanthomonas campestris pv. campestris str. ATCC 33913 190485 Leu GAG  
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>tdbD00006877 Xanthomonas campestris pv. campestris str. ATCC 33913 190485 Leu TAG  
-GCGAAAGTGGCGGAATT-GGTA-GACGCAACGATTTAGGTTCCTGACGCC-----GCAA-----GGCGTGGGGTTTCAGTCCCTCCTCGCACCA  
>tdbD00006994 Xylella fastidiosa Temecula 183190 Leu CAA  
-GCCGAAGTGGCGGAATT-GGTA-GACGCGAGCGACTCAAAATCCGCCACCT-----TAA-----AAGTG-TGTGGGTTTCAGTCCACCTTCGGCACCA  
>tdbD00006995 Xylella fastidiosa Temecula 183190 Leu CAG  
-GCCAGGTGGCGGAATT-GGTA-GACGCACTAGTTTCAGGTACTAGCGGGT-----AAA-----ACCG-TGGAGGTTTCAGTCCCTCCTCGCACCA  
>tdbD00006993 Xylella fastidiosa Temecula 183190 Leu GAG  
-GCCAGGTGGCGGAATT-GGTA-GACGCACTACCTTCAGGTGGTACGCGAC-----GTAA-----GTCGTAGGGGTTTCAGTCCCTCCTCGCACCA  
>tdbD00006996 Xylella fastidiosa Temecula 183190 Leu TAA  
-GCCCGGTGGCGGAATT-GGTA-GACCAAGGGACTTAAAATCCCTCGACC-----TTTA-----GGTTATGCGGGTTTCAGTCCCGCCCGGCACCA  
>tdbD00006997 Xylella fastidiosa Temecula 183190 Leu TAG  
-GCCGTTGTGGCGGAATT-GGTA-GACGCAACCGTTTAGGTCCGTTTCGCT-----TTT-----AGCGTGCAGGTTTCAGTCCCTCCTCGCACCA  
>tdbD00006634 Yersinia pestis CO92 214092 Leu CAA  
-GCCGAAGTGGCGGAATC-GGTA-GACGCGAGTTGACTCAAAATCAACCGCC-----GCGA-----GGCATGCCGGTTTCAGTCCCGCCTTCGGCACCA  
>tdbD00006631 Yersinia pestis CO92 214092 Leu CAG  
-GCGATGGTGGCGGAATT-GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTTC-----TTAC-----GGACGTGAGGGTTTCAGTCCCTCCTCGCACCA  
>tdbD00006636 Yersinia pestis CO92 214092 Leu GAG  
-GCGATGGTGGCGGAATT-GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTTC-----TTAC-----GGACGTGAGGGTTTCAGTCCCTCCTCGCACCA  
>tdbD00006635 Yersinia pestis CO92 214092 Leu GAG  
-GCCGCGGTGGTGAATT-GGTA-GACACGCTACCTTCAGGTGGTAGTGCCT-----GATT-----GGGCTTACGGGTTTCAGTCCCGTCCCTCGGTACCA  
>tdbD00006632 Yersinia pestis CO92 214092 Leu TAA  
-GCCCGGTGGTGAATC-GGTA-GACACAAGGGATTTAAAATCCCTCGGCT-----TAT-----GGCTGTGCGGGTTTCAGTCCCGCCCGGCACCA  
>tdbD00006633 Yersinia pestis CO92 214092 Leu TAG  
-GCGGAGTGGCGGAATT-GGTA-GACGCACTAGATTTAGGTTCAGCGCC-----GCAA-----GGTGTGCGAGTTTCAGTCTCGCCTCCCGCACCA  
>tdbD00006896 Yersinia pestis KIM 187410 Leu CAA  
-GCCGAAGTGGCGGAATC-GGTA-GACGCGAGTTGACTCAAAATCAACCGCC-----GCGA-----GGCATGCCGGTTTCAGTCCCGCCTTCGGCACCA  
>tdbD00006894 Yersinia pestis KIM 187410 Leu CAG  
-GCGATGGTGGCGGAATT-GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTTC-----TTAC-----GGACGTGAGGGTTTCAGTCCCTCCTCGCACCA  
>tdbD00006899 Yersinia pestis KIM 187410 Leu GAG  
-GCGATGGTGGCGGAATT-GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTTC-----TTAC-----GGACGTGAGGGTTTCAGTCCCTCCTCGCACCA  
>tdbD00006895 Yersinia pestis KIM 187410 Leu GAG  
-GCCGCGGTGGTGAATT-GGTA-GACACGCTACCTTCAGGTGGTAGTGCCT-----GATT-----GGGCTTACGGGTTTCAGTCCCGTCCCTCGGTACCA  
>tdbD00006898 Yersinia pestis KIM 187410 Leu TAA  
-GCCCGGTGGTGAATC-GGTA-GACACAAGGGATTTAAAATCCCTCGGCT-----TAT-----GGCTGTGCGGGTTTCAGTCCCGCCCGGCACCA  
>tdbD00006897 Yersinia pestis KIM 187410 Leu TAG  
-GCGGAGTGGCGGAATT-GGTA-GACGCACTAGATTTAGGTTCAGCGCC-----GCAA-----GGTGTGCGAGTTTCAGTCTCGCCTCCCGCACCA  
>tdbD00007162 Yersinia pseudotuberculosis IP\_32953 273123 Leu CAA  
-GCCGAAGTGGCGGAATC-GGTA-GACGCGAGTTGACTCAAAATCAACCGCC-----GCGA-----GGCATGCCGGTTTCAGTCCCGCCTTCGGCACCA  
>tdbD00007160 Yersinia pseudotuberculosis IP\_32953 273123 Leu CAG  
-GCGATGGTGGCGGAATT-GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTTC-----TTAC-----GGACGTGAGGGTTTCAGTCCCTCCTCGCACCA  
>tdbD00007163 Yersinia pseudotuberculosis IP\_32953 273123 Leu GAG  
-GCGATGGTGGCGGAATT-GGTA-GACGCGCTAGCTTCAGGTGTTAGTGTTC-----TTAC-----GGACGTGAGGGTTTCAGTCCCTCCTCGCACCA  
>tdbD00007161 Yersinia pseudotuberculosis IP\_32953 273123 Leu GAG  
-GCCGCGGTGGTGAATT-GGTA-GACACGCTACCTTCAGGTGGTAGTGCCT-----GATT-----GGGCTTACGGGTTTCAGTCCCGTCCCTCGGTACCA  
>tdbD00007165 Yersinia pseudotuberculosis IP\_32953 273123 Leu TAA  
-GCCGCGGTGGTGAATC-GGTA-GACACAAGGGATTTAAAATCCCTCGGCT-----TAT-----GGCTGTGCGGGTTTCAGTCCCGCCCGGCACCA

>tdbD00007164 *Yersinia pseudotuberculosis* IP\_32953 273123 Leu TAG  
-GCGGAGTGGCGAAATT-GGTA-GAGCAGCTAGATTAGGTTCTAGCGCC-----GCAA-----GGTGTGCGAGTTCAAGTCTCGCCTCCCGCACCA  
>tdbD00007620 *Escherichia coli* CFT073 199310 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACATCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007321 *Escherichia coli* K12 83333 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACATCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007327 *Escherichia coli* O157H7 83334 Met CAT:  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACATCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007333 *Escherichia coli* O157H7 EDL933 155864 Met CAT:  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACATCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007340 *Haemophilus influenzae* Rd KW20 71421 Met CAT  
-GGCTACATAGCTCAGTT-GGTT-AGAGCACAACTCATAATGTTGGG-----GTCGCAAGTTTGAATCTCGTGTAGCCACCA  
>tdbD00001808 *Photobacterium leiognathi* 658 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACATCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007411 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. CT18 220341 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACATCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007628 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. Ty2 209261 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACATCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007399 *Salmonella typhimurium* LT2 99287 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACATCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007561 *Shigella flexneri* 2a str. 301 198214 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACATCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007309 *Vibrio cholerae* O1 biovar *El Tor* str. N16961 243277 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACATCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007520 *Xanthomonas campestris* pv. *campestris* str. ATCC 33913 190485 Met CAT  
-GGCTATGTAGCTCAGTT-GGTT-AGAGCACAGCACTCATAATGATGGG-----GTCGTTGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007369 *Xylella fastidiosa* 9a5c 160492 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACATCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007599 *Xylella fastidiosa* Temecula 183190 Met CAT  
-GGCTATGTAGCTCAGTT-GGTT-AGAGCACAGCACTCATAATGATGGG-----GTCGTTGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007711 *Yersinia pestis* biovar *Microtus* str. 91001 229193 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACAGCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007398 *Yersinia pestis* CO92 214092 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACAGCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007529 *Yersinia pestis* KIM 187410 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACAGCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00007714 *Yersinia pseudotuberculosis* IP\_32953 273123 Met CAT  
-GGCTACGTAGCTCAGTT-GGTT-AGAGCACAGCACTCATAATGATGGG-----GTCACAGGTTTGAATCCCGTCGTAGCCACCA  
>tdbD00004310 *Bacillus anthracis* str. Ames 198094 Cys GCA  
-GGCGCATAGCCAAGT--GGT--AAGGCAGAGGTTGCAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTGCCGCCT---  
>tdbD00004320 *Bacillus anthracis* str. Sterne 260799 Cys GCA  
-GGCGCATAGCCAAGT--GGT--AAGGCAGAGGTTGCAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTGCCGCCT---  
>tdbD00004332 *Bacillus cereus* ATCC 10987 222523 Cys GCA  
-GGCGCATAGCCAAGT--GGT--AAGGCAGAGGTTGCAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTGCCGCCT---  
>tdbD00004298 *Bacillus cereus* ATCC 14579 226900 Cys GCA  
-GGCGCATAGCCAAGT--GGT--AAGGCAGAGGTTGCAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTGCCGCCT---  
>tdbD00004342 *Bacillus thuringiensis* serovar *konkukian* str. 97-27 281309 Cys GCA  
-GGCGCATAGCCAAGT--GGT--AAGGCAGAGGTTGCAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTGCCGCCT---  
>tdbD00004321 *Borrelia garinii* Pbi 290434 Cys GCA  
-GGCGCTTACCCAAGT--GGCT--AAGGGAGAAGTCTGCAAACTTTGA-----TTCGCCGGTTTGAATCCCGTCCAGCGCT---  
>tdbD00004301 *Escherichia coli* CFT073 199310 Cys GCA  
-GGCGGTTAAACAAAGC--GGT--TATGTAGCGGATTGCAAATCCGTCT-----A-GTCCGGTTTGAATCCCGTCCAGCGCT---  
>tdbD00004160 *Escherichia coli* K12 83333 Cys GCA  
-GGCGGTTAAACAAAGC--GGT--TATGTAGCGGATTGCAAATCCGTCT-----A-GTCCGGTTTGAATCCCGTCCAGCGCT---  
>tdbD00004162 *Escherichia coli* O157H7 83334 Cys GCA:  
-GGCGGTTAAACAAAGC--GGT--TATGTAGCGGATTGCAAATCCGTCT-----A-GTCCGGTTTGAATCCCGTCCAGCGCT---  
>tdbD00004162 *Escherichia coli* O157H7 EDL933 155864 Cys GCA:  
-GGCGGTTAAACAAAGC--GGT--TATGTAGCGGATTGCAAATCCGTCT-----A-GTCCGGTTTGAATCCCGTCCAGCGCT---  
>tdbD00004163 *Helicobacter pylori* 26695 85962 Cys GCA  
-GGCGCATAGCCAAGT--GGT--AAGGCATGGGTTGCAAAACCTTTGA-----TTCGCCGGTTTGAATCCCGTCCAGCGCT---  
>tdbD00004289 *Lactobacillus plantarum* WCF51 220668 Cys GCA  
-GGCGGTTAAACAAAGC--GGT--AAGGCAGAGGTTGCAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTACCGCT---  
>tdbD00004180 *Listeria monocytogenes* EGD-e 169963 Cys GCA  
-GGCGCATAGCCAAGT--GGT--AAGGCAGAGGTTGCAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTGCCGCCT---  
>tdbD00004334 *Listeria monocytogenes* str. 4b F2365 265669 Cys GCA  
-GGCGCATAGCCAAGT--GGT--AAGGCAGAGGTTGCAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTGCCGCCT---  
>tdbD00004153 *Neisseria meningitidis* Z2491 122587 Cys GCA  
-GGCGAGATAGCAAAGT--GGT--TATGCAGCGGATTGCAAATCCGTCT-----A-CGCCGGTTTGAATCCCGTCCAGCGCT---  
>tdbD00004172 *Pasteurella multocida* subsp. *multocida* str. Pm70 272843 Cys GCA  
-GGCGGTTAAACAAAGC--GGT--TATGCAGCGGATTGCAAATCCGTCT-----A-GTCCGGTTTGAATCCCGTCCAGCGCT---  
>tdbD00004260 *Rickettsia prowazekii* str. Madrid E 272947 Cys GCA  
-GGCTGGGTAGCAAAGT--GGT--AATGCCGTGGACTGCAAATCCTCTA-----TTCGTCGGTTTGAATCCCGTCCAGCGCT---  
>tdbD00004326 *Rickettsia typhi* str. Wilmington 257363 Cys GCA  
-GGCTGGGTAGCAAAGT--GGT--AATGCCGTGGACTGCAAATCCTCTA-----TTCGTCGGTTTGAATCCCGTCCAGCGCT---  
>tdbD00004196 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. CT18 220341 Cys GCA

-GGCGCGTTAACAAAGC--GGT--TATGTAGCGGATTGCAAAATCCGTCT-----A-GTCCGGTTCGACTCCGGAACGCGCCTCCA  
>tdbD00004304 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261 Cys GCA  
-GGCGCGTTAACAAAGC--GGT--TATGTAGCGGATTGCAAAATCCGTCT-----A-GTCCGGTTCGACTCCGGAACGCGCCTCCA  
>tdbD00004190 Salmonella\_typhimurium\_LT2\_99287 Cys GCA  
-GGCGCGTTAACAAAGC--GGT--TATGTAGCGGATTGCAAAATCCGTCT-----A-GTCCGGTTCGACTCCGGAACGCGCCTCCA  
>tdbD00004280 Shigella\_flexneri\_2a\_str.\_301\_198214 Cys GCA  
-GGCGCGTTAACAAAGC--GGT--TATGTAGCGGATTGCAAAATCCGTCT-----A-GTCCGGTTCGACTCCGGAACGCGCCTCCA  
>tdbD00004319 Staphylococcus\_aureus\_subsp.\_aureus\_MRSA252\_282458 Cys GCA  
-GGCGGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTCGCGCCTCCA  
>tdbD00004262 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620 Cys GCA  
-GGCGGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTCGCGCCTCCA  
>tdbD00004156 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879 Cys GCA  
-GGCGGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTCGCGCCTCCA  
>tdbD00004290 Staphylococcus\_epidermidis\_ATCC\_12228\_176280 Cys GCA  
-GGCGGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAAACCTTTA-----T-CACCGGTTCAAATCCGGTTCGCGCCTCCA  
>tdbD00004263 Streptococcus\_agalactiae\_NEM316\_211110 Cys GCA  
-GGCGGTATAGCCAAGT--GGT--AAGGCACGGCTCTGCAAAAACCTTTA-----T-CGTCGGTTCAAATCCGTCTACCGCCT---  
>tdbD00004282 Streptococcus\_mutans\_UA159\_210007 Cys GCA  
-GGCGGTATAGCCAAGT--GGT--AAGGCACGGCTCTGCAAAAACCTTTA-----T-CGTCGGTTCAAATCCGTCTACCGCCT---  
>tdbD00004184 Streptococcus\_pneumoniae\_TIGR4\_170187 Cys GCA  
-GGCGGTATAGCCAAGT--GGT--AAGGCACGGCTCTGCAAAAACCTTTA-----T-CGTCGGTTCAAATCCGTCTACCGCCT---  
>tdbD00004183 Streptococcus\_pyogenes\_M1\_GAS\_160490 Cys GCA  
-GGCGGTATAGCCAAGT--GGT--AAGGCACGGCTCTGCAAAAACCTTTA-----T-CGTCGGTTCAAATCCGTCTACCGCCT---  
>tdbD00004264 Streptococcus\_pyogenes\_MGAS315\_198466 Cys GCA  
-GGCGGTATAGCCAAGT--GGT--AAGGCACGGCTCTGCAAAAACCTTTA-----T-CGTCGGTTCAAATCCGTCTACCGCCT---  
>tdbD00004296 Streptococcus\_pyogenes\_SSI-1\_193567 Cys GCA  
-GGCGGTATAGCCAAGT--GGT--AAGGCACGGCTCTGCAAAAACCTTTA-----T-CGTCGGTTCAAATCCGTCTACCGCCT---  
>tdbD00004175 Synechocystis\_sp.\_PCC\_6803\_1148 Cys GCA  
-GGCGGCATAGCCAAGT--GGT--AAGGCAGAGGTCTGCAAAAATCTTTA-----C-CCCCAGTTCGAATCTGGGTGCGCCT---  
>tdbD00004173 Treponema\_pallidum\_subsp.\_pallidum\_str.\_Nichols\_243276 Cys GCA  
-GGCGCGGTGCCAAGT--GGT--AAGGGAGAGGTCTGCAAAAACCTTTA-----TGCATCAGTTCGATTCTGATCGCGCCT---  
>tdbD00011748 Bacillus\_anthraxis\_str.\_Ames\_198094 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTCGAATCTGCCCCCTCCACCA  
>tdbD00011759 Bacillus\_anthraxis\_str.\_Sterne\_260799 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTCGAATCTGCCCCCTCCACCA  
>tdbD00011772 Bacillus\_cereus\_ATCC\_10987\_222523 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTCGAATCTGCCCCCTCCACCA  
>tdbD00011736 Bacillus\_cereus\_ATCC\_14579\_226900 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTCGAATCTGCCCCCTCCACCA  
>tdbD00011565 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGCGGACTGTAAATCCGCTCCT-----TCAG-----GGTTCGGCAGTTTCGAATCTGCCCCCTCCACCA  
>tdbD00011782 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27\_281309 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTCGAATCTGCCCCCTCCACCA  
>tdbD00011784 Bartonella\_quintana\_str.\_Toulouse\_283165 Tyr GTA  
-GGAGGGGTGCCGAGT--GGTTAAAGGGGGCGGACTGTAAATCCGTTGCG-----TATG-----CTA-CGTTGGTTTCGAATCCACCCCTCCACCA  
>tdbD00011585 Borrelia\_burgdorferi\_B31\_24326 Tyr GTA  
-GGGGCGGTACCGAAGT--GGTTAAACGCGGAGCAGACTGTAAATCTGTTGGC-----TTTG-----CCTACGTGGGTTTCGAATCCACCCCTCCCA---  
>tdbD00011711 Brucella\_suis\_1330\_204722 Tyr GTA  
-GGAGGGATGCCGAGT--GGTTAAAGGGGGCGGACTGTAAATCCGTTGGC-----TATG-----CCTACGTGGTTTCGAATCCAACTCCCTCCACCA  
>tdbD00011586 Campylobacter\_jejuni\_subsp.\_jejuni\_NCTC\_11168\_192222 Tyr GTA  
-GGTGAGTTACTCAAGT--GGCCAAACGAGGAGCAGACTGTAAATCTGCTGGCT-----TTC-----GCCTCCGTTGGTTTCGAATCCACGACTCACCACCA  
>tdbD00011562 Chlamydia\_trachomatis\_D/UW-3/CX\_272561 Tyr GTA  
-GGGGGTGTCGCATAGC--GGTCAATGTCATCGGACTGTAAATCCGACTCCT-----TAC-----GGATACGTTGGTTTCGAATCCAGCCACCCCA---  
>tdbD00011561 Chlamydophila\_pneumoniae\_CWL029\_115713 Tyr GTA  
-GGGGGTGTCGCATAGT--GGTCAATGTCATCGGACTGTAAATCCGACTCCT-----TAC-----GGATACGTTGGTTTCGAATCCAGCCACCCCA---  
>tdbD00011575 Chlamydophila\_pneumoniae\_J138\_138677 Tyr GTA  
-GGGGGTGTCGCATAGT--GGTCAATGTCATCGGACTGTAAATCCGACTCCT-----TAC-----GGATACGTTGGTTTCGAATCCAGCCACCCCA---  
>tdbD00011696 Corynebacterium\_glutamicum\_ATCC\_13032\_196627 Tyr GTA  
-GCCGATTGCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCCGTCGGCT-----TGC-----GCCTACGTAGTTTCGAATCCTACATCTGGCA---  
>tdbD00011738 Escherichia\_coli\_CFT073\_199310 Tyr GTA  
-GGTGGGGTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ATCG-----ACTTCGAAGGTTTCGAATCCTTCCCCCACCACCA  
>tdbD00011739 Escherichia\_coli\_CFT073\_199310 Tyr GTA  
-GGTGGGGTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ATCG-----ACTTCGAAGGTTTCGAATCCTTCCCCCACCACCA  
>tdbD00011576 Escherichia\_coli\_K12\_83333 Tyr GTA  
-GGTGGGGTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ATCG-----ACTTCGAAGGTTTCGAATCCTTCCCCCACCACCA  
>tdbD00011577 Escherichia\_coli\_K12\_83333 Tyr GTA  
-GGTGGGGTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ATCG-----ACTTCGAAGGTTTCGAATCCTTCCCCCACCACCA  
>tdbD00011578 Escherichia\_coli\_O157H7\_83334 Tyr GTA:  
-GGTGGGGTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ATCG-----ACTTCGAAGGTTTCGAATCCTTCCCCCACCACCA  
>tdbD00011579 Escherichia\_coli\_O157H7\_83334 Tyr GTA:  
-GGTGGGGTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ATCG-----ACTTCGAAGGTTTCGAATCCTTCCCCCACCACCA  
>tdbD00011580 Escherichia\_coli\_O157H7\_EDL933\_155864 Tyr GTA:  
-GGTGGGGTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ATCG-----ACTTCGAAGGTTTCGAATCCTTCCCCCACCACCA  
>tdbD00011581 Escherichia\_coli\_O157H7\_EDL933\_155864 Tyr GTA:  
-GGTGGGGTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ATCG-----ACTTCGAAGGTTTCGAATCCTTCCCCCACCACCA

>tdbD00011602 *Listeria monocytogenes* EGD-e 169963 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGTGGTTTGAATCCACTCCCCTCCACCA  
>tdbD00011774 *Listeria monocytogenes* str. 4b\_F2365 265669 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGTGGTTTGAATCCACTCCCCTCCACCA  
>tdbD00011567 *Mycobacterium tuberculosis* CDC1551 83331 Tyr GTA  
-GGCAGGTTGCCCGAGC--GGCCAAATGGGAGCGGACTGTAAATCTGCGCGC-----AAAG-----CTA-CGCAGGTTTGAATCCTGCACCTGCCACCA  
>tdbD00011753 *Mycobacterium tuberculosis* H37Rv 83332 Tyr GTA  
-GGCAGGTTGCCCGAGC--GGCCAAATGGGAGCGGACTGTAAATCCGCTCCT-----AAAG-----CTA-CGCAGGTTTGAATCCTGCACCTGCCACCA  
>tdbD00011591 *Mycoplasma pneumoniae* M129 272634 Tyr GTA  
-GGACAGGTAGCGAAGT--GGCTAAACGCTTCTGACTGTAGATCAGACACCT-----TCAT-----GGTTCGGGAGTTTGAATCTCTCCTGTCCACCA  
>tdbD00011715 *Oceanobacillus iheyensis* HTE831 221109 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTGAATCTGCCCCCTCCACCA  
>tdbD00011755 *Photobacterium luminescens* subsp. *laumondii* T101 243265 Tyr GTA  
-GGTGGGTTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ACAG-----ACTTCGAAGGTTTGAATCCTTCCCCACCACCA  
>tdbD00011765 *Porphyromonas gingivalis* W83 242619 Tyr GTA  
-GGCAGTTTACCAGAGT--GGCCAAATGGGGCTGACTGTAACTCAGCTGGCT-----TAC-----GCCTTCGGTGGTTTGAATCCATCACTGCCCA---  
>tdbD00011766 *Rickettsia typhi* str. Wilmington 257363 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAATGGCAGCAGACTGTAAATCTGCGCGC-----TAAG-----CGTT-CGAAGGTTTGAATCCTTCTCCTCCACCA  
>tdbD00011621 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. CT18 220341 Tyr GTA  
-GGTGGGTTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ACAG-----ACTTCGAAGGTTTGAATCCTTCCCCACCACCA  
>tdbD00011742 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. Ty2 209261 Tyr GTA  
-GGTGGGTTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ACAG-----ACTTCGAAGGTTTGAATCCTTCCCCACCACCA  
>tdbD00011614 *Salmonella typhimurium* LT2 99287 Tyr GTA  
-GGTGGGTTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ATCG-----ACTTCGAAGGTTTGAATCCTTCCCCACCACCA  
>tdbD00011615 *Salmonella typhimurium* LT2 99287 Tyr GTA  
-GGTGGGTTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ACAG-----ACTTCGAAGGTTTGAATCCTTCCCCACCACCA  
>tdbD00011718 *Shigella flexneri* 2a str. 301 198214 Tyr GTA  
-GGTGGGTTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ATCG-----ACTTCGAAGGTTTGAATCCTTCCCCACCACCA  
>tdbD00011758 *Staphylococcus aureus* subsp. *aureus* MRSA252 282458 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTGAATCTGCCCCCTCCACCA  
>tdbD00011697 *Staphylococcus aureus* subsp. *aureus* MW2 196620 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTGAATCTGCCCCCTCCCA---  
>tdbD00011698 *Staphylococcus aureus* subsp. *aureus* MW2 196620 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTGAATCTGCCCCCTCCACCA  
>tdbD00011571 *Staphylococcus aureus* subsp. *aureus* N315 158879 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTGAATCTGCCCCCTCCCA---  
>tdbD00011572 *Staphylococcus aureus* subsp. *aureus* N315 158879 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTGAATCTGCCCCCTCCACCA  
>tdbD00011728 *Staphylococcus epidermidis* ATCC 12228 176280 Tyr GTA  
-GGAGGGGTAGCGAAGT--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGCAGTTTGAATCTGCCCCCTCCACCA  
>tdbD00011699 *Streptococcus agalactiae* NEM316 211110 Tyr GTA  
-GGAGAGATAGCGAAGA--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGGGTTTGAATCCCTCTCTCTCCA---  
>tdbD00011700 *Streptococcus agalactiae* NEM316 211110 Tyr GTA  
-GGAAAGATAGCGAAGA--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGGGTTTGAATCCCTCTCTTTCCA---  
>tdbD00011606 *Streptococcus pneumoniae* TIGR4 170187 Tyr GTA  
-GGAGAGATAGCGAAGA--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGGGTTTGAATCCCTCTCTCTCCA---  
>tdbD00011607 *Streptococcus pneumoniae* TIGR4 170187 Tyr GTA  
-GGAAGGTAGCGAAGA--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGGGTTTGAATCCCTCCCCTTCCA---  
>tdbD00011605 *Streptococcus pyogenes* M1 GAS 160490 Tyr GTA  
-GGAAGATAGCGAAGA--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGGGTTTGAATCCCTCTCTTTCCA---  
>tdbD00011701 *Streptococcus pyogenes* MGAS315 198466 Tyr GTA  
-GGAAGATAGCGAAGA--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGGGTTTGAATCCCTCTCTTTCCA---  
>tdbD00011734 *Streptococcus pyogenes* SSI-1 193567 Tyr GTA  
-GGAAGATAGCGAAGA--GGCTAAACGCGGCGGACTGTAAATCCGCTCCT-----TCG-----GGTTCGGGGTTTGAATCCCTCTCTTTCCA---  
>tdbD00011716 *Streptomyces coelicolor* A3(2) 100226 Tyr GTA  
-GGCGGTGTGCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGCG-----TCAG-----CCTTCCCAGGTTTGAATCCTGGCGCGGCCA---  
>tdbD00003519 *Streptomyces lividans* 1916 Tyr GTA  
-GGCGGTGTGCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGCG-----TCAG-----CCTTCCCAGGTTTGAATCCTGGCGCGGCCA---  
>tdbD00011595 *Synechocystis* sp. PCC 6803 1148 Tyr GTA  
-GGTTCGATGCCCGAGT--GGTTAATGGGGCGGACTGTAAATCCGCTGGC-----TATG-----CCTACGCTGGTTTCAAATCCAGCTCGGCCA---  
>tdbD00011593 *Treponema pallidum* subsp. *pallidum* str. Nichols 243276 Tyr GTA  
-GGGGAGTTTCCCGAGT--GGTCAAAGGGAGCAGACTGTAAATCTGTTGGCG-----TTG-----TCTT-CCAAGGTTTGAATCCTTACTCCCCA---  
>tdbD00011730 *Tropheryma whipplei* TW08/27 218496 Tyr GTA  
-GGCGAGTTACCCAAGT--GGCCAAAGGGATCTGACTGTAAATCAGCTGTCA-----TTC-----GACTTCGGGGTTTGAATCCCTCACTCGCCA---  
>tdbD00011705 *Xanthomonas campestris* pv. *campestris* str. ATCC 33913 190485 Tyr GTA  
-GGAGGGATACCCAAGC--GGCCAAAGGGGGCAGACTGTAAATCTGCTGGCT-----TAC-----GCCTTCGGTGGTTTGAATCCACCTCCCTCCACCA  
>tdbD00011731 *Xylella fastidiosa* Temecula 183190 Tyr GTA  
-GGAGGGATACCCAAGC--GGCCAAAGGGGGCAGACTGTAAATCTGCTGGCT-----TGC-----GCCTTCGGTGGTTTGAATCCACCTCCCTCCACCA  
>tdbD00011769 *Yersinia pestis* biovar *Microtus* str. 91001 229193 Tyr GTA  
-GGTGGGTTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ATCG-----ACTTCGAAGGTTTGAATCCTTCCCCACCACCA  
>tdbD00011613 *Yersinia pestis* C092 214092 Tyr GTA  
-GGTGGGTTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ATCG-----ACTTCGAAGGTTTGAATCCTTCCCCACCACCA  
>tdbD00011708 *Yersinia pestis* KIM 187410 Tyr GTA  
-GGTGGGTTCCCGAGC--GGCCAAAGGGAGCAGACTGTAAATCTGCGGTC-----ATCG-----ACTTCGAAGGTTTGAATCCTTCCCCACCACCA  
>tdbD00011770 *Yersinia pseudotuberculosis* IP\_32953 273123 Tyr GTA

-GGTGGGGTCCCGAGC--GGCCAAAGGGAGCAGACTGTAATCTGCCGTC-----ATCG-----ACTTCGAAGGTTCGAATCCTTCCCCACCACCA  
>tdbD00011438 *Bacillus anthracis*\_str.\_Sterne\_260799 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAAGTGGGTCTCCAAAACCTCCA-----G-TGTGGGTTTCGATTCTACTGCCCTGCCA  
>tdbD00011439 *Bacillus anthracis*\_str.\_Sterne\_260799 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAAGTGGGTCTCCAAAACCTCCA-----G-TGTGGGTTTCGATTCTACTGCCCTG---  
>tdbD00011451 *Bacillus cereus*\_ATCC\_10987\_222523 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAAGTGGGTCTCCAAAACCTCCA-----G-TGTGGGTTTCGATTCTACTGCCCTGCCA  
>tdbD00011452 *Bacillus cereus*\_ATCC\_10987\_222523 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAAGTGGGTCTCCAAAACCTCCA-----G-TGTGGGTTTCGATTCTACTGCCCTG---  
>tdbD00011414 *Bacillus cereus*\_ATCC\_14579\_226900 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAAGTGGGTCTCCAAAACCTCCA-----G-TGTGGGTTTCGATTCTACTGCCCTGCCA  
>tdbD00011415 *Bacillus cereus*\_ATCC\_14579\_226900 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAAGTGGGTCTCCAAAACCTCCA-----G-TGTGGGTTTCGATTCTACTGCCCTG---  
>tdbD00003288 *Bacillus subtilis*\_1423 Trp CCA  
-AGGGGCATAGTTTAAAC--GGT--AGAAGCAGAGGTCTCCAAAACCTCCG-----G-TGTGGGTTTCGATTCTACTGCCCTGCCA  
>tdbD00011462 *Bacillus thuringiensis*\_serovar\_konkukian\_str.\_97-27\_281309 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAAGTGGGTCTCCAAAACCTCCA-----G-TGTGGGTTTCGATTCTACTGCCCTG---  
>tdbD00011463 *Bacillus thuringiensis*\_serovar\_konkukian\_str.\_97-27\_281309 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAAGTGGGTCTCCAAAACCTCCA-----G-TGTGGGTTTCGATTCTACTGCCCTGCCA  
>tdbD00011306 *Borrelia burgdorferi*\_B31\_224326 Trp CCA  
-AGGTCAGTAGTTCCAAC--GGT--AGAAGCAGAGGTCTCCAAAACCTGTAT-----GCTGGGGGTTTCGAACTCCTGACCTG---  
>tdbD00011440 *Borrelia garinii*\_PBi\_290434 Trp CCA  
-AGGTCAGTAGTTCCAAC--GGT--AGAAGCAGAGGTCTCCAAAACCTGTAT-----GCTGGGGGTTTCGAACTCCTGACCTG---  
>tdbD00011387 *Brucella suis*\_1330\_204722 Trp CCA  
-AGGGGTATAGCTCAGTT--GGT--AGAGCGACGGTCTCCAAAACCGTAG-----GTCGCGGGTTTCGAACTCCTGACCTG---  
>tdbD00011418 *Escherichia coli*\_CFT073\_199310 Trp CCA  
-AGGGGCGTAGTTCGAATT--GGT--AGAGCACCAGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTGCCA  
>tdbD00011300 *Escherichia coli*\_K12\_83333 Trp CCA  
-AGGGGCGTAGTTCGAATT--GGT--AGAGCACCAGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTGCCA  
>tdbD00011301 *Escherichia coli*\_O157H7\_83334 Trp CCA:  
-AGGGGCGTAGTTCGAATT--GGT--AGAGCACCAGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTGCCA  
>tdbD00011302 *Escherichia coli*\_O157H7\_EDL933\_155864 Trp CCA:  
-AGGGGCGTAGTTCGAATT--GGT--AGAGCACCAGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTGCCA  
>tdbD00011305 *Haemophilus influenzae*\_Rd\_KW20\_71421 Trp CCA  
-AGGGGCGTAGTTCGAATT--GGT--AGAGCACCAGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGCTCTCCGCCCTGCCA  
>tdbD00011303 *Helicobacter pylori*\_26695\_85962 Trp CCA  
-AGGTCAGTAGCTCCAAT--GGT--AGAGCGTCCGGTCTCCAAAACCGGGT-----GTTGGGGGTTTCGAGTCCCTCCTGGCCTGCCA  
>tdbD00011304 *Helicobacter pylori*\_J99\_85963 Trp CCA  
-AGGTCAGTAGCTCCAAT--GGT--AGAGCGTCCGGTCTCCAAAACCGGGT-----GTTGGGGGTTTCGAGTCCCTCCTGGCCTGCCA  
>tdbD00011320 *Listeria innocua*\_Clp11262\_272626 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAAGTGGGTCTCCAAAACCTCCA-----G-TGTGGGTTTCGATTCTACTGCCCTGCCA  
>tdbD00011321 *Listeria monocytogenes*\_EGD-e\_169963 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAAGTGGGTCTCCAAAACCTCCA-----G-TGTGGGTTTCGATTCTACTGCCCTGCCA  
>tdbD00011454 *Listeria monocytogenes*\_str.\_4b\_F2365\_265669 Trp CCA  
-AGGGGCATAGTTTAAA--GGT--AGAAGTGGGTCTCCAAAACCTCCA-----G-TGTGGGTTTCGATTCTACTGCCCTGCCA  
>tdbD00011292 *Mycobacterium tuberculosis*\_CDC1551\_83331 Trp CCA  
-AGGGGCGTAGCTCAACT--GGC--AGAGCAGCGGTCTCCAAAACCGGAG-----GTTGCAGGTTCAAGTCTGTGCGCCCTG---  
>tdbD00011433 *Mycobacterium tuberculosis*\_H37Rv\_83332 Trp CCA  
-AGGGGCGTAGCTCAACT--GGC--AGAGCAGCGGTCTCCAAAACCGGAG-----GTTGCAGGTTCAAGTCTGTGCGCCCTG---  
>tdbD00011294 *Neisseria meningitidis*\_Z2491\_122587 Trp CCA  
-AGGCCAATAGCTCAATT--GGT--AGAGTATCGGTCTCCAAAACCGGAG-----GTTGGGGGTTTCGAGACCCTCTGGCCTGCCA  
>tdbD00011312 *Pasteurella multocida*\_subsp.\_multocida\_str.\_Pm70\_272843 Trp CCA  
-AGGGGCGTAGTTCGAATT--GGT--AGAGCACCAGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGCTCTCCGCCCTGCCA  
>tdbD00011435 *Photobacterium luminescens*\_subsp.\_laumondii\_TTO1\_243265 Trp CCA  
-AGGGGCGTAGTTCGAATT--GGT--AGAGCACCAGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTGCCA  
>tdbD00011436 *Rhodospseudomonas palustris*\_CGA009\_258594 Trp CCA  
-AGGAGTGTAGCTCAATT--GGT--AGAGCACCAGGTCTCCAAAACCGGGG-----GTCGCGAGTTTCGAGCCTGCCACTCCTGCCA  
>tdbD00011373 *Rickettsia prowazekii*\_str.\_Madrid\_E\_272947 Trp CCA  
-AGGAGTGTAGCTCAATT--GGT--AGAGCACCAGGTCTCCAAAACCGGAG-----GTTGCAGGTTTCGATTCTGTGCGCTCCTGCCA  
>tdbD00011337 *Salmonella enterica*\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341 Trp CCA  
-AGGGGCGTAGTTCGAATT--GGT--AGAGCACCAGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTGCCA  
>tdbD00011420 *Salmonella enterica*\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261 Trp CCA  
-AGGGGCGTAGTTCGAATT--GGT--AGAGCACCAGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTGCCA  
>tdbD00011332 *Salmonella typhimurium*\_LT2\_99287 Trp CCA  
-AGGGGCGTAGTTCGAATT--GGT--AGAGCACCAGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTGCCA  
>tdbD00011437 *Staphylococcus aureus*\_subsp.\_aureus\_MRSA252\_282458 Trp CCA  
-AGGGCATAAGTTCGAATT--GGT--AGAATAGAGGTCTCCAAAACCTTTG-----G-TGTGGGTTTCGATTCTACTGCCCTGCCA  
>tdbD00011375 *Staphylococcus aureus*\_subsp.\_aureus\_MW2\_196620 Trp CCA  
-AGGGGCATAGTTCGAATT--GGT--AGAATAGAGGTCTCCAAAACCTTTG-----G-TGTGGGTTTCGATTCTACTGCCCTGCCA  
>tdbD00011296 *Staphylococcus aureus*\_subsp.\_aureus\_N315\_158879 Trp CCA  
-AGGGCATAAGTTCGAATT--GGT--AGAATAGAGGTCTCCAAAACCTTTG-----G-TGTGGGTTTCGATTCTACTGCCCTGCCA  
>tdbD00011391 *Streptomyces coelicolor*\_A3(2)\_100226 Trp CCA  
-AGGGTCGTAGCTCAATT--GGT--AGAGCAGTGGTCTCCAAAACCGG-----GTTGGGGGTTTCAGTCCCTCCGCCCTG---  
>tdbD00003285 *Streptomyces griseus*\_1911 Trp CCA  
-AGGGTCGTAGCTCAATT--GGT--AGAGCAGTGGTCTCCAAAACCGG-----GTTGGGGGTTTCAGTCCCTCCGCCCTG---

>tdbD00011408 Tropheryma whipplei\_TW08/27 218496 Trp CCA  
-AGGGCGGTGCTCAATT-GGT--AGAGCACGGTCTCCAAAACCGGAG-----GTTGCAGGTTCAAGTCTCTCCGCCCTG---  
>tdbD00011318 Xylella fastidiosa\_9a5c 160492 Trp CCA  
-AGGGCGTAGTTCAATT-GGT--AGAGCACCGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTGCCA  
>tdbD00011448 Yersinia pestis biovar\_Microtus\_str.\_91001 229193 Trp CCA  
-AGGGCGTAGTTCAATT-GGT--AGAGCACCGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTGCCA  
>tdbD00011331 Yersinia pestis\_CO92 214092 Trp CCA  
-AGGGCGTAGTTCAATT-GGT--AGAGCACCGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTGCCA  
>tdbD00011384 Yersinia pestis\_KIM 187410 Trp CCA  
-AGGGCGTAGTTCAATT-GGT--AGAGCACCGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTGCCA  
>tdbD00011449 Yersinia pseudotuberculosis\_IP\_32953 273123 Trp CCA  
-AGGGCGTAGTTCAATT-GGT--AGAGCACCGGTCTCCAAAACCGGGT-----GTTGGGAGTTTCGAGTCTCTCCGCCCTGCCA  
>tdbD00004802 Escherichia coli\_CFT073 199310 Glu TTC  
-GTCCCTTCGTCTAGA--GGCCCAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00004617 Escherichia coli\_K12 83333 Glu TTC  
-GTCCCTTCGTCTAGA--GGCCCAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00004618 Escherichia coli\_O157H7 83334 Glu TTC:  
-GTCCCTTCGTCTAGA--GGCCCAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00004619 Escherichia coli\_O157H7\_EDL933 155864 Glu TTC:  
-GTCCCTTCGTCTAGA--GGCCCAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00000543 Haemophilus influenzae 727 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACATCGCCCTTTCACGGCGGTA-----A-CCGGGGTTTCGAATCCCCGTGGGGACGCCA  
>tdbD00004625 Haemophilus influenzae\_Rd\_KW20 71421 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACATCGCCCTTTCACGGCGGTA-----A-CCGGGGTTTCGAATCCCCGTGGGGACGCCA  
>tdbD00004632 Pasteurella multocida subsp.\_multocida\_str.\_Pm70 272843 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACATCGCCCTTTCACGGCGGTA-----A-CCGGGGTTTCGAATCCCCGTGGGGACGCCA  
>tdbD00004812 Pseudomonas syringae pv.\_tomato\_str.\_DC3000 223283 Glu TTC  
-GTCCCTTCGTCTAGT--GGCCTAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAGTCCCCTAGGGGACGCCA  
>tdbD00004665 Salmonella enterica subsp.\_enterica\_serovar\_Typhi\_str.\_CT18 220341 Glu TTC  
-GTCCCTTCGTCTAGA--GGCCCAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00004805 Salmonella enterica subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2 209261 Glu TTC  
-GTCCCTTCGTCTAGA--GGCCCAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00000544 Salmonella enteritidis 592 Glu TTC  
-GTCCCTTCGTCTAGA--GGCCCAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00004658 Salmonella typhimurium\_LT2 99287 Glu TTC  
-GTCCCTTCGTCTAGA--GGCCCAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00004659 Salmonella typhimurium\_LT2 99287 Glu TTC  
-GTCCCTTCGTCTAGA--GGCCCAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00004660 Salmonella typhimurium\_LT2 99287 Glu TTC  
-GTCCCTTCGTCTAGA--GGCCCAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00004768 Shigella flexneri\_2a\_str.\_301 198214 Glu TTC  
-GTCCCTTCGTCTAGA--GGCCCAGGACACCGCCCTTTCACGGCGGTA-----A-CAGGGGTTTCGAATCCCCTAGGGGACGCCA  
>tdbD00004749 Xanthomonas campestris pv.\_campestris\_str.\_ATCC\_33913 190485 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACACCCTTTCACGGTGGAC-----A-CCGGGGTTTCGAATCCCCGTGGGGACGCCA  
>tdbD00004791 Xylella fastidiosa\_Temecula 183190 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACATCACCTTTCACGGTGGC-----A-CCGGGGTTTCGAATCCCCGTGGGGACGCCA  
>tdbD00004657 Yersinia pestis\_CO92 214092 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACACTGCCCTTTCACGGCTGTA-----A-CAGGGGTTTCGAATCCCCTTGGGGACGCCA  
>tdbD00004754 Yersinia pestis\_KIM 187410 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACACTGCCCTTTCACGGCTGTA-----A-CAGGGGTTTCGAATCCCCTTGGGGACGCCA  
>tdbD00004853 Yersinia pseudotuberculosis\_IP\_32953 273123 Glu TTC  
-GTCCCATCGTCTAGA--GGCCTAGGACACTGCCCTTTCACGGCTGTA-----A-CAGGGGTTTCGAATCCCCTTGGGGACGCCA  
>tdbD00008639 Buchnera aphidicola\_str.\_Sg\_(Schizaphis\_graminum) 198804 Gln TTG  
-TGGGGTATAGCCAAGT--GGTT--AAGGCACCGGTTTTTGATACCGGCA-----T-CCCTGGTTTCGAATCCAGGTACCCCAGCCA  
>tdbD00008704 Escherichia coli\_CFT073 199310 Gln CTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGATTCTGATTCGGCA-----TTCCGAGGTTTCGAATCCTCGTACCCCAGCCA  
>tdbD00008705 Escherichia coli\_CFT073 199310 Gln TTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATACCGGCA-----TTCCCTGGTTTCGAATCCAGGTACCCCAGCCA  
>tdbD00008503 Escherichia coli\_K12 83333 Gln CTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGATTCTGATTCGGCA-----TTCCGAGGTTTCGAATCCTCGTACCCCAGCCA  
>tdbD00008504 Escherichia coli\_K12 83333 Gln TTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATACCGGCA-----TTCCCTGGTTTCGAATCCAGGTACCCCAGCCA  
>tdbD00008505 Escherichia coli\_O157H7 83334 Gln CTG:  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGATTCTGATTCGGCA-----TTCCGAGGTTTCGAATCCTCGTACCCCAGCCA  
>tdbD00008506 Escherichia coli\_O157H7 83334 Gln TTG:  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATACCGGCA-----TTCCCTGGTTTCGAATCCAGGTACCCCAGCCA  
>tdbD00008511 Escherichia coli\_O157H7\_EDL933 155864 Gln CTG:  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGATTCTGATTCGGCA-----TTCCGAGGTTTCGAATCCTCGTACCCCAGCCA  
>tdbD00008508 Escherichia coli\_O157H7\_EDL933 155864 Gln TTG:  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATACCGGCA-----TTCCCTGGTTTCGAATCCAGGTACCCCAGCCA  
>tdbD00008511 Haemophilus influenzae\_Rd\_KW20 71421 Gln TTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCCCTGGTTTTGATCTCAGCA-----TTCCTAGGTTTCGAATCCTAGTACCCCAGCCA  
>tdbD00008512 Haemophilus influenzae\_Rd\_KW20 71421 Gln TTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATCTCAGCA-----TTCCTAGGTTTCGAATCCTAGTACCCCAGCCA  
>tdbD00008532 Listeria monocytogenes\_EGD-e 169963 Gln TTG

-TGGGCTATAGCCAAGC--GGT--AAGGCAACGGATTTTGATTCCGTCA-----TGCGCTGGTTTCAATCCAGCTAGCCCAG---  
>tdbD00008755 *Listeria\_monocytogenes\_str\_4b\_F2365\_265669* Gln TTG  
-TGGGCTATAGCCAAGC--GGT--AAGGCAACGGATTTTGATTCCGTCA-----TGCGCTGGTTTCAATCCAGCTAGCCCAG---  
>tdbD00008493 *Neisseria\_meningitidis\_Z2491\_122587* Gln TTG  
-TGGGGAGTTCGTAAGC--GGTT--AAGACTGGATTTTGATTCCAGCA-----TGCGAAGGTTTCAATCCTTCTCCAGCCAGCCA  
>tdbD00008558 *Salmonella\_enterica\_subsp\_enterica\_serovar\_Typhi\_str\_CT18\_220341* Gln CTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGATTTTGATTCCGGCA-----TTCCGAGGTTTCAATCCTCGTACCCAGCCAGCCA  
>tdbD00008559 *Salmonella\_enterica\_subsp\_enterica\_serovar\_Typhi\_str\_CT18\_220341* Gln TTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATACCGGCA-----TTCCCTGGTTTCAATCCAGGTACCCAGCCAGCCA  
>tdbD00008710 *Salmonella\_enterica\_subsp\_enterica\_serovar\_Typhi\_str\_Ty2\_209261* Gln CTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGATTTTGATTCCGGCA-----TTCCGAGGTTTCAATCCTCGTACCCAGCCAGCCA  
>tdbD00008709 *Salmonella\_enterica\_subsp\_enterica\_serovar\_Typhi\_str\_Ty2\_209261* Gln TTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATACCGGCA-----TTCCCTGGTTTCAATCCAGGTACCCAGCCAGCCA  
>tdbD00008549 *Salmonella\_typhimurium\_LT2\_99287* Gln CTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGATTTTGATTCCGGCA-----TTCCGAGGTTTCAATCCTCGTACCCAGCCAGCCA  
>tdbD00008550 *Salmonella\_typhimurium\_LT2\_99287* Gln TTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATACCGGCA-----TTCCCTGGTTTCAATCCAGGTACCCAGCCAGCCA  
>tdbD00008674 *Shigella\_flexneri\_2a\_str\_301\_198214* Gln CTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGATTTTGATTCCGGCA-----TTCCGAGGTTTCAATCCTCGTACCCAGCCAGCCA  
>tdbD00008673 *Shigella\_flexneri\_2a\_str\_301\_198214* Gln TTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATACCGGCA-----TTCCCTGGTTTCAATCCAGGTACCCAGCCAGCCA  
>tdbD00008547 *Yersinia\_pestis\_CO92\_214092* Gln CTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGATTTTGATTCCAGCA-----TTCCGAGGTTTCAATCCTCGTACCCAGCCAGCCA  
>tdbD00008548 *Yersinia\_pestis\_CO92\_214092* Gln TTG  
-TGGGATATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATCCTGGCA-----TTCCAGGTTTCAATCCTGGTATCCAGCCAGCCA  
>tdbD00008658 *Yersinia\_pestis\_KIM\_187410* Gln CTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGATTTTGATTCCAGCA-----TTCCGAGGTTTCAATCCTCGTACCCAGCCAGCCA  
>tdbD00008659 *Yersinia\_pestis\_KIM\_187410* Gln TTG  
-TGGGATATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATCCTGGCA-----TTCCAGGTTTCAATCCTGGTATCCAGCCAGCCA  
>tdbD00008748 *Yersinia\_pseudotuberculosis\_IP\_32953\_273123* Gln CTG  
-TGGGGTATCGCCAAGC--GGT--AAGGCACCGGATTTTGATTCCAGCA-----TTCCGAGGTTTCAATCCTCGTACCCAGCCAGCCA  
>tdbD00008749 *Yersinia\_pseudotuberculosis\_IP\_32953\_273123* Gln TTG  
-TGGGATATCGCCAAGC--GGT--AAGGCACCGGTTTTTGATCCTGGCA-----TTCCAGGTTTCAATCCTGGTATCCAGCCAGCCA  
>tdbD00009416 *Bacillus\_anthraxis\_str\_Sterne\_260799* Arg ACG  
-GCGCCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAGAG-----GTTAGGGGTTTCAATCCTCTCGGGCGGCCA  
>tdbD00009417 *Bacillus\_anthraxis\_str\_Sterne\_260799* Arg ACG  
-GCGCCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAGAG-----GTTAGGGGTTTCAATCCTCTCGGGCGGCCA  
>tdbD00009419 *Bacillus\_anthraxis\_str\_Sterne\_260799* Arg CCG  
-GCGCCCATAGCTCAGTC--GGAT--AGAGCGTGGTTTCCGGTACCAGT-----CT-----GCCGGGGGTTTCAATCCCTCTGGGGCGCG---  
>tdbD00009418 *Bacillus\_anthraxis\_str\_Sterne\_260799* Arg TCT  
-GTCCAGTAGCTCAGCC--GGAT--AGAGCATACGCCTTCTAAGCGTACG-----GTCGGGAGTTTCAATCCTCTCTGGGACG---  
>tdbD00009460 *Bacillus\_cereus\_ATCC\_10987\_222523* Arg ACG  
-GCGCCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAGAG-----GTTAGGGGTTTCAATCCTCTCGGGCGGCCA  
>tdbD00009461 *Bacillus\_cereus\_ATCC\_10987\_222523* Arg ACG  
-GCGCCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAGAG-----GTTAGGGGTTTCAATCCTCTCGGGCGGCCA  
>tdbD00009462 *Bacillus\_cereus\_ATCC\_10987\_222523* Arg ACG  
-GCGCCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAGAG-----GTTAGGGGTTTCAATCCTCTCGGGCGGCCA  
>tdbD00009463 *Bacillus\_cereus\_ATCC\_10987\_222523* Arg CCG  
-GCGCCCATAGCTCAGTC--GGAT--AGAGCGTGGTTTCCGGTACCAGT-----CT-----GCCGGGGGTTTCAATCCCTCTGGGGCGCG---  
>tdbD00009332 *Bacillus\_cereus\_ATCC\_14579\_226900* Arg ACG  
-GCGCCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAGAG-----GTTAGGGGTTTCAATCCTCTCGGGCGGCCA  
>tdbD00009333 *Bacillus\_cereus\_ATCC\_14579\_226900* Arg ACG  
-GCGCCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAGAG-----GTTAGGGGTTTCAATCCTCTCGGGCGGCCA  
>tdbD00009335 *Bacillus\_cereus\_ATCC\_14579\_226900* Arg CCG  
-GCGCCCATAGCTCAGTC--GGAT--AGAGCGTGGTTTCCGGTACCAGT-----CT-----GCCGGGGGTTTCAATCCCTCTGGGGCGCG---  
>tdbD00009334 *Bacillus\_cereus\_ATCC\_14579\_226900* Arg TCT  
-GTCCAGTAGCTCAGCC--GGAT--AGAGCATACGCCTTCTAAGCGTACG-----GTCGGGAGTTTCAATCCTCTCTGGGACG---  
>tdbD00002449 *Bacillus\_subtilis\_1423* Arg ACG  
-GCGCCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAAAAG-----GTTAGGGGTTTCAATCCTCTCGGGCGGCCA  
>tdbD00008817 *Bacillus\_subtilis\_subsp\_subtilis\_str\_168\_224308* Arg ACG  
-GCGCCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAAAAG-----GTTAGGGGTTTCAATCCTCTCGGGCGGCCA  
>tdbD00009496 *Bacillus\_thuringiensis\_serovar\_konkukian\_str\_97-27\_281309* Arg ACG  
-GCGCCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAGAG-----GTTAGGGGTTTCAATCCTCTCGGGCGGCCA  
>tdbD00009497 *Bacillus\_thuringiensis\_serovar\_konkukian\_str\_97-27\_281309* Arg ACG  
-GCGCCCGTAGCTCAATT--GGAT--AGAGCGTTTACTACGGATCAAGAG-----GTTAGGGGTTTCAATCCTCTCGGGCGGCCA  
>tdbD00009498 *Bacillus\_thuringiensis\_serovar\_konkukian\_str\_97-27\_281309* Arg CCG  
-GCGCCCATAGCTCAGTC--GGAT--AGAGCGTGGTTTCCGGTACCAGT-----CT-----GCCGGGGGTTTCAATCCCTCTGGGGCGCG---  
>tdbD00009382 *Bartonella\_henselae\_str\_Houston-1\_283166* Arg ACG  
-GCACCCGTAGCTCAGCT--GGAT--AGAGCACCAGACTACGAATCTGGGG-----GTCAGGAGTTTCAATCCTCTCTGGGTGCGCCA  
>tdbD00009502 *Bartonella\_quintana\_str\_Toulouse\_283165* Arg ACG  
-GCACCCGTAGCTCAGCT--GGAT--AGAGCACCAGACTACGAATCTGGGG-----GTCAGGAGTTTCAATCCTCTCTGGGTGCGCCA  
>tdbD00009504 *Bartonella\_quintana\_str\_Toulouse\_283165* Arg TCT  
-GGTCCCGTAGCTCAGCT--GGAT--AGAGCAACCGCCTTCTAAGCCGTGG-----GTCACAGGTTTCAATCCTGTCTGGGATCGCCA  
>tdbD00008898 *Borrelia\_burgdorferi\_B31\_24326* Arg GCG  
-GTGTCCATAGCTCAGTT--GGAT--AGAGCGTTAGATTGCGATTCTTAAG-----GTCGGAGGTTTCAAGTCTCTCTGGACACG---

>tdbD00008899 *Borrelia burgdorferi*\_B31 224326 Arg TCG  
-GCATCATAGCTCAATT-GGAT-AGAGCGCGGACTTCGAATCCGAAG-----GTTGCAGGTTTCGACTCCTGCTGAGTGCG---  
>tdbD00008900 *Borrelia burgdorferi*\_B31 224326 Arg TCT  
-GCACCAATAGCTCAATT-GGAT-AGAGCAACAGACTTCTAATCTGTAG-----GTTTTAGGTTTCGAGTCTTAATGGTGCG---  
>tdbD00009420 *Borrelia garinii*\_PBi 290434 Arg GCG  
-GTGTCCATAGCTCAGTT-GGAT-AGAGCGTTAGATTGCGATTCTTAAG-----GTCGGAGGTTCAAGTCTCTTGGACACG---  
>tdbD00009231 *Brucella suis*\_1330 204722 Arg ACG  
-GCACCCGTAGCTCAGCT-GGAT-AGAGCACCAGACTACGAATCTGGGG-----GTCAGAGGTTTCAATCCTTTCCGGTGCGCCA  
>tdbD00009232 *Brucella suis*\_1330 204722 Arg CCT  
-GGTCCCGTAGCTCAGTA-GGAT-AGAGCGACAGATTCCCTAATCTGTAG-----GTCACAGGTTTCGATTCTGTGCGGGATCACCA  
>tdbD00009233 *Brucella suis*\_1330 204722 Arg TCT  
-GGTCCCGTAGCTCAGTT-GGAT-AGAGCACCAGGCTTCTAAGCCGATG-----GTCGCAGGTTTCGAATCCTGCCGGATCGCCA  
>tdbD00009172 *Buchnera aphidicola*\_str.\_Sg (Schizaphis graminum) 198804 Arg ACG  
-GTACTCCGTAGCTCAGTT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAGGTTTCGAATCCTTCCGGATGCA---  
>tdbD00008905 *Caulobacter crescentus*\_CB15 190650 Arg ACG  
-GCGCCCGTAGCTCAGCT-GGAT-AGAGCATCAGACTACGAATCTGAGG-----GTCGGACGTTTCGAATCGTTCGGGGCGCGCCA  
>tdbD00008906 *Caulobacter crescentus*\_CB15 190650 Arg CCG  
-GCACCCGTAGCTCAGT-GGAT-AGAGCGTTGCCCTCCCTAAGCGAAG-----GTCACACGTTTCGAATCGTGTGCGGGTGCGCCA  
>tdbD00008811 *Chlamydia trachomatis*\_D/UW-3/CX 272561 Arg TCG  
-GCACCGATAGCTCAACT-GGAT-AGAGTACTGGCTTCGGACCAGGTG-----GTTGGAGGTTTCGAACCTCTTCGGTGCG---  
>tdbD00008812 *Chlamydia trachomatis*\_D/UW-3/CX 272561 Arg TCT  
-GGACCGATAGCTCAGT-GGAT-AGAGCATCCGCTTCTAAGCGAATG-----GTCGCAGGTTTCGAATCCTGCTCGGTCCG---  
>tdbD00008806 *Chlamydomydia pneumoniae*\_CWL029 115713 Arg ACG  
-GCACCGATAGCTCAGT-GGAT-AGAGTACTGGCTTCGAACCGAGGTG-----GTCAGAGGTTTCGAGTCTCTCTGGTGCG---  
>tdbD00008807 *Chlamydomydia pneumoniae*\_CWL029 115713 Arg CCT  
-GTCTCGTAGCTCAGTA-GGAT-AGAGCGGTTGCCCTCCCTAAGCGAAG-----GCCATGCGTTTCGAATCGCATCGAGGACG---  
>tdbD00008808 *Chlamydomydia pneumoniae*\_CWL029 115713 Arg TCG  
-GCACCGATAGCTCAATT-GGAT-AGAGTACTGGCTTCGGACCAGGTG-----GTTGGAGGTTTCGAGCCCTCTTCGGTGCG---  
>tdbD00008809 *Chlamydomydia pneumoniae*\_CWL029 115713 Arg TCT  
-GGACCGATAGCTCAGT-GGAT-AGAGCATTCGCTTCTAAGCGAATG-----GTCGCAGGTTTCGAGTCTCTCGGTCCG---  
>tdbD00008852 *Chlamydomydia pneumoniae*\_J138 138677 Arg ACG  
-GCACCGATAGCTCAGT-GGAT-AGAGTACTGGCTTCGAACCGAGGTG-----GTCAGAGGTTTCGAGTCTCTCTGGTGCG---  
>tdbD00008853 *Chlamydomydia pneumoniae*\_J138 138677 Arg CCT  
-GTCTCGTAGCTCAGTA-GGAT-AGAGCGGTTGCCCTCCCTAAGCGAAG-----GCCATGCGTTTCGAATCGCATCGAGGACG---  
>tdbD00008854 *Chlamydomydia pneumoniae*\_J138 138677 Arg TCG  
-GCACCGATAGCTCAATT-GGAT-AGAGTACTGGCTTCGGACCAGGTG-----GTTGGAGGTTTCGAGCCCTCTTCGGTGCG---  
>tdbD00008855 *Chlamydomydia pneumoniae*\_J138 138677 Arg TCT  
-GGACCGATAGCTCAGT-GGAT-AGAGCATTCGCTTCTAAGCGAATG-----GTCGCAGGTTTCGAGTCTCTCGGTCCG---  
>tdbD00009235 *Corynebacterium efficiens*\_YS-314 196164 Arg ACG  
-GCGCCCGTAGCTCAAC--GGAT-AGAGCATCTGACTACGGATCAGAAG-----GTTGGGGGTTTCGAATCCCTCCGGGCGCA---  
>tdbD00009178 *Corynebacterium glutamicum*\_ATCC 13032 196627 Arg ACG  
-GCGCCCGTAGCTCAAC--GGAT-AGAGCATCTGACTACGGATCAGAAG-----GTTGGGGGTTTCGAATCCCTCCGGGCGCA---  
>tdbD00009179 *Corynebacterium glutamicum*\_ATCC 13032 196627 Arg ACG  
-GCGCCCGTAGCTCAAC--GGAT-AGAGCATCTGACTACGGATCAGAAG-----GTTGGGGGTTTCGAATCCCTCCGGGCGCA---  
>tdbD00009181 *Corynebacterium glutamicum*\_ATCC 13032 196627 Arg CCG  
-GCCTCCGTAGCTCAGT-GGAT-AGAGCACCAGGTTTCCGGTACCAGAG-----GTCGTAGGTTTCGACTCCTATCGGGGGCA---  
>tdbD00009344 *Escherichia coli*\_CFT073 199310 Arg ACG  
-GCATCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAGGTTTCGAATCCTCCCGATGCACCA  
>tdbD00009345 *Escherichia coli*\_CFT073 199310 Arg CCG  
-GCGCCCGTAGCTCAGCT-GGAT-AGAGCGCTGCCCTCCGGAGGCAGAG-----GTCTCAGGTTTCGAATCCTGTGCGGGCGCGCCA  
>tdbD00009343 *Escherichia coli*\_CFT073 199310 Arg CCT  
-GTCCTCTTAGTTAAAT--GGAT-ATAACGAGCCCCCTCCTAAGGGCTAA-----T-TGCAGGTTTCGATCCTGCAGGGGACACCA  
>tdbD00009339 *Escherichia coli*\_CFT073 199310 Arg TCT  
-GCGCCCTTAGCTCAGTT-GGAT-AGAGCAACGACCTTCTAAGTCGTGG-----GCCCGAGGTTTCGAATCCTGCAGGGCGCGCCA  
>tdbD00008856 *Escherichia coli*\_K12 83333 Arg ACG  
-GCATCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAGGTTTCGAATCCTCCCGATGCACCA  
>tdbD00008857 *Escherichia coli*\_K12 83333 Arg CCG  
-GCGCCCGTAGCTCAGCT-GGAT-AGAGCGCTGCCCTCCGGAGGCAGAG-----GTCTCAGGTTTCGAATCCTGTGCGGGCGCGCCA  
>tdbD00008858 *Escherichia coli*\_K12 83333 Arg CCT  
-GTCCTCTTAGTTAAAT--GGAT-ATAACGAGCCCCCTCCTAAGGGCTAA-----T-TGCAGGTTTCGATCCTGCAGGGGACACCA  
>tdbD00008859 *Escherichia coli*\_K12 83333 Arg TCT  
-GCGCCCTTAGCTCAGTT-GGAT-AGAGCAACGACCTTCTAAGTCGTGG-----GCCCGAGGTTTCGAATCCTGCAGGGCGCGCCA  
>tdbD00008860 *Escherichia coli*\_O157H7 83334 Arg ACG:  
-GCATCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAGGTTTCGAATCCTCCCGATGCACCA  
>tdbD00008861 *Escherichia coli*\_O157H7 83334 Arg CCG:  
-GCGCCCGTAGCTCAGCT-GGAT-AGAGCGCTGCCCTCCGGAGGCAGAG-----GTCTCAGGTTTCGAATCCTGTGCGGGCGCGCCA  
>tdbD00008862 *Escherichia coli*\_O157H7 83334 Arg CCT:  
-GTCCTCTTAGTTAAAT--GGAT-ATAACGAGCCCCCTCCTAAGGGCTAA-----T-TGCAGGTTTCGATCCTGCAGGGGACACCA  
>tdbD00008871 *Escherichia coli*\_O157H7 83334 Arg TCT:  
-GCGCCCTTAGCTCAGTT-GGAT-AGAGCAACGACCTTCTAAGTCGTGG-----GCCCGAGGTTTCGAATCCTGCAGGGCGCGCCA  
>tdbD00008872 *Escherichia coli*\_O157H7\_EDL933 155864 Arg ACG:  
-GCATCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAGGTTTCGAATCCTCCCGATGCACCA  
>tdbD00008874 *Escherichia coli*\_O157H7\_EDL933 155864 Arg CCG:  
-GCGCCCGTAGCTCAGCT-GGAT-AGAGCGCTGCCCTCCGGAGGCAGAG-----GTCTCAGGTTTCGAATCCTGTGCGGGCGCGCCA  
>tdbD00008875 *Escherichia coli*\_O157H7\_EDL933 155864 Arg CCT:



-GTCCTCTTAGTTAAAT--GGAT-ATAACGAGCCCCCTCTAAGGGCTAA-----T-TGCAGGTTTCGATTCTCTGCAGGGGACACCA  
>tdbD00008878 Escherichia\_coli\_O157H7\_EDL933\_155864\_Arg\_TCT:  
-GCGTTTTTAGCTCAGCA-GGAC-AGAGCAATTGCCTTCTAAGCAATCG-----GTCAGTGGTTCGACTCCAGTACAACGCGCCA  
>tdbD00008879 Escherichia\_coli\_O157H7\_EDL933\_155864\_Arg\_TCT:  
-GCGTTTTTAGCTCAGCC-GGAC-AGAGCAATTGCCTTCTAAGCAATCG-----GTCAGTGGTTCGAACCCAGTACAACGCACCA  
>tdbD00008881 Escherichia\_coli\_O157H7\_EDL933\_155864\_Arg\_TCT:  
-GCGTTGTTAGCTCAGCC-GGAC-AGAGCAATTGCCTTCTAAGCAATCG-----GTCAGTGGTTCGACTCCACTACAACGCGCCA  
>tdbD00008882 Escherichia\_coli\_O157H7\_EDL933\_155864\_Arg\_TCT:  
-GCGTTGTTAGCTCAGCC-GGAC-AGAGCAATTGCCTTCTGAGCAATCG-----GTCAGTGGTTCGAATCCAGTACAACGCGCCA  
>tdbD00008883 Escherichia\_coli\_O157H7\_EDL933\_155864\_Arg\_TCT:  
-GCGTTGTTAGCTCAGCC-GGAC-AGAGCAATTGCCTTCTAAGCAATCG-----GTCAGTGGTTCGAATCCAGTACAACGCGCCA  
>tdbD00008884 Escherichia\_coli\_O157H7\_EDL933\_155864\_Arg\_TCT:  
-GCGTTGTTAGCTCAGCC-GGAC-AGAGCAATTGCCTTCTAAGCAATCG-----GTCAGTGGTTCGAATCCAGTACAACGCACCA  
>tdbD00008885 Haemophilus\_influenzae\_Rd\_KW20\_71421\_Arg\_ACG  
-GCGCCCTTAGCTCAGTT-GGAT-AGAGCAACGACCTTCTAAGTCGTGG-----GCCGCAGGTTTCGAATCCTGCAGGGCGCGCCA  
>tdbD00008886 Haemophilus\_influenzae\_Rd\_KW20\_71421\_Arg\_CCG  
-GCACCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCAGAGGTTTCGAATCCTCTCGGGTGCGCCA  
>tdbD00008887 Haemophilus\_influenzae\_Rd\_KW20\_71421\_Arg\_TCT  
-GCGTTCGTAGCTCAGTT-GGAT-AGAGCGTTGGCCTCCGGAGCCAAAG-----GTCGCAAGTTCGAATCTGTGCGAGCGCGCCA  
>tdbD00008888 Haemophilus\_influenzae\_Rd\_KW20\_71421\_Arg\_TCT  
-GCGCCCTTAGCTCAGCT-GGAT-AGAGCAACGCCCTTCTAAGGCGTGG-----GTCAAAGGTTTCGAATCCTTTAGGGCGTGCCA  
>tdbD00008889 Helicobacter\_pylori\_26695\_85962\_Arg\_CCT  
-GTCCTTGTAGCTCAGCT-GGAT-AGAGCGTATGATTCCTAATCGTAAG-----GTCGTGGGTTTCGAATCCCGCAAGGACACCA  
>tdbD00008887 Helicobacter\_pylori\_26695\_85962\_Arg\_GCG  
-GTGTCGTAGCTCAGCT-GAAT-AGAGCAACAGGTTGCGGTCTGTAG-----GTCGGGGGTTTGAATCCCTCCGAGCACACCA  
>tdbD00008888 Helicobacter\_pylori\_26695\_85962\_Arg\_TCG  
-GCGTTCGTAGCTCAATT-GGAT-AGAGCAACAGACTTCCGGATCTGGGG-----GTTAGGGGTTTCGACTCCCTTCGGGCGTACCA  
>tdbD00008889 Helicobacter\_pylori\_26695\_85962\_Arg\_TCT  
-GCGCTTGTAGCTCAGCT-GGAT-AGAGCAACAGCCTTCTAAGCCGTAG-----GTCGCAGGTTTCGAGTCTGCCAAGCGCACCA  
>tdbD00008890 Helicobacter\_pylori\_J99\_85963\_Arg\_CCT  
-GTCCTTGTAGCTCAGCT-GGAT-AGAGCGTATGATTCCTAATCGTAAG-----GTCGTGGGTTTCGAATCCCGCAAGGACACCA  
>tdbD00008891 Helicobacter\_pylori\_J99\_85963\_Arg\_GCG  
-GTGTCGTAGCTCAGCT-GAAT-AGAGCAACAGGTTGCGGTCTGTAG-----GTCGGGGGTTTGAATCCCTCCGAGCACACCA  
>tdbD00008892 Helicobacter\_pylori\_J99\_85963\_Arg\_TCG  
-GCGTTCGTAGCTCAATT-GGAT-AGAGCAACAGACTTCCGGATCTGGGG-----GTTAGGGGTTTCGACTCCCTTCGGGCGTACCA  
>tdbD00008893 Helicobacter\_pylori\_J99\_85963\_Arg\_TCT  
-GCGCTTGTAGCTCAGCT-GGAT-AGAGCAACAGCCTTCTAAGCCGTAG-----GTCGCAGGTTTCGAGTCTGCCAAGCGCACCA  
>tdbD00008955 Listeria\_monocytogenes\_EGD-e\_169963\_Arg\_ACG  
-GCGCCCATAGCTCAACT-GGAT-AGAGTACTTGACTACGAATCAAGCG-----GTTAGAGGTTTCGACTCCTCTTGGGCGCA---  
>tdbD00008958 Listeria\_monocytogenes\_EGD-e\_169963\_Arg\_CCG  
-GCCCTCGTGGTGCAAC--GGAT-AGCAGCTAAGATTCGGGTCTTTAAA-----A-TGGGGGTTTCGATTCCCTCCGAGGGCA---  
>tdbD00008957 Listeria\_monocytogenes\_EGD-e\_169963\_Arg\_CCT  
-GCCCATATAGTTAAAC--GGAT-ATAACAAGCCCCCTCTAAGGGCTAG-----T-TCGTGGTTTCGATTCCGCGTATGGGCG---  
>tdbD00008956 Listeria\_monocytogenes\_EGD-e\_169963\_Arg\_TCT  
-GTCCTGATAGCTCAGCT-GGAT-AGAGCAACGGCCTTCTAAGCCGTAG-----GTCGGGGGTTTCGAATCCCTCTCAGGACG---  
>tdbD00009470 Listeria\_monocytogenes\_str\_4b\_F2365\_265669\_Arg\_ACG  
-GCGCCCATAGCTCAACT-GGAT-AGAGTACTTGACTACGAATCAAGCG-----GTTAGAGGTTTCGACTCCTCTTGGGCGCA---  
>tdbD00009473 Listeria\_monocytogenes\_str\_4b\_F2365\_265669\_Arg\_CCG  
-GCCCTCGTGGTGCAAC--GGAT-AGCAGCTAAGATTCGGGTCTTTAAA-----A-TGGGGGTTTCGATTCCCTCCGAGGGCA---  
>tdbD00009472 Listeria\_monocytogenes\_str\_4b\_F2365\_265669\_Arg\_CCT  
-GCCCATATAGTTAAAC--GGAT-ATAACAAGCCCCCTCTAAGGGCTAG-----T-TCGTGGTTTCGATTCCGCGTATGGGCG---  
>tdbD00009471 Listeria\_monocytogenes\_str\_4b\_F2365\_265669\_Arg\_TCT  
-GTCCTGATAGCTCAGCT-GGAT-AGAGCAACGGCCTTCTAAGCCGTAG-----GTCGGGGGTTTCGAATCCCTCTCAGGACG---  
>tdbD00008848 Mycobacterium\_leprae\_TN\_272631\_Arg\_TCT  
-GCCTCCGTAGCTCAGGT-GGAT-AGAGCAAGGGCCTTCTAATCCCTAG-----GTCGCACGTTTCGAGTCGTGCCGGGGGCA---  
>tdbD00008824 Mycobacterium\_tuberculosis\_CDC1551\_83331\_Arg\_ACG  
-GCGCCCGTAGCTCAAC--GGAT-AGAGCATCTGACTACGGATCAGAAG-----GTTGGGAGTTTCGAATCTCTTCGGGCGCG---  
>tdbD00008825 Mycobacterium\_tuberculosis\_CDC1551\_83331\_Arg\_CCG  
-GCCCCGTAGCTCAGG--GGAT-AGAGCGTCTGCCTCCGGAGCAGAAG-----GCCGCAGGTTTCGAATCCTGCCGGGGGCA---  
>tdbD00008826 Mycobacterium\_tuberculosis\_CDC1551\_83331\_Arg\_CCT  
-GCCCTCGTAGCTCAGG--GGAT-AGAGCACGGCTCCTAAAGCCGGT-----GTCGCAGGTTTCGAATCCTGCCGGGGGCA---  
>tdbD00008827 Mycobacterium\_tuberculosis\_CDC1551\_83331\_Arg\_TCT  
-GCCTCCGTAGCTCAGGT-GGAT-AGAGCAAGGGCCTTCTAATCCCTAG-----GTCGCACGTTTCGAGTCGTGCCGGGGGCA---  
>tdbD00009398 Mycobacterium\_tuberculosis\_H37Rv\_83332\_Arg\_ACG  
-GCGCCCGTAGCTCAAC--GGAT-AGAGCATCTGACTACGGATCAGAAG-----GTTGGGAGTTTCGAATCTCTTCGGGCGCG---  
>tdbD00009396 Mycobacterium\_tuberculosis\_H37Rv\_83332\_Arg\_CCG  
-GCCCCGTAGCTCAGG--GGAT-AGAGCGTCTGCCTCCGGAGCAGAAG-----GCCGCAGGTTTCGAATCCTGCCGGGGGCA---  
>tdbD00009395 Mycobacterium\_tuberculosis\_H37Rv\_83332\_Arg\_CCT  
-GCCCTCGTAGCTCAGG--GGAT-AGAGCACGGCTCCTAAAGCCGGT-----GTCGCAGGTTTCGAATCCTGCCGGGGGCA---  
>tdbD00009397 Mycobacterium\_tuberculosis\_H37Rv\_83332\_Arg\_TCT  
-GCCTCCGTAGCTCAGGT-GGAT-AGAGCAAGGGCCTTCTAATCCCTAG-----GTCGCACGTTTCGAGTCGTGCCGGGGGCA---  
>tdbD00008913 Mycoplasma\_genitalium\_G37\_243273\_Arg\_CCT  
-CTTCCCTTGGTGCAAT--GGAC-AGCACAAGTCTGCTAATCAGTAA-----A-TAGAGGTTCAACTCCTCTAGGGAAGGCCA  
>tdbD00008914 Mycoplasma\_genitalium\_G37\_243273\_Arg\_GCG  
-GTCATCATAGCTCAATA-GGAC-AGAGTATCAGCTTGCGGAGCTGAG-----GTTACAGGTTTCGATTCTGTGGTGAGGCCA

>tdbD00008915 *Mycoplasma genitalium* G37 243273 Arg TCG  
-GCGCCCATAGCTCAATC-GGAT-AGAGTGTCTGGCTTCGGACCAGAAAG-----GTTATGGGTTCAAGTCTATTTGGGCGCGCCA  
>tdbD00002425 *Mycoplasma mycoides* 2102 Arg ACG  
-GCGCCCGTAGATCAATT-GGAT-AGATCGCTTGACTACGGATCAAAAAG-----GTTGGGGGTTTCGAGTCCCTCCGGGCGCACCA  
>tdbD00002426 *Mycoplasma mycoides* 2102 Arg TCT  
-GCCCATGTAGCTCAGTA-GGAT-AGAGCACGCGCCTTCTAAGCGGTAG-----GTCGGAAGTTTCGAGCCTTCTCGTGGGCACCA  
>tdbD00002427 *Mycoplasma pneumoniae* 2104 Arg GCG  
-GTCATCATAGCTCAATA-GGAC-AGAGTATCAGCTTTCGGGAGCTGAGG-----GTTACAGGTTTCGATTCTGTGTTGGTACGCCA  
>tdbD00008918 *Mycoplasma pneumoniae* M129 272634 Arg GCG  
-GTCATCATAGCTCAATA-GGAC-AGAGTATCAGCTTTCGGGAGCTGAGG-----GTTACAGGTTTCGATTCTGTGTTGGTACGCCA  
>tdbD00008919 *Mycoplasma pneumoniae* M129 272634 Arg TCG  
-GCGCCCATAGCTCAATT-GGAT-AGAGTGTCTGGCTTCGGACCAGAAAG-----GTTATGGGTTCAAGTCTATTTGGGCGCGCCA  
>tdbD00008829 *Neisseria meningitidis* MC58 122586 Arg ACG  
-GCACCCGTAGCTCAGTT-GGAT-AGAGTATCTGGCTTCGGACCAGAGG-----GTTACAGGTTTCGATTCTGTGTTGGTACGCCA  
>tdbD00008833 *Neisseria meningitidis* Z2491 122587 Arg ACG  
-GCACCCGTAGCTCAGTT-GGAT-AGAGTATCTGGCTTCGGACCAGAGG-----GTTACAGGTTTCGATTCTGTGTTGGTACGCCA  
>tdbD00008834 *Neisseria meningitidis* Z2491 122587 Arg CCT  
-TCTCGCCGTAGCTCAACC-GGAT-AGAAGTATGCCTCCTAAGCGTAAA-----A-TACAGGTTTCGATTCTGTGTTGGCGAGG---  
>tdbD00008835 *Neisseria meningitidis* Z2491 122587 Arg TCT  
-GCGCCCGTAGCTCAACC-GGAT-AGAGCACCGACCTTCTAAGTTCGGGG-----GTTACAGGTTTCGATTCTGTGTTGGCGGTGCCA  
>tdbD00008921 *Pasteurella multocida* subsp. *multocida* str. Pm70 272843 Arg ACG  
-GCACCCGTAGCTCAGTT-GGAT-AGAGTACTCGGCTACGAACCGAGAG-----GTCAGAGGTTTCGAACTCCTCTCGGGTGCGCCA  
>tdbD00009406 *Photobacterium luminescens* subsp. *laumondii* T101 243265 Arg CCG  
-GCGCCCGTAGCTCAGCT-GGAT-AGAGCGCTGCCCTCCGGAGGCAGAG-----GTCTCAGGTTTCGAACTCCTGTGTTGGCGGTGCCA  
>tdbD00009435 *Porphyromonas gingivalis* W83 242619 Arg ACG  
-GGCCGCGTAGCTCAACT-GAAT-AGAGTACTGACTACGGATACGGCCG-----GTTACAGGTTTGAATCCTGTGTTGGCGGTCA---  
>tdbD00009409 *Rhodopseudomonas palustris* CGA009 258594 Arg CCG  
-GCACCCGTAGCTCAGCT-GGAT-AGAGCGTTGCCCTCCGAAAGCAAG-----GTCACACGTTTCGAACTCCTGTGTTGGCGGTGCCA  
>tdbD00009407 *Rhodopseudomonas palustris* CGA009 258594 Arg CCT  
-GGTCCCGTAGCTCAGCC-GGAT-AGAGCGCGGTTTCTAACCCTGAG-----GTCGGATGTTTCGAGTTCATCCCGGGATGCGCCA  
>tdbD00009411 *Rhodopseudomonas palustris* CGA009 258594 Arg TCG  
-GCGCTCGTAGCTCAGCT-GGAT-AGAGCATCGGATTTTCGATTCCGAGG-----GTCGGAGGTTTCGAACTCCTTCGAGCGCGCCA  
>tdbD00009175 *Rickettsia prowazekii* str. Madrid E 272947 Arg ACG  
-GCACCCGTAGCTCAATT-GGAT-AGAGTATATGACTACGGATCATAAG-----GTTAGGGGTTTCGACTCCTCTCGGGTGCGCCA  
>tdbD00009177 *Rickettsia prowazekii* str. Madrid E 272947 Arg TCT  
-GCACCCCTTAGCTCAGCT-GGAT-AGAGCAACAGATTTCTAATCTGTGG-----GTCAGAGGTTTCGAACTCCTTTAGGGTGCGCCA  
>tdbD00009439 *Rickettsia typhi* str. Wilmington 257363 Arg ACG  
-GCACCCGTAGCTCAATT-GGAT-AGAGTATATGACTACGGATCATAAG-----GTTAGGGGTTTCGACTCCTCTCGGGTGCGCCA  
>tdbD00009438 *Rickettsia typhi* str. Wilmington 257363 Arg CCG  
-GCATTGCTAGCTCAGTT-GGAT-AGAGCATTTGCCCTCCGAAAGCAAG-----GTCATTGGTTTCAAATCCAATCGAATGCACCA  
>tdbD00009440 *Rickettsia typhi* str. Wilmington 257363 Arg TCT  
-GCACCCCTTAGCTCAGCT-GGAT-AGAGCAACAGATTTCTAATCTGTGG-----GTCAGAGGTTTCGAACTCCTTTAGGGTGCGCCA  
>tdbD00009021 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. CT18 220341 Arg ACG  
-GCATCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAGGTTTCGAACTCCTCCGGATGCACCA  
>tdbD00009022 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. CT18 220341 Arg CCG  
-GCATCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAGGTTTCGAACTCCTCCGGATGCACCA  
>tdbD00009354 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. Ty2 209261 Arg ACG  
-GCATCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAGGTTTCGAACTCCTCCGGATGCACCA  
>tdbD00009355 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. Ty2 209261 Arg CCG  
-GCATCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAGGTTTCGAACTCCTCCGGATGCACCA  
>tdbD00009350 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. Ty2 209261 Arg CCT  
-GTCCCTTAGTTAAAT--GGAT-ATAACGAGCCCTCCTAAGGGCTAG-----T-TGCAGGTTTCGATTCTGCAGGGGACACCA  
>tdbD00009352 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. Ty2 209261 Arg TCT  
-CCGCCATTAGCTCAACC-GGAT-AGAGCATAGAGCTTCTACTCTAAG-----GTTCCGGGTTTCAATCCTCGATGGCGGACCA  
>tdbD00009353 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. Ty2 209261 Arg TCT  
-GCGCCCTTAGCTCAGTT-GGAT-AGAGCAACGCTTCTAAGCCGTGG-----GTCGAGGTTTCGAACTCCTGCAGGGCGCGCCA  
>tdbD00002454 *Salmonella typhimurium* 602 Arg CCG  
-GCGCCCGTAGCTCAGCT-GGAT-AGAGCGCTGCCCTCCGGAGGCAGAG-----GTCTCAGGTTTCGAACTCCTGTGTTGGCGGTACCA  
>tdbD00008999 *Salmonella typhimurium* LT2 99287 Arg ACG  
-GCATCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAGGTTTCGAACTCCTCCGGATGCACCA  
>tdbD00009000 *Salmonella typhimurium* LT2 99287 Arg CCG  
-GCGCCCGTAGCTCAGCT-GGAT-AGAGCGCTGCCCTCCGGAGGCAGAG-----GTCTCAGGTTTCGAACTCCTGTGTTGGCGGTACCA  
>tdbD00008997 *Salmonella typhimurium* LT2 99287 Arg CCT  
-GTCCCTTAGTTAAAT--GGAT-ATAACGAGCCCTCCTAAGGGCTAG-----T-TGCAGGTTTCGATTCTGCAGGGGACACCA  
>tdbD00008996 *Salmonella typhimurium* LT2 99287 Arg TCT  
-CCGCCATTAGCTCAACC-GGAT-AGAGCATAGAGCTTCTACTCTAAG-----GTTCCGGGTTTCAATCCTCGATGGCGGACCA  
>tdbD00009265 *Shigella flexneri* 2a str. 301 198214 Arg ACG  
-GCATCCGTAGCTCAGCT-GGAT-AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAGGTTTCGAACTCCTCCGGATGCACCA  
>tdbD00009263 *Shigella flexneri* 2a str. 301 198214 Arg CCG  
-GCGCCCGTAGCTCAGCT-GGAT-AGAGCGCTGCCCTCCGGAGGCAGAG-----GTCTCAGGTTTCGAACTCCTGTGTTGGCGGTGCCA  
>tdbD00009259 *Shigella flexneri* 2a str. 301 198214 Arg CCT  
-GTCCTCTTAGTTAAAT--GGAT-ATAACGAGCCCTCCTAAGGGCTAA-----T-TGCAGGTTTCGATTCTGCAGGGGACACCA  
>tdbD00009260 *Shigella flexneri* 2a str. 301 198214 Arg TCT  
-GCGCCCTTAGCTCAGTT-GGAT-AGAGCAACGACCTTCTAAGTCGTGG-----GCCGAGGTTTCGAACTCCTGCAGGGCGCGCCA  
>tdbD00009415 *Staphylococcus aureus* subsp. *aureus* MRSA252 282458 Arg ACG

-GCGCCCGTAGCTCAATT-GGAT-AGAGCGTTTGACTACGGATCAAGAG-----GTTATGGGTTTCGACTCCTATCGGGCGCG---  
>tdbD00009183 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620 Arg ACG  
-GCGCCCGTAGCTCAATT-GGAT-AGAGCGTTTGACTACGGATCAAGAG-----GTTATGGGTTTCGACTCCTATCGGGCGCGCCA  
>tdbD00009186 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620 Arg ACG  
-GCGCCCGTAGCTCAATT-GGAT-AGAGCGTTTGACTACGGATCAAGAG-----GTTATGGGTTTCGACTCCTATCGGGCGCG---  
>tdbD00009185 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620 Arg TCT  
-GTCCTGGTAGCTCAGCT-GGAT-AGAGCAATGGCCTTCTAAGCCATCG-----GTCGGGGGTTTCGAATCCCTCCCAGGACG---  
>tdbD00008841 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879 Arg ACG  
-GCGCCCGTAGCTCAATT-GGAT-AGAGCGTTTGACTACGGATCAAGAG-----GTTATGGGTTTCGACTCCTATCGGGCGCG---  
>tdbD00008842 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879 Arg ACG  
-GCGCCCGTAGCTCAATT-GGAT-AGAGCGTTTGACTACGGATCAAGAG-----GTTATGGGTTTCGACTCCTATCGGGCGCGCCA  
>tdbD00008843 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879 Arg CCG  
-CTCCTTGTGGTGAAT--GGAT-AACACGTAAGATTCGGTTCTTAAAG-----A-TAGGGGTTCAATTCCCTTCAAGGAGG---  
>tdbD00008844 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879 Arg TCT  
-GTCCTGGTAGCTCAGCT-GGAT-AGAGCAATGGCCTTCTAAGCCATCG-----GTCGGGGGTTTCGAATCCCTCCCAGGACG---  
>tdbD00009296 Staphylococcus\_epidermidis\_ATCC\_12228\_176280 Arg TCT  
-GTCCTGGTAGCTCAGCT-GGAT-AGAGCAATGGCCTTCTAAGCCATCG-----GTCGGGGGTTTCGAATCCCTCCCAGGACG---  
>tdbD00009187 Streptococcus\_agalactiae\_NEM316\_211110 Arg ACG  
-GCACCCCTTAGCTCAACT-GGAT-AGAGTACCTGACTACGAATCAGGCG-----GTTAGAGGTTTCGACTCCTCTAGGGTGCA---  
>tdbD00009189 Streptococcus\_agalactiae\_NEM316\_211110 Arg CCG  
-CCATCTTTAGTGAAT--GGAT-ATCACACAAGATTCGGTTCTTGGG-----A-TAGGGGTTTCGATTCCCTTAAAGATGGA---  
>tdbD00009188 Streptococcus\_agalactiae\_NEM316\_211110 Arg CCT  
-GTCCCTTTAGTCAAT--GGAT-ATAACAACCTCCCTCCTAAGGAGTAA-----T-TGCTGGTTTCGATTCCGGCAGGGGACA---  
>tdbD00009190 Streptococcus\_agalactiae\_NEM316\_211110 Arg TCT  
-GGTTCATAGCTCAGCT-GGAT-AGAGCATTCGCCTTCTAAGCGAAGC-----GTCGCAGGTTTCGAATCCTTGCTGGAATCA---  
>tdbD00008973 Streptococcus\_pneumoniae\_TIGR4\_170187 Arg ACG  
-GCACCCCTTAGCTCAACT-GGAT-AGAGTACCTGACTACGAATCAGGCG-----GTTAGAGGTTTCGACTCCTCTAGGGTGCA---  
>tdbD00008974 Streptococcus\_pneumoniae\_TIGR4\_170187 Arg TCT  
-GGTTCATAGCTCAGCT-GGAT-AGAGCATTCGCCTTCTAAGCGAAGC-----GTCGCAGGTTTCGAATCCTTGCTGGGATCA---  
>tdbD00008966 Streptococcus\_pyogenes\_M1\_GAS\_160490 Arg ACG  
-GCACCCCTTAGCTCAACT-GGAT-AGAGTACCTGACTACGAATCAGGCG-----GTTAGAGGTTTCGACTCCTCTAGGGTGCA---  
>tdbD00008967 Streptococcus\_pyogenes\_M1\_GAS\_160490 Arg ACG  
-GCACCCCTTAGCTCAACT-GGAT-AGAGTACCTGACTACGAATCAGGCG-----GTTAGAGGTTTCGACTCCTCTAGGGTGCA---  
>tdbD00008969 Streptococcus\_pyogenes\_M1\_GAS\_160490 Arg CCG  
-CCACCTTTAGTGAAT--GGAT-ATCACGTAAGATTCGGTTCTTGGAG-----A-TGGGGGTTTCGATTCCCTCAAGGTGGA---  
>tdbD00008970 Streptococcus\_pyogenes\_M1\_GAS\_160490 Arg TCT  
-GGTTCATAGCTCAGCT-GGAT-AGAGCATTCGCCTTCTAAGCGAAGC-----GTCGCAGGTTTCGAATCCTTGCTGGGATCA---  
>tdbD00009191 Streptococcus\_pyogenes\_MGAS315\_198466 Arg ACG  
-GCACCCCTTAGCTCAACT-GGAT-AGAGTACCTGACTACGAATCAGGCG-----GTTAGAGGTTTCGACTCCTCTAGGGTGCA---  
>tdbD00009193 Streptococcus\_pyogenes\_MGAS315\_198466 Arg CCG  
-CCACCTTTAGTGAAT--GGAT-ATCACGTAAGATTCGGTTCTTGGAG-----A-TGGGGGTTTCGATTCCCTCAAGGTGGA---  
>tdbD00009192 Streptococcus\_pyogenes\_MGAS315\_198466 Arg CCT  
-GACCCCTTAGTTCAT--GGAT-ATAACAACCTCCCTCCTAAGGAGTAG-----T-TGCTGGTTTCGATTCCGGCAGGGGTCA---  
>tdbD00009323 Streptococcus\_pyogenes\_SSI-1\_193567 Arg ACG  
-GCACCCCTTAGCTCAACT-GGAT-AGAGTACCTGACTACGAATCAGGCG-----GTTAGAGGTTTCGACTCCTCTAGGGTGCA---  
>tdbD00009324 Streptococcus\_pyogenes\_SSI-1\_193567 Arg ACG  
-GCACCCCTTAGCTCAACT-GGAT-AGAGTACCTGACTACGAATCAGGCG-----GTTAGAGGTTTCGACTCCTCTAGGGTGCA---  
>tdbD00009325 Streptococcus\_pyogenes\_SSI-1\_193567 Arg CCG  
-CCACCTTTAGTGAAT--GGAT-ATCACGTAAGATTCGGTTCTTGGAG-----A-TGGGGGTTTCGATTCCCTCAAGGTGGA---  
>tdbD00009326 Streptococcus\_pyogenes\_SSI-1\_193567 Arg CCT  
-GACCCCTTAGTTCAT--GGAT-ATAACAACCTCCCTCCTAAGGAGTAG-----T-TGCTGGTTTCGATTCCGGCAGGGGTCA---  
>tdbD00009327 Streptococcus\_pyogenes\_SSI-1\_193567 Arg TCT  
-GGTTCATAGCTCAGCT-GGAT-AGAGCATTCGCCTTCTAAGCGAAGC-----GTCGCAGGTTTCGAATCCTTGCTGGGATCA---  
>tdbD00009248 Streptomyces\_coelicolor\_A3(2)\_100226 Arg ACG  
-GCACCTGTAGCTTAAC--GGAT-AGAGCATCTGACTACGGATCAGAAG-----GTTGCAGGTTTCGAATCCTGCCGAGTGCA---  
>tdbD00009250 Streptomyces\_coelicolor\_A3(2)\_100226 Arg CCG  
-GCCCCCGTAGCTCAGG--GGAT-AGAGCAACGGCCTCCGGAGCCGCTGT-----G-CGCAGGTTTCGAATCCTGCCGGGGGCA---  
>tdbD00009249 Streptomyces\_coelicolor\_A3(2)\_100226 Arg TCT  
-GCCCCCGTAGCTCAGT--GGAT-AGAGCAGGCGCCTTCTAAGCGCTTG-----GCCGCAGGTTTCGAGTCTGCCGGGGGCG---  
>tdbD00002463 Streptomyces\_venezuelae\_54571 Arg CCT  
-GCCTTCGTAGCTCAGG--GGAT-AGAGCACCGCTCTCCTAAGCGGGT-----GTCGCAGGTTTCGAATCCTGCCGGGGGACCA  
>tdbD00008934 Synechocystis\_sp.\_PCC\_6803\_1148 Arg ACG  
-GGGCTGTAGCTTAGT--GGATTAGAGCGCGTGGCTACGGACCCAGAG-----GTCGGGGGTTTCGAGTCCCTCCAAGCCCG---  
>tdbD00008935 Synechocystis\_sp.\_PCC\_6803\_1148 Arg CCG  
-GGACACGTAGCTCAGT--GGAT-AGAGCATCAGGTTCGGTCTTGGAG-----GTCGGGGGTTTCGAATCCCTCCGTGTTCG---  
>tdbD00008936 Synechocystis\_sp.\_PCC\_6803\_1148 Arg CCT  
-GAGGTGTAGCTCAGAC--GGAT-AGAGCAAGCGCCTCCTAAGCGCTGG-----GCCGCGGTTTCGACTCCGGCCAACCTCG---  
>tdbD00008937 Synechocystis\_sp.\_PCC\_6803\_1148 Arg TCT  
-GGGTGCTAGCTCAGT--GGAT-AGAGCATCCGCCTTCTAAGCGGACG-----GTCGCAGGTTTCGAATCCTGCCGCACCCG---  
>tdbD00008924 Treponema\_pallidum\_subsp.\_pallidum\_str.\_Nichols\_243276 Arg CCG  
-GGAAGATTAGCTCATTC--GGAT-AGAGCGTTGGCCTCCGGAGCCAAAG-----GCGGTGGGTTCAATCCCGCATCTTCCA---  
>tdbD00008925 Treponema\_pallidum\_subsp.\_pallidum\_str.\_Nichols\_243276 Arg CCT  
-GATCCATTAGCTCAGC--GGAG-AGAGCGGCGCCTCCTAAGCGGACG-----GTCGGACGTTCAAGTCGTCATGGATCA---  
>tdbD00008926 Treponema\_pallidum\_subsp.\_pallidum\_str.\_Nichols\_243276 Arg GCG  
-GAGACTATAGCTCAGT--GGAT-AGAGTGTGATTCGGGATCTGAAG-----GTCGACGGTTTCGAATCCGCCTAGTCTCA---

>tdbD00008927 *Treponema pallidum* subsp. *pallidum* str. *Nichols* 243276 Arg TCG  
-GCGCTCGTAGCTCAGGT--GGAT--AGAGCAACAGACTTCGAATCTGTAG-----GTCGCACGTTCAAGTCTGTGCGGGCGCA---  
>tdbD00008928 *Treponema pallidum* subsp. *pallidum* str. *Nichols* 243276 Arg TCT  
-GGGATCATAGCTCACCC--GGAT--AGAGCGACTGCCTTCTAAGCAGTAG-----GGAGGGGGTTCGAGTCCCTCTGGTCCCA---  
>tdbD00009306 *Tropheryma whipplei* TW08/27 218496 Arg ACG  
-GCGCCCGTAGCTCAACT--GGAT--AGAGCATCTGACTACGGATCAGAAG-----GTTGGGGGTTTCAATCCCTTCCGGGCGCG---  
>tdbD00009304 *Tropheryma whipplei* TW08/27 218496 Arg CCG  
-GCCCCATAGCTCAGG--GGAT--AGAGCGTCTGCCTCCGGAGCAGAAG-----GCCGTGGGTTCAAATCCCGTGGGGGCG---  
>tdbD00009305 *Tropheryma whipplei* TW08/27 218496 Arg CCT  
-GCCTCTGTAGCTCAAT--GGA--AGAGCGGTTCCCGTCCCTAAGGAAATG-----GTTGGGGGTTTCGAGTCCCTCCAGGGGCG---  
>tdbD00009303 *Tropheryma whipplei* TW08/27 218496 Arg TCT  
-GCCCTCGTAGCTCAGC--GGAT--AGAGCAGAAGACTTCTAATCTTTGT-----GTCGCAGGTTTCGATTCTGTGCGGGGCG---  
>tdbD00009210 *Xanthomonas campestris* pv. *campestris* str. *ATCC 33913* 190485 Arg ACG  
-GCGCCCGTAGCTCAGTT--GGAT--AGAGTACCTGGCTACGAACCGAGCG-----GTCGGGAGTTTCAATCTCTCCGGGCGCACCA  
>tdbD00009208 *Xanthomonas campestris* pv. *campestris* str. *ATCC 33913* 190485 Arg CCG  
-GCGCTCGTAGCTCAGC--GGAT--AGAGTAGTGGCTTCCGAAGCCATTG-----GTCGGGGGTTTCAATCCCTCCGGGCGCACCA  
>tdbD00009211 *Xanthomonas campestris* pv. *campestris* str. *ATCC 33913* 190485 Arg CCT  
-GCACCCATAGCTCAGT--GGAT--AGAGCTCCCCCTCCTAAGGGAAAG-----GTCGCCCGTTCGAATCGGGCCGGGGTCCACCA  
>tdbD00009209 *Xanthomonas campestris* pv. *campestris* str. *ATCC 33913* 190485 Arg TCT  
-GCGCCCGTAGCTCAACC--GGAT--AGAGCACCGCCTTCTAAGCCGCG-----GTTACAGGTTTCGAGTCTGTGCGGGCGGCCA  
>tdbD00009309 *Xylella fastidiosa* Temeculal 183190 Arg ACG  
-GCGCCCGTAGCTCAGT--GGAT--AGAGTACCTGGCTACGAACCGAGCG-----GTCGGGAGTTTCAATCTCTCCGGGCGGCCA  
>tdbD00009307 *Xylella fastidiosa* Temeculal 183190 Arg CCG  
-GCGCTCGTAGCTCAGT--GGATAAGAGTAGTGGCTTCCGAAGCCATTG-----GTCGGGGGTTTCAATCCCTCCGGGCGGCCA  
>tdbD00009310 *Xylella fastidiosa* Temeculal 183190 Arg TCT  
-GCGCCCGTAGCTCAATCGGAATAAGAGCACCGCCCTTCTAAGCCGGGG-----GTTGCAGGTTTCGAGTCTGTGCGGGTGCGCCA  
>tdbD00008992 *Yersinia pestis* CO92 214092 Arg ACG  
-GCACCCATAGCTCAGCT--GGAT--AGAGTACTCGGCTACGAACCTGAGCG-----GTCGGAAGTTTCAATCTTCTGGGTGCACCA  
>tdbD00008993 *Yersinia pestis* CO92 214092 Arg ACG  
-GCACCCATAGCTCAGCT--GGAT--AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAAGTTTCAATCTTCTGGGTGCACCA  
>tdbD00008994 *Yersinia pestis* CO92 214092 Arg CCG  
-GCGCCCGTAGCTCAGCT--GGAT--AGAGCGCTGCCCTCCGGAGGCAGAG-----GTCTCAGGTTTCAATCTGTGCGGGCGCACCA  
>tdbD00008990 *Yersinia pestis* CO92 214092 Arg CCT  
-GTCCCCGTAGTTAAAC--GGAT--ATAACAAGCCCCCTCCTAAGGGCTAG-----T-TACTGGTTTCGATTCCAGTCCGGGACACCA  
>tdbD00008991 *Yersinia pestis* CO92 214092 Arg TCT  
-GCGCCCTTAGCTCAGTT--GGAT--AGAGCAACGGCCTTCTAAGCCGTAG-----GTCACAGGTTTCGAGCCCTGTAGGGCGTACCA  
>tdbD00009221 *Yersinia pestis* KIM 187410 Arg ACG  
-GCACCCATAGCTCAGCT--GGAT--AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAAGTTTCAATCTTCTGGGTGCACCA  
>tdbD00009222 *Yersinia pestis* KIM 187410 Arg ACG  
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>tdbD00009220 *Yersinia pestis* KIM 187410 Arg CCG  
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>tdbD00009224 *Yersinia pestis* KIM 187410 Arg CCT  
-GTCCCCGTAGTTAAAC--GGAT--ATAACAAGCCCCCTCCTAAGGGCTAG-----T-TACTGGTTTCGATTCCAGTCCGGGACACCA  
>tdbD00009223 *Yersinia pestis* KIM 187410 Arg TCT  
-GCGCCCTTAGCTCAGTT--GGAT--AGAGCAACGGCCTTCTAAGCCGTAG-----GTCACAGGTTTCGAGCCCTGTAGGGCGTACCA  
>tdbD00009453 *Yersinia pseudotuberculosis* IP 32953 273123 Arg ACG  
-GCACCCATAGCTCAGCT--GGAT--AGAGTACTCGGCTACGAACCGAGCG-----GTCGGAAGTTTCAATCTTCTGGGTGCACCA  
>tdbD00009452 *Yersinia pseudotuberculosis* IP 32953 273123 Arg CCG  
-GCGCCCGTAGCTCAGCT--GGAT--AGAGCGCTGCCCTCCGGAGGCAGAG-----GTCTCAGGTTTCAATCTGTGCGGGCGCACCA  
>tdbD00009455 *Yersinia pseudotuberculosis* IP 32953 273123 Arg CCT  
-GTCCCCGTAGTTAAAC--GGAT--ATAACAAGCCCCCTCCTAAGGGCTAG-----T-TACTGGTTTCGATTCCAGTCCGGGACACCA  
>tdbD00009454 *Yersinia pseudotuberculosis* IP 32953 273123 Arg TCT  
-GCGCCCTTAGCTCAGTT--GGAT--AGAGCAACGGCCTTCTAAGCCGTAG-----GTCACAGGTTTCGAGCCCTGTAGGGCGTACCA  
>tdbD00010131 *Bacillus anthracis* str. *Sterne* 260799 Ser GGA  
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>tdbD00010179 *Bacillus cereus* ATCC 10987 222523 Ser GGA  
-GGAGAGCTGTCCGAGTT--GGCCGAAGGAGCAGGATTGGAAATCGTGTATACGTC--ACA--AGCGTAT--CAAGGGTTTCAATCCCTTGTCTCCGCCA  
>tdbD00009591 *Bacillus subtilis* subsp. *subtilis* str. 168 224308 Ser GGA  
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>tdbD00009593 *Bacillus subtilis* subsp. *subtilis* str. 168 224308 Ser TGA  
-GGAGGAATACCCAAGTCTGGCTGAAGGGATCGGTCTTGAACCCGACAGGGTG--TCAA--AGCCCG--CGGGGTTTCAATCCCTTCTCCGCCA  
>tdbD00010214 *Bacillus thuringiensis* serovar *konkukian* str. 97-27 281309 Ser GGA  
-GGAGAGCTGTCCGAGTT--GGCCGAAGGAGCAGGATTGGAAATCGTGTATACGTC--ACA--AGCGTAT--CAAGGGTTTCAATCCCTTGTCTCCGCCA  
>tdbD00010223 *Bartonella quintana* str. *Toulouse* 283165 Ser GCT  
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>tdbD00009649 *Borrelia burgdorferi* B31 224326 Ser GCT  
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>tdbD00009650 *Borrelia burgdorferi* B31 224326 Ser GGA  
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>tdbD00010136 *Borrelia garinii* PBI 290434 Ser TGA  
-GGAGAGGTGGCAGAGT--GGTTTAAATGCTACGGCTTGAACCCGTTGTAGGT---GTAA--GCCTAC--CGTGAAGTTTCAATCTCACCTCTCCG---  
>tdbD00009973 *Brucella suis* 1330 204722 Ser CGA  
-GGAGAGGTGGCTGAGT--GGTTGAAAGCACCGCACTCGAAATCGGGCATGGGG---GCAA--CTCCAT--CGGGGTTTCAATCCCTCCCTCTCCGCCA  
>tdbD00009971 *Brucella suis* 1330 204722 Ser GCT

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>tdbD00009974 Brucella\_suis\_1330\_204722 Ser TGA  
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>tdbD00009582 Chlamydia\_trachomatis\_D/UW-3/CX\_272561 Ser CGA  
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>tdbD00009576 Chlamydophila\_pneumoniae\_AR39\_115711 Ser TGA  
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>tdbD00009577 Chlamydophila\_pneumoniae\_CWL029\_115713 Ser CGA  
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-GGAGAGATGTCGAGT--GGTTCGAAGGAGCAGCCTGGAACGCGTGTGTAGGG---GAAA--CTCTAC--CGAGGGTTTCAATCCCCTCTCTCTCCGCCA  
>tdbD00009920 Corynebacterium\_glutamicum\_ATCC\_13032\_196627 Ser TGA  
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>tdbD00010062 Escherichia\_coli\_CFT073\_199310 Ser CGA  
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-GGAGAAATACCCAAGTCCGGCTGAAGGGGACAGACTCGAAATCTGTAGGCGG---TGTA--TGCCGCGCCGGGGTTTCAATCCCCTCTCTCTCCG---  
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-GGAGAAATACCCAAGTCTGGCTGAAGGGGATCGGTCTTGAAAACCGACAGGCGGG---TAA--TACCGCG--CGGGGGTTTCAATCCCCTCTCTCTCCG---  
>tdbD00010188 Listeria\_monocytogenes\_str\_4b\_F2365\_265669 Ser CGA  
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>tdbD00009598 Mycobacterium\_tuberculosis\_CDC1551\_83331 Ser GCT  
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>tdbD00002621 Mycoplasma\_mycoides\_2102 Ser TGA  
-GGAAGATTACCCAAGTCCGGCTGAAGGGGATCGGTCTTGAAAACCGAGAGTCCGG---GAA--ACCCGAG--CGGGGGTTTCAATCCCCTCTCTCCGCCA  
>tdbD00009605 Neisseria\_meningitidis\_Z2491\_122587 Ser CGA  
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>tdbD00009606 Neisseria\_meningitidis\_Z2491\_122587 Ser GCT  
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>tdbD00010120 Rhodopseudomonas\_palustris\_CGA009\_258594\_Ser\_CGA  
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>tdbD00009917 Rickettsia\_prowazekii\_str.\_Madrid\_E\_272947\_Ser\_GCT  
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>tdbD00009769 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341\_Ser\_CGA  
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>tdbD00009768 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341\_Ser\_TGA  
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>tdbD00010068 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261\_Ser\_CGA  
-GGAGAGATGCCGGAGC--GGCTGAACCGGACCGGTCTCGAAAACCGGAGTAGGG---GCAA--CTCTAC-CGGGGGTTCAAATCCCCCTCTCTCCGCCA  
>tdbD00010070 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261\_Ser\_TGA  
-GGAAGTGTGGCCGAGC--GGTTGAAGGCACCGGTCTTGAAAACCGGCGACCC---GAAA---GGGTT-CCAGAGTTCGAATCTCTGCGCTTCCGCCA  
>tdbD00009751 Salmonella\_typhimurium\_LT2\_99287\_Ser\_CGA  
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>tdbD00009749 Salmonella\_typhimurium\_LT2\_99287\_Ser\_TGA  
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>tdbD00009994 Shigella\_flexneri\_2a\_str.\_301\_198214\_Ser\_CGA  
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>tdbD00009992 Shigella\_flexneri\_2a\_str.\_301\_198214\_Ser\_TGA  
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>tdbD00009924 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620\_Ser\_TGA  
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>tdbD00009927 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620\_Ser\_TGA  
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>tdbD00009928 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620\_Ser\_TGA  
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>tdbD00009614 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879\_Ser\_GGA  
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>tdbD00009616 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879\_Ser\_TGA  
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>tdbD00009617 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879\_Ser\_TGA  
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>tdbD00010024 Staphylococcus\_epidermidis\_ATCC\_12228\_176280\_Ser\_TGA  
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>tdbD00002639 Streptomyces\_lividans\_1916\_Ser\_GCT  
-GGAGGCGTCGCTAGTCCGGTCTATGGCCCGCAGTCTAATGCGGTTTGGGTC--TTAA-AGCCCAT-CGAGGGTTCGAATCCCTCCGCTCCG---  
>tdbD00009683 Synechocystis\_sp.\_PCC\_6803\_1148\_Ser\_CGA  
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>tdbD00009693 Xylella\_fastidiosa\_9a5c\_160492\_Ser\_GGA  
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>tdbD00009743 Yersinia\_pestis\_C092\_214092\_Ser\_TGA  
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>tdbD00010169 *Yersinia\_pseudotuberculosis\_IP\_32953\_273123* Ser TGA  
-GGAAGGATGGCCGAGT--GGTTTAAAGGCAACGGTCTTGAAAACCGTCGACTG---TAA---CAGGTCCTAGAGTTTCAATCTCTATCTCTCCGCCA  
>tdbD00010170 *Yersinia\_pseudotuberculosis\_IP\_32953\_273123* Ser TGA  
-GGAGGGGTGGCCGAGT--GGCTGAAGGCAACGGTCTTGAAAACCGTCGACGG---GTAA---CCGTT-CGAGAGTTTCAATCTCTCTCTCCCTCCGCCA  
>tdbD00010698 *Bacillus\_anthraxis\_str.\_Sterne\_260799* Thr GGT  
-GCTTCCATAGCTCAGCT--GGT--AGAGCACTTCCATGGTAAGGAAGAG-----GTCACCGGTTCAAGCCCAGTTGGAAGCT---  
>tdbD00010735 *Bacillus\_cereus\_ATCC\_10987\_222523* Thr GGT  
-GCTTCCATAGCTCAGCT--GGT--AGAGCACTTCCATGGTAAGGAAGAG-----GTCACCGGTTCAAGCCCAGTTGGAAGCT---  
>tdbD00010641 *Bacillus\_cereus\_ATCC\_14579\_226900* Thr GGT  
-GCTTCCATAGCTCAGCT--GGT--AGAGCACTTCCATGGTAAGGAAGAG-----GTCACCGGTTCAAGCCCAGTTGGAAGCT---  
>tdbD00010302 *Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308* Thr GGT  
-GCTTCCATAGCTCAGCA--GGT--AGAGCACTTCCATGGTAAGGAAGAG-----GTCAGCGGTTTCGAGCCCAGTTGGAAGCT---  
>tdbD00010763 *Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27\_281309* Thr GGT  
-GCTTCCATAGCTCAGCT--GGT--AGAGCACTTCCATGGTAAGGAAGAG-----GTCACCGGTTCAAGCCCAGTTGGAAGCT---  
>tdbD00010348 *Borrelia\_burgdorferi\_B31\_224326* Thr GGT  
-GCCCTTATAGCTCAGTT--GGT--AGAGCACCACCATGGTAAGGTGGGG-----GTCGTCGGTTCAAGTCCGATTGAGGGCT---  
>tdbD00010702 *Borrelia\_garinii\_PBi\_290434* Thr GGT  
-GCCCTTATAGCTCAGTT--GGT--AGAGCACCACCATGGTAAGGTGGGG-----GTCGTCGGTTCAAGTCCGATTGAGGGCT---  
>tdbD00010412 *Brucella\_melitensis\_16M\_224914* Thr GGT  
-GCTGCGGTAGCTCAGT--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GTCGAGAGTTCAATCTCTCTCGCAGCACCA  
>tdbD00010297 *Chlamydia\_trachomatis\_D/UW-3/CX\_272561* Thr GGT  
-GCCAGGTAGCTCAGT--GGT--AGAGCACTTGCATGGTAAGCAAGTG-----GCCGTAGGTTCAATTCCTATTTCTGGGCA---  
>tdbD00010294 *Chlamydophila\_pneumoniae\_CWL029\_115713* Thr GGT  
-GCCAGATAGCTCAGT--GGT--AGAGCACTTGCATGGTAAGCAAGCG-----GTCGTAGGTTCAATTCCTATTTCTGGGCA---  
>tdbD00010327 *Chlamydophila\_pneumoniae\_J138\_138677* Thr GGT  
-GCCAGATAGCTCAGT--GGT--AGAGCACTTGCATGGTAAGCAAGCG-----GTCGTAGGTTCAATTCCTATTTCTGGGCA---  
>tdbD00010331 *Escherichia\_coli\_K12\_83333* Thr GGT  
-GCTGATATGGCTCAGTT--GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCCCGAGTTTCGACTCTGGGTATCAGCACCA  
>tdbD00010332 *Escherichia\_coli\_K12\_83333* Thr GGT  
-GCTGATATAGCTCAGTT--GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCGAATCTGCCTATCAGCACCA  
>tdbD00010335 *Escherichia\_coli\_O157H7\_83334* Thr GGT:  
-GCTGATATGGCTCAGTT--GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCCCGAGTTTCGACTCTGGGTATCAGCACCA  
>tdbD00010336 *Escherichia\_coli\_O157H7\_83334* Thr GGT:  
-GCTGATATAGCTCAGTT--GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCGAATCTGCCTATCAGCACCA  
>tdbD00010339 *Escherichia\_coli\_O157H7\_EDL933\_155864* Thr GGT:  
-GCTGATATGGCTCAGTT--GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCCCGAGTTTCGACTCTGGGTATCAGCACCA  
>tdbD00010340 *Escherichia\_coli\_O157H7\_EDL933\_155864* Thr GGT:  
-GCTGATATAGCTCAGTT--GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCGAATCTGCCTATCAGCACCA  
>tdbD00010346 *Haemophilus\_influenzae\_Rd\_KW20\_71421* Thr GGT  
-GCTGATATAGCTCAGTT--GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCGAATCTGCCTATCAGCACCA  
>tdbD00010342 *Helicobacter\_pylori\_26695\_85962* Thr GGT  
-GCCTATATAGCTCAGA--GGC--AGAGCACTTCCCTTGGTAAGGAAGAG-----GTCGGCGGTTCAATTCGGCTTATAGGCTCCA  
>tdbD00010344 *Helicobacter\_pylori\_J99\_85963* Thr GGT  
-GCCTATATAGCTCAGA--GGC--AGAGCACTTCCCTTGGTAAGGAAGAG-----GTCGGCGGTTCAATTCGGCTTATAGGCTCCA  
>tdbD00002961 *Listeria\_ivanovii\_1638* Thr GGT  
-GCCGCTTATAGCTCAGTT--GGT--AGAGCACTTCCATGGTAAGGAAGGG-----GTCGTCGGTTCAATTCGGCAAGTGAGGCT---  
>tdbD00010394 *Listeria\_monocytogenes\_EGD-e\_169963* Thr GGT  
-GCCGCTTATAGCTCAGTT--GGT--AGAGCACTTCCATGGTAAGGAAGGG-----GTCGTCGGTTCAATTCGGCAAGTGAGGCT---  
>tdbD00010746 *Listeria\_monocytogenes\_str.\_4b\_F2365\_265669* Thr GGT  
-GCCGCTTATAGCTCAGTT--GGT--AGAGCACTTCCATGGTAAGGAAGGG-----GTCGTCGGTTCAATTCGGCAAGTGAGGCT---  
>tdbD00010416 *Mesorhizobium\_lotii\_MAFF303099\_266835* Thr GGT  
-GCTGCGGTAGCTCAGT--GGT--AGAGCACTCCCTTGGTAAGGGAGAG-----GTCGAGAGTTCAATCTCTCTCGCAGCACCA  
>tdbD00010309 *Mycobacterium\_tuberculosis\_CDC1551\_83331* Thr GGT  
-GCCCCCTTAGCTCAGTC--GGC--AGAGCGTTTCCATGGTAAGGAAAAG-----GTCAACGGTTTCGATTCCGTTAGGGGGCT---  
>tdbD00010684 *Mycobacterium\_tuberculosis\_H37Rv\_83332* Thr GGT  
-GCCCCCTTAGCTCAGTC--GGC--AGAGCGTTTCCATGGTAAGGAAAAG-----GTCAACGGTTTCGATTCCGTTAGGGGGCT---  
>tdbD00010359 *Mycoplasma\_genitalium\_G37\_243273* Thr GGT  
-GCCGAATTGGTTTAGG--GGC--AAAACAGATCCATGGTAAGGATCAG-----A-GAACAGTTTCGACTCTGTTATTCCGGCACCA  
>tdbD00010364 *Pasteurella\_multocida\_subsp.\_multocida\_str.\_Pm70\_272843* Thr GGT  
-GCTGATATAGCTCAGTT--GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCGGCGGTTCAATTCGGCTATCAGCACCA  
>tdbD00010370 *Pseudomonas\_aeruginosa\_PA01\_208964* Thr GGT  
-GCTCATGTAGCTCAGTT--GGT--AGAGCACACCCTTGGTAAGGGTGAG-----GTCAGCGGTTCAATTCGGCTCATGAGCTCCA  
>tdbD00010435 *Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341* Thr GGT  
-GCTGATATAGCTCAGTT--GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCCCGAGTTTCGACTCTGGGTATCAGCACCA  
>tdbD00010436 *Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341* Thr GGT  
-GCTGATATAGCTCAGTT--GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCGAATCTGCCTATCAGCACCA  
>tdbD00010654 *Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261* Thr GGT  
-GCTGATATAGCTCAGTT--GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCCCGAGTTTCGACTCTGGGTATCAGCACCA  
>tdbD00010655 *Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261* Thr GGT  
-GCTGATATAGCTCAGTT--GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCGAATCTGCCTATCAGCACCA  
>tdbD00010420 *Salmonella\_typhimurium\_LT2\_99287* Thr GGT  
-GCTGATATAGCTCAGTT--GGT--AGAGCGCACCCCTTGGTAAGGGTGAG-----GTCCCGAGTTTCGACTCTGGGTATCAGCACCA

>tdbD00010422 Salmonella\_typhimurium LT2 99287 Thr GGT  
-GCTGATATAGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCAATCTGCCTATCAGCACCA  
>tdbD00010593 Shigella\_flexneri\_2a\_str.\_301 198214 Thr GGT  
-GCTGATATGGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCCCAGTTTCTGACTCTGGGTATCAGCACCA  
>tdbD00010596 Shigella\_flexneri\_2a\_str.\_301 198214 Thr GGT  
-GCTGATATAGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCAATCTGCCTATCAGCACCA  
>tdbD00010439 Sinorhizobium\_meliloti\_1021 266834 Thr GGT  
-GCTGTATAGCTCAGG--GGT--AGAGCACTCCCTTGGTAAGGGGAG-----GCCGAGAGTTCAAATCTCTCTAGCAGCACCA  
>tdbD00010545 Streptococcus\_pyogenes MGAS315 198466 Thr GGT  
-GCCCGTGTAGTTAAAT--GGT--ATAATAAAGCAATGGTAATGCTTCG-----T-TCCGAGTTTCGATTCTCGGTGGTGCA---  
>tdbD00010636 Streptococcus\_pyogenes SSI-1 193567 Thr GGT  
-GCCCGTGTAGTTAAAT--GGT--ATAATAAAGCAATGGTAATGCTTCG-----T-TCCGAGTTTCGATTCTCGGTGGTGCA---  
>tdbD00010373 Synechocystis\_sp.\_PCC 6803 1148 Thr GGT  
-GCCCTGTAGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCACGAGTTTCAATCCTCGTCAAGGGCT---  
>tdbD00010367 Treponema\_pallidum\_subsp.\_pallidum\_str.\_Nichols 243276 Thr GGT  
-GCTTCTGTAGCTCAGTT-GGT--AGAGCGCAACCATGGTAAGGGTGAG-----GTCAGCGGTTTCAATCCCGCTCGGAAGCT---  
>tdbD00010624 Tropheryma\_whipplei\_TW08/27 218496 Thr GGT  
-GCCCGGTGTAGCTCAGTT-GGT--AGAGCACTTCATGGTAAGGGGAG-----GTCGTGAGTTTCAATCCTGACCCGGGGCT---  
>tdbD00010317 Vibrio\_cholerae\_O1\_biovar\_El\_Tor\_str.\_N16961 243277 Thr GGT  
-GCTGATATGGCTCAGTC-GGT--AGAGCGCATCCTTGGTAAGGGATGAG-----GTCCCAGTTTTCGATTCTGGGTATCAGCACCA  
>tdbD00010556 Xanthomonas\_campestris\_pv.\_campestris\_str.\_ATCC\_33913 190485 Thr GGT  
-GCTCAGTAGCTCAGTT-GGT--AGAGCACTTCATGGTAAGGGGAG-----GTCGAAGTTTTCGATTCTCTTTCGTGAGCACCA  
>tdbD00010383 Xylella\_fastidiosa\_9a5c\_160492 Thr GGT  
-GCTGATATGGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCCCAGTTTCTGACTCTGGGTATCAGCACCA  
>tdbD00010384 Xylella\_fastidiosa\_9a5c\_160492 Thr GGT  
-GCTGATATAGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCAATCTGCCTATCAGCACCA  
>tdbD00010629 Xylella\_fastidiosa\_Temecula\_183190 Thr GGT  
-GCTCAGTAGCTCAGTC-GGT--AGAGCACCTCCTTGGTAAGGGAGGAG-----GTCGATGTTTTCGATTCCATTCGTGAGCACCA  
>tdbD00010727 Yersinia\_pestis\_biovar\_Microtus\_str.\_91001 229193 Thr GGT  
-GCTGATATGGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCCCAGTTTCTGACTCTGGGTATCAGCACCA  
>tdbD00010728 Yersinia\_pestis\_biovar\_Microtus\_str.\_91001 229193 Thr GGT  
-GCTGATATAGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCAATCTGCCTATCAGCACCA  
>tdbD00010418 Yersinia\_pestis\_CO92\_214092 Thr GGT  
-GCTGATATGGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCCCAGTTTCTGACTCTGGGTATCAGCACCA  
>tdbD00010419 Yersinia\_pestis\_CO92\_214092 Thr GGT  
-GCTGATATAGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCAATCTGCCTATCAGCACCA  
>tdbD00010565 Yersinia\_pestis\_KIM\_187410 Thr GGT  
-GCTGATATGGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCCCAGTTTCTGACTCTGGGTATCAGCACCA  
>tdbD00010567 Yersinia\_pestis\_KIM\_187410 Thr GGT  
-GCTGATATAGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCAATCTGCCTATCAGCACCA  
>tdbD00010730 Yersinia\_pseudotuberculosis\_IP\_32953\_273123 Thr GGT  
-GCTGATATAGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCGGCAGTTTCAATCTGCCTATCAGCACCA  
>tdbD00010731 Yersinia\_pseudotuberculosis\_IP\_32953\_273123 Thr GGT  
-GCTGATATGGCTCAGTT-GGT--AGAGCGACCCTTGGTAAGGGTGAG-----GTCCCAGTTTCTGACTCTGGGTATCAGCACCA  
>tdbD00008403 Bacillus\_anthraxis\_str.\_Sterne\_260799 Pro TGG  
-CGGAAGTGGCTCAGCTTGGT--AGAGCACCTGGTTTGGGACCAGGGG-----GTCGCAGTTTCAAATCCTGTCTTCCCGACCA  
>tdbD00008404 Bacillus\_anthraxis\_str.\_Sterne\_260799 Pro TGG  
-CGGAAGTGGCTCAGCTTGGT--AGAGCACCTGGTTTGGGACCAGGGG-----GTCGCAGTTTCAAATCCTGTCTTCCCGA---  
>tdbD00008427 Bacillus\_cereus\_ATCC\_10987\_222523 Pro TGG  
-CGGAAGTGGCTCAGCTTGGT--AGAGCACCTGGTTTGGGACCAGGGG-----GTCGCAGTTTCAAATCCTGTCTTCCCGACCA  
>tdbD00008428 Bacillus\_cereus\_ATCC\_10987\_222523 Pro TGG  
-CGGAAGTGGCTCAGCTTGGT--AGAGCACCTGGTTTGGGACCAGGGG-----GTCGCAGTTTCAAATCCTGTCTTCCCGA---  
>tdbD00008354 Bacillus\_cereus\_ATCC\_14579\_226900 Pro TGG  
-CGGAAGTGGCTCAGCTTGGT--AGAGCACCTGGTTTGGGACCAGGGG-----GTCGCAGTTTCAAATCCTGTCTTCCCGA---  
>tdbD00008355 Bacillus\_cereus\_ATCC\_14579\_226900 Pro TGG  
-CGGAAGTGGCTCAGCTTGGT--AGAGCACCTGGTTTGGGACCAGGGG-----GTCGCAGTTTCAAATCCTGTCTTCCCGACCA  
>tdbD00008069 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308 Pro TGG  
-CGGAAGTAGCTCAGCTTGGT--AGAGCACATGGTTTGGGACCATGGG-----GTCGCAGTTTCAATCCTGTCTTCCCGACCA  
>tdbD00008445 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27\_281309 Pro TGG  
-CGGAAGTGGCTCAGCTTGGT--AGAGCACCTGGTTTGGGACCAGGGG-----GTCGCAGTTTCAAATCCTGTCTTCCCGA---  
>tdbD00008446 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27\_281309 Pro TGG  
-CGGAAGTGGCTCAGCTTGGT--AGAGCACCTGGTTTGGGACCAGGGG-----GTCGCAGTTTCAAATCCTGTCTTCCCGACCA  
>tdbD00008377 Bacteroides\_thetaiotaomicron\_VPI-5482\_226186 Pro TGG  
-CGGGGTGTAGCGCAGTCCGGTT-AGCGCACCTGCTTTGGGAGCAGGGG-----GTCGTGGTTTCAATCCCGTACCCCGA---  
>tdbD00008451 Bartonella\_quintana\_str.\_Toulouse\_283165 Pro TGG  
-CGGAGCGTAGCGCAGCCTGGT--AGCGCACCTGATTTGGGATCAGGGG-----GTCGTAGTTTCAATCCTATCGCTCCGACCA  
>tdbD00008105 Borrelia\_burgdorferi\_B31\_224326 Pro TGG  
-CGGGATGTGGCTTAGT--GGCT-AAGGCACCTGCTTTGGGAGCAGGGG-----ATCGTGAGTTTCAATCCACCATCCCGA---  
>tdbD00008405 Borrelia\_garinii\_PBI\_290434 Pro TGG  
-CGGGATGTGGCTTAGT--GGCT-AAGGCACCTGCTTTGGGAGCAGGGG-----ATCGTGAGTTTCAATCCACCATCCCGA---  
>tdbD00008148 Brucella\_melitensis\_16M\_224914 Pro GGG  
-CGGAGCGTAGCGCAGCCGGT--AGCGCACTTGACTGGGGTCAAGGG-----GTCGTGGTTTCAATCCCGCCGCTCCGACCA  
>tdbD00008306 Brucella\_suis\_1330\_204722 Pro CGG  
-CGGAGTGTAGCGCAGCCTGGT--AGCGCACCTCGTTCCGGACGAGGG-----GTCGGAGTTTCAATCCTCTCACTCCGACCA  
>tdbD00008305 Brucella\_suis\_1330\_204722 Pro GGG



-CGGAGCGTAGCGCAGCCCGGT--AGCGCACTTGACTGGGGTCAAGGG-----GTCGTGGGTTCAATCCCGCCGCTCCGACCA  
>tdbD00008307 Brucella\_suis\_1330\_204722 Pro TGG  
-CGGAGCGTAGCGCAGTCTGGT--AGCGCACTGATTTGGGATCAGGGG-----GTCGCAGGTTCAATCCTGCCGCTCCGACCA  
>tdbD00008065 Chlamydia\_trachomatis\_D/UW-3/CX\_272561 Pro GGG  
-CTGGATGTAGCGCAGCCTGGT--AGCGCACTTGCAATGGGGTCAAGGG-----GGCGGAGGTTCAAATCCTCTCATCCAGA---  
>tdbD00008066 Chlamydia\_trachomatis\_D/UW-3/CX\_272561 Pro TGG  
-CGGAGTATAGCGCAGCCTGGT--AGCGCGGTTGCTTTGGGAGCAATAG-----GTCGGGGGTTCAATCCTCTACTCCGA---  
>tdbD00008063 Chlamydia\_pneumoniae\_CWL029\_115713 Pro GGG  
-CTGGGTGTAGCGCAGCCTGGT--AGCGCACTTGCAATGGGGTCAAGGG-----GGCGGAGGTTCAAATCCTCTCATCCAGA---  
>tdbD00008064 Chlamydia\_pneumoniae\_CWL029\_115713 Pro TGG  
-CGGAGTATAGCGCAGCCTGGT--AGCGCGGTTGCTTTGGGAGCAATAG-----GTCGGGGGTTCAATCCTCTACTCCGA---  
>tdbD00008088 Chlamydia\_pneumoniae\_J138\_138677 Pro GGG  
-CTGGGTGTAGCGCAGCCTGGT--AGCGCACTTGCAATGGGGTCAAGGG-----GGCGGAGGTTCAAATCCTCTCATCCAGA---  
>tdbD00008089 Chlamydia\_pneumoniae\_J138\_138677 Pro TGG  
-CGGAGTATAGCGCAGCCTGGT--AGCGCGGTTGCTTTGGGAGCAATAG-----GTCGGGGGTTCAATCCTCTACTCCGA---  
>tdbD00008308 Corynebacterium\_efficiens\_YS-314\_196164 Pro CGG  
-CGGGATATGGCGCAGCTTGGT--AGCGCGCCTCGTTCGGGACGAGGAG-----GTCGCAGGTTCAAATCCTGTATCCCGACCA  
>tdbD00008357 Escherichia\_coli\_CFT073\_199310 Pro CGG  
-CGGTGATTGGCGCAGCCTGGT--AGCGCACTTCGTTTCGGGACGAAGGG-----GTCGGAGGTTCAATCCTCTATCACCAGACCA  
>tdbD00008357 Escherichia\_coli\_CFT073\_199310 Pro GGG  
-CGGCACGTAGCGCAGCCTGGT--AGCGCACCGTCATGGGGTTCGGGG-----GTCGGAGGTTCAAATCCTCTCGTGCCGACCA  
>tdbD00008359 Escherichia\_coli\_CFT073\_199310 Pro TGG  
-CGGCGAGTAGCGCAGCCTGGT--AGCGCAACTGGTTGGGACCAGTGG-----GTCGGAGGTTCAATCCTCTCTCGCCGACCA  
>tdbD00008090 Escherichia\_coli\_K12\_83333 Pro CGG  
-CGGTGATTGGCGCAGCCTGGT--AGCGCACTTCGTTTCGGGACGAAGGG-----GTCGGAGGTTCAATCCTCTATCACCAGACCA  
>tdbD00008091 Escherichia\_coli\_K12\_83333 Pro GGG  
-CGGCACGTAGCGCAGCCTGGT--AGCGCACCGTCATGGGGTTCGGGG-----GTCGGAGGTTCAAATCCTCTCGTGCCGACCA  
>tdbD00008092 Escherichia\_coli\_K12\_83333 Pro TGG  
-CGGCGAGTAGCGCAGCCTGGT--AGCGCAACTGGTTGGGACCAGTGG-----GTCGGAGGTTCAATCCTCTCTCGCCGACCA  
>tdbD00008093 Escherichia\_coli\_O157H7\_83334 Pro CGG:  
-CGGTGATTGGCGCAGCCTGGT--AGCGCACTTCGTTTCGGGACGAAGGG-----GTCGGAGGTTCAATCCTCTATCACCAGACCA  
>tdbD00008094 Escherichia\_coli\_O157H7\_83334 Pro GGG:  
-CGGCACGTAGCGCAGCCTGGT--AGCGCACCGTCATGGGGTTCGGGG-----GTCGGAGGTTCAAATCCTCTCGTGCCGACCA  
>tdbD00008097 Escherichia\_coli\_O157H7\_EDL933\_155864 Pro CGG:  
-CGGTGATTGGCGCAGCCTGGT--AGCGCACTTCGTTTCGGGACGAAGGG-----GTCGGAGGTTCAATCCTCTATCACCAGACCA  
>tdbD00008098 Escherichia\_coli\_O157H7\_EDL933\_155864 Pro GGG:  
-CGGCACGTAGCGCAGCCTGGT--AGCGCACCGTCATGGGGTTCGGGG-----GTCGGAGGTTCAAATCCTCTCGTGCCGACCA  
>tdbD00008099 Escherichia\_coli\_O157H7\_EDL933\_155864 Pro TGG:  
-CGGCGAGTAGCGCAGCCTGGT--AGCGCAACTGGTTGGGACCAGTGG-----GTCGGAGGTTCAATCCTCTCTCGCCGACCA  
>tdbD00008104 Haemophilus\_influenzae\_Rd\_KW20\_71421 Pro TGG  
-CGGCGAGTAGCGCAGCCTGGT--AGCGCAACTGGTTGGGACCAGTGG-----GTCGTAGGTTCAAATCCTATCTCGCCGACCA  
>tdbD00002110 Helicobacter\_pylori\_210 Pro TGG  
-CGGGCGTAGCGCAGTCTGGT--AGCGCACTTGTTGGGACCAAGGG-----GTCGAAGGTTCAATCCTTTTCGCCCGACCA  
>tdbD00008101 Helicobacter\_pylori\_26695\_85962 Pro TGG  
-CGGGCGTAGCGCAGTCTGGT--AGCGCACTTGTTGGGACCAAGGG-----GTCGAAGGTTCAATCCTTTTCGCCCGACCA  
>tdbD00008102 Helicobacter\_pylori\_J99\_85963 Pro GGG  
-CGGAGTATGGCGCAGCCTGGT--AGCGCGCACCCCTGGGGTGGGTGAG-----GTCGTGGGTTTGAATCCCGTACTCCGACCA  
>tdbD00008103 Helicobacter\_pylori\_J99\_85963 Pro TGG  
-CGGGCGTAGCGCAGTCTGGT--AGCGCACTTGTTGGGACCAAGGG-----GTCGAAGGTTCAATCCTTTTCGCCCGACCA  
>tdbD00008137 Listeria\_innocua\_Clip11262\_272626 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGCACTTGTTGGGACCAAGGG-----GTCGCAGGTTCAATCCTGTCTTCCCAG---  
>tdbD00008138 Listeria\_monocytogenes\_EGD-e\_169963 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGCACTTGTTGGGACCAAGGG-----GTCGCAGGTTCAATCCTGTCTTCCCAG---  
>tdbD00008432 Listeria\_monocytogenes\_str\_4b\_F2365\_265669 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGCACTTGTTGGGACCAAGGG-----GTCGCAGGTTCAATCCTGTCTTCCCAG---  
>tdbD00008084 Mycobacterium\_leprae\_TN\_272631 Pro CGG  
-CGGGGTGTGGCGCAGCTTGGT--AGCGCGCTTCGTTTCGGGACGAAGAG-----GCCGTGGGTTCAAATCCCGCCACCCCGA---  
>tdbD00008085 Mycobacterium\_leprae\_TN\_272631 Pro GGG  
-CGGGCTGTGGCGCAGCTTGGT--AGCGCACTTGACTGGGGTCAAGTG-----GTCGCAGGTTCAAATCCTGTCTCAGCCCGA---  
>tdbD00008086 Mycobacterium\_leprae\_TN\_272631 Pro TGG  
-CGGGGTGTAGCGCAGCTTGGT--AGCGCATCCGCTTTGGGAGCGGAAG-----GCCGCAGGTTCAAATCCTGTCTCAGCCCGA---  
>tdbD00002106 Mycobacterium\_tuberculosis\_1773 Pro CGG  
-CGGGGTGTGGCGCAGCTTGGT--AGCGCGCTTCGTTTCGGGACGAAGAG-----GCCGTGGGTTCAAATCCCGCCACCCCGA---  
>tdbD00008071 Mycobacterium\_tuberculosis\_CDC1551\_83331 Pro CGG  
-CGGGGTGTGGCGCAGCTTGGT--AGCGCGCTTCGTTTCGGGACGAAGAG-----GCCGTGGGTTCAAATCCCGCCACCCCGA---  
>tdbD00008072 Mycobacterium\_tuberculosis\_CDC1551\_83331 Pro GGG  
-CGGGCTGTGGCGCAGCTTGGT--AGCGCACTTGACTGGGGTCAAGTG-----GTCGCAGGTTCAAATCCTGTCTCAGCCCGA---  
>tdbD00008073 Mycobacterium\_tuberculosis\_CDC1551\_83331 Pro TGG  
-CGGGGTGTAGCGCAGCTTGGT--AGCGCATCCGCTTTGGGAGCGGAAG-----GCCGCAGGTTCAAATCCTGTCTCAGCCCGA---  
>tdbD00008394 Mycobacterium\_tuberculosis\_H37Rv\_83332 Pro CGG  
-CGGGGTGTGGCGCAGCTTGGT--AGCGCGCTTCGTTTCGGGACGAAGAG-----GCCGTGGGTTCAAATCCCGCCACCCCGA---  
>tdbD00008392 Mycobacterium\_tuberculosis\_H37Rv\_83332 Pro GGG  
-CGGGCTGTGGCGCAGCTTGGT--AGCGCACTTGACTGGGGTCAAGTG-----GTCGCAGGTTCAAATCCTGTCTCAGCCCGA---  
>tdbD00008393 Mycobacterium\_tuberculosis\_H37Rv\_83332 Pro TGG  
-CGGGGTGTAGCGCAGCTTGGT--AGCGCATCCGCTTTGGGAGCGGAAG-----GCCGCAGGTTCAAATCCTGTCTCAGCCCGA---  
-CGGGGTGTAGCGCAGCTTGGT--AGCGCATCCGCTTTGGGAGCGGAAG-----GCCGCAGGTTCAAATCCTGTCTCAGCCCGA---

>tdbD00008113 Mycoplasma genitalium G37 243273 Pro TGG  
-CGGGAAGTAGCTTAGTTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTCAAATCCTGTCTTCCCGACCA  
>tdbD00002098 Mycoplasma mycoides 2102 Pro TGG  
-CGGGAAGTGGCTCAGTTTGGT--AGAGCATTCGGTTTGGGACCAAGGG-----GTCGCAGGTTCAAATCCTGTCTTCCCGACCA  
>tdbD00008114 Mycoplasma pneumoniae M129 272634 Pro TGG  
-CGGGAAGTGGCTTAGTTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTCAAATCCTGTCTTCCCGACCA  
>tdbD00008078 Neisseria meningitidis Z2491 122587 Pro GGG  
-CGGAGTGTGGCGCAGTCTGGT--AGCGCACTTGCATGGGGTGCAAGGG-----GTCGAAGGTTTCAATCCTTTTACTCCGACCA  
>tdbD00008079 Neisseria meningitidis Z2491 122587 Pro TGG  
-CGGGGCGTAGCGCAGCCCGTT--AGCGCATCTGCCTTGGGAGCAGAGG-----GTCGTGAGTTTCAATCCCACCGCCCGACCA  
>tdbD00008115 Pasteurella multocida subsp. multocida str. Pm70 272843 Pro TGG  
-CGGGGAGTAGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGTAGGTTCAAATCCTATCTCGCCGACCA  
>tdbD00008397 Phototribadus luminescens subsp. laumondii T101 243265 Pro TGG  
-CGGGGAGTAGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGGAGGTTTCAATCCTCTCTCGCCGACCA  
>tdbD00008414 Porphyromonas gingivalis W83 242619 Pro TGG  
-CGGGGTGTAGCGCAGTCCGGTT--AGCGCACTTGCCTTGGGAGCAGGGG-----GTCGTGGGTTTCAATCCCCTACTCCCGA---  
>tdbD00008399 Rhodospseudomonas palustris CGA009 258594 Pro CGG  
-CGGAGTGTGGCTAGCGCAGCTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTTCAATCCTGCCACTCCGACCA  
>tdbD00008400 Rhodospseudomonas palustris CGA009 258594 Pro TGG  
-CGGGGTATAGCGCAGCTTGGT--AGCGCGGAGTTTGGGTTACTGCAG-----GTCGTGTTTCAATCCAGTGCCTCCGACCA  
>tdbD00008273 Rickettsia prowazekii str. Madrid E 272947 Pro TGG  
-CGGGGCGTAGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGGGAGTTTCAATCCTCTCCGCCCGACCA  
>tdbD00008417 Rickettsia typhi str. Wilmington 257363 Pro TGG  
-CGGGGCGTAGCGCAGCTTGGT--AGCGCATCTGGTTTGGGACCAAGGG-----GTCGGGAGTTTCAATCCTCTCCGCCCGACCA  
>tdbD00008172 Salmonella enterica subsp. enterica serovar Typhi str. CT18 220341 Pro CGG  
-CGGTGATTGGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGGAGGTTTCAATCCTCTATCACCAGACCA  
>tdbD00008170 Salmonella enterica subsp. enterica serovar Typhi str. CT18 220341 Pro GGG  
-CGGCACGTAGCGCAGCTTGGT--AGCGCACCGTTCATGGGGTGTCCGGG-----GTCGGAGGTTTCAAATCCTCTCGTCCGACCA  
>tdbD00008171 Salmonella enterica subsp. enterica serovar Typhi str. CT18 220341 Pro TGG  
-CGGGGAGTAGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGGAGGTTTCAATCCTCTCTCGCCGACCA  
>tdbD00008367 Salmonella enterica subsp. enterica serovar Typhi str. Ty2 209261 Pro CGG  
-CGGTGATTGGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGGAGGTTTCAATCCTCTATCACCAGACCA  
>tdbD00008365 Salmonella enterica subsp. enterica serovar Typhi str. Ty2 209261 Pro GGG  
-CGGCACGTAGCGCAGCTTGGT--AGCGCACCGTTCATGGGGTGTCCGGG-----GTCGGAGGTTTCAAATCCTCTCGTCCGACCA  
>tdbD00008366 Salmonella enterica subsp. enterica serovar Typhi str. Ty2 209261 Pro TGG  
-CGGGGAGTAGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGGAGGTTTCAATCCTCTCTCGCCGACCA  
>tdbD00002116 Salmonella typhimurium 602 Pro TGG  
-CGGGGAGTAGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGGAGGTTTCAATCCTCTCTCGCCGACCA  
>tdbD00008157 Salmonella typhimurium LT2 99287 Pro CGG  
-CGGTGATTGGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGGAGGTTTCAATCCTCTATCACCAGACCA  
>tdbD00008156 Salmonella typhimurium LT2 99287 Pro GGG  
-CGGCACGTAGCGCAGCTTGGT--AGCGCACCGTTCATGGGGTGTCCGGG-----GTCGGAGGTTTCAAATCCTCTCGTCCGACCA  
>tdbD00008158 Salmonella typhimurium LT2 99287 Pro TGG  
-CGGGGAGTAGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGGAGGTTTCAATCCTCTCTCGCCGACCA  
>tdbD00008321 Shigella flexneri 2a str. 301 198214 Pro CGG  
-CGGTGATTGGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGGAGGTTTCAATCCTCTATCACCAGACCA  
>tdbD00008319 Shigella flexneri 2a str. 301 198214 Pro TGG  
-CGGGGAGTAGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGGAGGTTTCAATCCTCTCTCGCCGACCA  
>tdbD00008174 Sinorhizobium meliloti 1021 266834 Pro GGG  
-CGGAGCGTAGCGCAGCCCGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGTGGGTTTCAATCCCCTCCGCTCCGACCA  
>tdbD00002107 Staphylococcus aureus 1280 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00008402 Staphylococcus aureus subsp. aureus MRSA252 282458 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00008277 Staphylococcus aureus subsp. aureus MW2 196620 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00008083 Staphylococcus aureus subsp. aureus N315 158879 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00008278 Streptococcus agalactiae NEM316 211110 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGTACTTGGTTTGGGACCAAGGT-----GTCGCAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00008323 Streptococcus mutans UA159 210007 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGTACTTGGTTTGGGACCAAGGT-----GTCGCAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00008143 Streptococcus pneumoniae TIGR4 170187 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGTACTTGGTTTGGGACCAAGGT-----GTCGCAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00008142 Streptococcus pyogenes M1 GAS 160490 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGTACTTGGTTTGGGACCAAGGT-----GTCGCAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00008279 Streptococcus pyogenes MGAS315 198466 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGTACTTGGTTTGGGACCAAGGT-----GTCGCAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00008350 Streptococcus pyogenes SSI-1 193567 Pro TGG  
-CGGGAAGTAGCTCAGCTTGGT--AGAGTACTTGGTTTGGGACCAAGGT-----GTCGCAGGTTTCAATCCTGTCTTCCCGA---  
>tdbD00008361 Streptomyces avermitilis MA-4680 227882 Pro GGG  
-CGGGACGTGGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTTCAAATCCTGTCTCCCGA---  
>tdbD00008364 Streptomyces avermitilis MA-4680 227882 Pro GGG  
-CGGGACGTGGCGCAGCTTGGT--AGCGCACTTGGTTTGGGACCAAGGG-----GTCGCAGGTTTCAAATCCTGTCTCCCGA---  
>tdbD00008314 Streptomyces coelicolor A3(2) 100226 Pro CGG

-CGGGGTGTGGCGCAGCTTGGT--AGCGCGCTTCGTTCCGGGACGAAGAG-----GTCGTGGGTTCAAATCCCGCCACCCCGA---  
>tdbD00008315 Streptomyces coelicolor\_A3(2) 100226 Pro GGG  
-CGGGACGTGGCGCAGCTTGGT--AGCGCACTTGACTGGGGGTCAAGGG-----GTCGCAGGTTCAAATCCTGTCTGCCGACCA---  
>tdbD00008316 Streptomyces coelicolor\_A3(2) 100226 Pro TGG  
-CGGGGTGTGGCGCAGCTTGGT--AGCGCGTCCGCTTTGGGAGCGGAAG-----GCCGTGGGTTCAAATCCCGCCACCCCGACCA  
>tdbD00008122 Synechocystis\_sp.\_PCC\_6803\_1148 Pro CGG  
-CGGGATGTAGCGCAGCTTGGT--AGCGCACTTCGTTCCGGGACGAAGGG-----GCCGCAGGTTCGAATCCTGTCTGCCGACCA---  
>tdbD00008123 Synechocystis\_sp.\_PCC\_6803\_1148 Pro GGG  
-CGGGCGTAGCGCAGCTTGGT--AGCGCACCCTTTGGGGTAGTGGGG-----GTCGTGGGTTCAAATCCCGCCGCTCCGA---  
>tdbD00008124 Synechocystis\_sp.\_PCC\_6803\_1148 Pro TGG  
-CGGGATGTAGCGCAGCTTGGT--AGCGCGCTGCTTTGGGAGCAGGAT-----GTCGCAGGTTCAAATCCTGTCTGCCGACCA---  
>tdbD00008282 Thermosynechococcus\_elongatus\_BP-1\_197221 Pro GGG  
-CGGGCGTAGCGCAGCTTGGT--AGCGCACCCTTTGGGGTAGTGGGG-----GTCGTGGGTTCAAATCCCGCCGCTCCGA---  
>tdbD00008116 Treponema pallidum\_subsp.\_pallidum\_str.\_Nichols\_243276 Pro CGG  
-CGGGTGGTAGCGCAGT--GGT--AGCGCGCTCGGTTCCGGGACTGAGAG-----GTCGGGGGTTCAAATCCCGCTGCCCGACCA  
>tdbD00008117 Treponema pallidum\_subsp.\_pallidum\_str.\_Nichols\_243276 Pro GGG  
-CGGGCAATGGCGCAGTA--GGT--AGCGTACAAGTCTGGGGGACTTGGG-----GTCCCGGTTTCGAGTCCGGGTTGCCGACCA---  
>tdbD00008118 Treponema pallidum\_subsp.\_pallidum\_str.\_Nichols\_243276 Pro TGG  
-CGGGACGTGGCCTAGG--GGCT--AGGGCACCCGGTTGGGACCGGAAG-----ATCGAGGTTCAAATCCCGCTGCCGACCA---  
>tdbD00008340 Tropheryma whipplei\_TW08/27\_218496 Pro CGG  
-CGGGGTGTGGCGCAGCTTGGT--AGCGCGCTCGTTCGGGACGAGGAG-----GTCGTGGGTTCAAATCCCGCCACCCCGA---  
>tdbD00008338 Tropheryma whipplei\_TW08/27\_218496 Pro GGG  
-CGGGCTGTGGCGCAGCTTGGT--AGCGCACTTGACTGGGGGTCAAGGG-----GTCGTGGGTTCAAATCCCGCCAGCCCGA---  
>tdbD00008339 Tropheryma whipplei\_TW08/27\_218496 Pro TGG  
-CGGGGTGTAGCTCAGTTTGGT--AGAGCGCCCGCTTTGGGAGCGGGAG-----GTCGCAGGTTCAAATCCTGTCTGCCGACCA---  
>tdbD00008081 Vibrio cholerae\_O1\_biovar\_El\_Tor\_str.\_N16961\_243277 Pro TGG  
-CGGTGAATAGCGCAGTTTGGT--AGCGCATCTGGTTTGGGACCGAGG-----GTCGGGGGTTCAAATCCCGCTTCCCGACCA  
>tdbD00008290 Xanthomonas campestris\_pv.\_campestris\_str.\_ATCC\_33913\_190485 Pro CGG  
-CGGGGTGTAGCTCAGTCTGGT--AGAGCGCTACGTTCCGGGACGTAGAG-----GTCGCAGGTTCAAATCCTGTCTGCCGACCA  
>tdbD00008291 Xanthomonas campestris\_pv.\_campestris\_str.\_ATCC\_33913\_190485 Pro GGG  
-CGGGGTATAGCGCAGCCTGGT--AGCGCACTAGTCTGGGGGACTAGTG-----GTCGTGGGTTCAAATCCCGCTGCCGACCA  
>tdbD00008289 Xanthomonas campestris\_pv.\_campestris\_str.\_ATCC\_33913\_190485 Pro TGG  
-CGGGGTATAGCGCAGTCTGGT--AGCGCGCTGCTTTGGGAGCAGGAT-----GTCGGGGGTTCAAATCCCGCTGCCGACCA  
>tdbD00008128 Xylella fastidiosa\_9a5c\_160492 Pro CGG  
-CGGGGTGTAGCTCAGTCTGGT--AGAGCGCTACGTTCCGGGACGTAGAG-----GTCGCAGGTTCAAATCCTGTCTGCCGACCA  
>tdbD00008131 Xylella fastidiosa\_9a5c\_160492 Pro CGG  
-CGGTGATTGGCGCAGCCTGGT--AGCGCACTTCGTTCCGGGACGAAGGG-----GTCGGAGGTTCAAATCCTCTATCACCAGCA  
>tdbD00008132 Xylella fastidiosa\_9a5c\_160492 Pro GGG  
-CGGCACGTAGCGCAGCCTGGT--AGCGCACCGTCACTGGGGTGTCCGGG-----GTCGGAGGTTCAAATCCTCTCGTCCGACCA  
>tdbD00008133 Xylella fastidiosa\_9a5c\_160492 Pro TGG  
-CGGGAGTAGCGCAGCTTGGT--AGCGCACTGGTTTGGGACCGAGTGG-----GTCGGAGGTTCAAATCCTCTCGCCGACCA  
>tdbD00008341 Xylella fastidiosa\_Temecula\_183190 Pro CGG  
-CGGGGTGTAGCTCAGTCTGGT--AGAGCGCTACGTTCCGGGACGTAGAG-----GTCGCAGGTTCAAATCCTGTCTGCCGACCA  
>tdbD00008342 Xylella fastidiosa\_Temecula\_183190 Pro GGG  
-CGGGGTATAGCGCAGCCTGGT--AGCGCACCGTCTGGGGGACTGTGT-----GTCGTGGGTTCAAATCCCGCTGCCGACCA  
>tdbD00008343 Xylella fastidiosa\_Temecula\_183190 Pro TGG  
-CGGGGTATAGCGCAGTCTGGT--AGCGCGCTGCTTTGGGAGCAGGAT-----GTCGGGGGTTCAAATCCCGCTGCCGACCA  
>tdbD00008422 Yersinia pestis\_biovar\_Microtus\_str.\_91001\_229193 Pro TGG  
-CGGGAGTAGCGCAGCTTGGT--AGCGCACTGGTTTGGGACCGAGTGG-----GTCGGAGGTTCAAATCCTCTCGCCGACCA  
>tdbD00008154 Yersinia pestis\_CO92\_214092 Pro GGG  
-CGGCATGTAGCGCAGCTTGGT--AGCGCACCGTCACTGGGGTGTCCGGG-----GTCGAAGGTTCAAATCCTTTTCATGCCGACCA  
>tdbD00008155 Yersinia pestis\_CO92\_214092 Pro TGG  
-CGGGAGTAGCGCAGCTTGGT--AGCGCACTGGTTTGGGACCGAGTGG-----GTCGGAGGTTCAAATCCTCTCGCCGACCA  
>tdbD00008299 Yersinia pestis\_KIM\_187410 Pro GGG  
-CGGCATGTAGCGCAGCTTGGT--AGCGCACCGTCACTGGGGTGTCCGGG-----GTCGAAGGTTCAAATCCTTTTCATGCCGACCA  
>tdbD00008298 Yersinia pestis\_KIM\_187410 Pro TGG  
-CGGGAGTAGCGCAGCTTGGT--AGCGCACTGGTTTGGGACCGAGTGG-----GTCGGAGGTTCAAATCCTCTCGCCGACCA  
>tdbD00008424 Yersinia pseudotuberculosis\_IP\_32953\_273123 Pro GGG  
-CGGCATGTAGCGCAGCTTGGT--AGCGCACCGTCACTGGGGTGTCCGGG-----GTCGAAGGTTCAAATCCTTTTCATGCCGACCA  
>tdbD00008423 Yersinia pseudotuberculosis\_IP\_32953\_273123 Pro TGG  
-CGGGAGTAGCGCAGCTTGGT--AGCGCACTGGTTTGGGACCGAGTGG-----GTCGGAGGTTCAAATCCTCTCGCCGACCA  
>tdbD00005264 Agrobacterium tumefaciens\_str.\_C58\_176299 Gly GCC  
-CGGGGTGTAGCTCAGG--GGT--AGAGCACAACTTGCCAAGGTTGGG-----GTCGAGGTTCAAATCCCGTTCGCCGCTCCA  
>tdbD00005506 Bacillus anthracis\_str.\_Ames\_198094 Gly GCC  
-CGGGAAGTAGTTCAGT--GGT--AGAATACAACCTTGCCAAGGTTGGG-----GTCGCGGGTTCAAATCCCGTCTCCGCTCCA  
>tdbD00005533 Bacillus anthracis\_str.\_Sterne\_260799 Gly GCC  
-CGGGAAGTAGTTCAGT--GGT--AGAATACAACCTTGCCAAGGTTGGG-----GTCGCGGGTTCAAATCCCGTCTCCGCTCCA  
>tdbD00005535 Bacillus anthracis\_str.\_Sterne\_260799 Gly GCC  
-CGGGAAGTAGTTCAGT--GGT--AGAATACAACCTTGCCAAGGTTGGG-----GTCGCGGGTTCAAATCCCGTCTCCGCTCCA  
>tdbD00005534 Bacillus anthracis\_str.\_Sterne\_260799 Gly TCC  
-CGGGGTGTAGTTTGTAGT--GGT--AAAACAAGAGCCTTCCAAGCTCTGG-----T-CGAGAGTTTCGATTCTCTTCCACCCGCT---  
>tdbD00005536 Bacillus anthracis\_str.\_Sterne\_260799 Gly TCC  
-CGGGGTGTAGTTTGTAGT--GGT--AAAACAAGAGCCTTCCAAGCTCTGG-----T-CGAGAGTTTCGATTCTCTTCCACCCGCTCCA  
>tdbD00005568 Bacillus cereus\_ATCC\_10987\_222523 Gly GCC  
-CGGGAAGTAGTTCAGT--GGT--AGAATACAACCTTGCCAAGGTTGGG-----GTCGCGGGTTCAAATCCCGTCTCCGCT---

>tdbD00005570 *Bacillus cereus*\_ATCC\_10987\_222523\_Gly\_GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAATACAACCTTGCCAAGGTTGGG-----GTCGCGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00005569 *Bacillus cereus*\_ATCC\_10987\_222523\_Gly\_TCC  
-GCGGGTGTAGTTTAGT--GGT--AAAACAAGAGCCTTCCAAGCTCTGG-----T-CGAGAGTTCGATTCTCTTCAACCCGCT---  
>tdbD00005571 *Bacillus cereus*\_ATCC\_10987\_222523\_Gly\_TCC  
-GCGGGTGTAGTTTAGT--GGT--AAAACAAGAGCCTTCCAAGCTCTGG-----T-CGAGAGTTCGATTCTCTTCAACCCGCTCCA  
>tdbD00005474 *Bacillus cereus*\_ATCC\_14579\_226900\_Gly\_GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAATACAACCTTGCCAAGGTTGGG-----GTCGCGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00005475 *Bacillus cereus*\_ATCC\_14579\_226900\_Gly\_GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAATACAACCTTGCCAAGGTTGGG-----GTCGCGGGTTTCAATCCCCTCTTCCGCT---  
>tdbD00005476 *Bacillus cereus*\_ATCC\_14579\_226900\_Gly\_TCC  
-GCGGGTGTAGTTTAGT--GGT--AAAACAAGAGCCTTCCAAGCTCTGG-----T-CGAGAGTTCGATTCTCTTCAACCCGCT---  
>tdbD00005477 *Bacillus cereus*\_ATCC\_14579\_226900\_Gly\_TCC  
-GCGGGTGTAGTTTAGT--GGT--AAAACAAGAGCCTTCCAAGCTCTGG-----T-CGAGAGTTCGATTCTCTTCAACCCGCTCCA  
>tdbD00000830 *Bacillus subtilis*\_1423\_Gly\_TCC  
-GCGGGTGTAGTTTAGT--GGT--AAAACCTCAGCCTTCCAAGCTGATG-----T-CGTGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00000832 *Bacillus subtilis*\_1423\_Gly\_TCC  
-GCGGGTGTAGTTTAGT--GGT--AAAACCTCAGCCTTCCAAGCTGATG-----T-CGTGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00005144 *Bacillus subtilis*\_subsp.\_subtilis\_str.\_168\_224308\_Gly\_GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAACACCACCTTGCCAAGGTTGGG-----GTCGCGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00005145 *Bacillus subtilis*\_subsp.\_subtilis\_str.\_168\_224308\_Gly\_TCC  
-GCGGGTGTAGTTTAGT--GGT--AAAACCTCAGCCTTCCAAGCTGATG-----T-CGTGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00005146 *Bacillus subtilis*\_subsp.\_subtilis\_str.\_168\_224308\_Gly\_TCC  
-GCGGGTGTAGTTTAGT--GGT--AAAACCTCAGCCTTCCAAGCTGATG-----T-CGTGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00005594 *Bacillus thuringiensis*\_serovar\_konkukian\_str.\_97-27\_281309\_Gly\_GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAATACAACCTTGCCAAGGTTGGG-----GTCGCGGGTTTCAATCCCCTCTTCCGCT---  
>tdbD00005595 *Bacillus thuringiensis*\_serovar\_konkukian\_str.\_97-27\_281309\_Gly\_GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAATACAACCTTGCCAAGGTTGGG-----GTCGCGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00005596 *Bacillus thuringiensis*\_serovar\_konkukian\_str.\_97-27\_281309\_Gly\_TCC  
-GCGGGTGTAGTTTAGT--GGT--AAAACAAGAGCCTTCCAAGCTCTGG-----T-CGAGAGTTCGATTCTCTTCAACCCGCT---  
>tdbD00005597 *Bacillus thuringiensis*\_serovar\_konkukian\_str.\_97-27\_281309\_Gly\_TCC  
-GCGGGTGTAGTTTAGT--GGT--AAAACAAGAGCCTTCCAAGCTCTGG-----T-CGAGAGTTCGATTCTCTTCAACCCGCTCCA  
>tdbD00005498 *Bacteroides thetaiotaomicron*\_VPI-5482\_226186\_Gly\_GCC  
-GCGGAATAGCTCAGTT--GGT--AGAGCACAACCTTGCCAAGGTTAGG-----GTCGCGAGTTCGAGTCTCGTTTTCCGCT---  
>tdbD00005601 *Bartonella quintana*\_str.\_Toulouse\_283165\_Gly\_GCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGTTGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00005602 *Bartonella quintana*\_str.\_Toulouse\_283165\_Gly\_TCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGTTGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00005408 *Bifidobacterium longum*\_NCC2705\_206672\_Gly\_GCC  
-GCGGACATAGCTTAGTT--GGT--AAAGCGCAACCTTGCCAAGGTTGAG-----ACCGCGGGTTTCAATCCCCTCTTCCGCT---  
>tdbD00005186 *Borrelia burgdorferi*\_B31\_224326\_Gly\_TCC  
-GCTCCTTCGTATAAT--GGCT--ATTACCTTAGCCTTCCAAGCTAATG-----A-TGTCGGTTTCAATCCCCTCTTCCGCT---  
>tdbD00005538 *Borrelia garinii*\_PBi\_290434\_Gly\_GCC  
-GCGAAAGTAACTCAGG--GGT--AGAGTGTACCTTGCCAAGGTTGAA-----GTCGCGGGTTTCAATCCCCTCTTCCGCT---  
>tdbD00005537 *Borrelia garinii*\_PBi\_290434\_Gly\_TCC  
-GCTCCTTCGTATAAT--GGCT--ATTACCTTAGCCTTCCAAGCTAATG-----A-TGTCGGTTTCAATCCCCTCTTCCGCT---  
>tdbD00005243 *Brucella melitensis*\_16M\_224914\_Gly\_GCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGAGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00005411 *Brucella suis*\_1330\_204722\_Gly\_GCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGAGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00005412 *Brucella suis*\_1330\_204722\_Gly\_TCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCACAACCTTGCCAAGGTTGGG-----GTCGAGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00005188 *Campylobacter jejuni*\_subsp.\_jejuni\_NCTC\_11168\_192222\_Gly\_TCC  
-GCGGGAGTAGCTCAGTT--GGCT--AGAGCATCAGCCTTCCAAGCTGAGG-----GTCGCGGGTTTCAATCCCCTCTTCCGCTCCA  
>tdbD00005140 *Chlamydia trachomatis*\_D/UW-3/CX\_272561\_Gly\_GCC  
-GCGGGTGTAGCTCAGT--GGT--AGAGCGCCAGTTTGCCAACGTTGAAG-----GTCGTTGAGTTTCAAGCCTCATCACCCGCT---  
>tdbD00005141 *Chlamydia trachomatis*\_D/UW-3/CX\_272561\_Gly\_TCC  
-GCGCCCGTAGCTCAAT--GGT--AGAGCTGTAGCCTTCCAAGCTACCG-----G-TGTCAGTTTCAAGCCTCATCACCCGCT---  
>tdbD00005137 *Chlamydia pneumoniae*\_AR39\_115711\_Gly\_TCC  
-GCGCCCGTAGCTCAAT--GGT--AGAGCTGTAGCCTTCCAAGCTACCG-----G-TGTCAGTTTCAAGCCTCATCACCCGCT---  
>tdbD00005138 *Chlamydia pneumoniae*\_CWL029\_115713\_Gly\_GCC  
-GCGGGTGTAGCTCAGT--GGT--AGAGCGTCACGTTTGCCAACGTTGAAG-----GTCGTTGAGTTTCAAGCCTCATCACCCGCT---  
>tdbD00005139 *Chlamydia pneumoniae*\_CWL029\_115713\_Gly\_TCC  
-GCGCCCGTAGCTCAAT--GGT--AGAGCTGTAGCCTTCCAAGCTACCG-----G-TGTCAGTTTCAAGCCTCATCACCCGCT---  
>tdbD00005167 *Chlamydia pneumoniae*\_J138\_138677\_Gly\_GCC  
-GCGGGTGTAGCTCAGT--GGT--AGAGCGTCACGTTTGCCAACGTTGAAG-----GTCGTTGAGTTTCAAGCCTCATCACCCGCT---  
>tdbD00005168 *Chlamydia pneumoniae*\_J138\_138677\_Gly\_TCC  
-GCGCCCGTAGCTCAAT--GGT--AGAGCTGTAGCCTTCCAAGCTACCG-----G-TGTCAGTTTCAAGCCTCATCACCCGCT---  
>tdbD00005413 *Corynebacterium efficiens*\_YS-314\_196164\_Gly\_GCC  
-GCGGATGTAGCGCAGTT--GGT--AGCGCATCACCTTGCCAAGGTTGAGG-----GTCGCGAGTTCGAGTCTCGTCATCCGCT---  
>tdbD00005371 *Corynebacterium glutamicum*\_ATCC\_13032\_196627\_Gly\_GCC  
-GCGGATGTAGCGCAGTT--GGT--AGCGCATCACCTTGCCAAGGTTGAGG-----GTCGCGAGTTCGAGTCTCGTCATCCGCT---  
>tdbD00005372 *Corynebacterium glutamicum*\_ATCC\_13032\_196627\_Gly\_GCC  
-GCGGATGTAGCGCAGTT--GGT--AGCGCATCACCTTGCCAAGGTTGAGG-----GTCGCGAGTTCGAGTCTCGTCATCCGCT---  
>tdbD00005481 *Escherichia coli*\_CFT073\_199310\_Gly\_CCC

-GCGGGCGTAGTTCAAT--GGT--AGAACGAGAGCTTCCCAAGCTCTAT-----A-CGAGGGTTCGATTCCCTTCGCCCGCTCCA  
>tdbD00005480 Escherichia\_coli\_CFT073\_199310 Gly GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACGACCTTGCCAAGGTCGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005482 Escherichia\_coli\_CFT073\_199310 Gly TCC  
-GCGGGCATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCGCTGCCCGCTCCA  
>tdbD00005169 Escherichia\_coli\_K12\_83333 Gly CCC  
-GCGGGCGTAGTTCAAT--GGT--AGAACGAGAGCTTCCCAAGCTCTAT-----A-CGAGGGTTCGATTCCCTTCGCCCGCTCCA  
>tdbD00005170 Escherichia\_coli\_K12\_83333 Gly GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACGACCTTGCCAAGGTCGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005171 Escherichia\_coli\_K12\_83333 Gly TCC  
-GCGGGCATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCGCTGCCCGCTCCA  
>tdbD00005172 Escherichia\_coli\_O157H7\_83334 Gly CCC:  
-GCGGGCGTAGTTCAAT--GGT--AGAACGAGAGCTTCCCAAGCTCTAT-----A-CGAGGGTTCGATTCCCTTCGCCCGCTCCA  
>tdbD00005173 Escherichia\_coli\_O157H7\_83334 Gly GCC:  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACGACCTTGCCAAGGTCGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005174 Escherichia\_coli\_O157H7\_83334 Gly TCC:  
-GCGGGCATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCGCTGCCCGCTCCA  
>tdbD00005175 Escherichia\_coli\_O157H7\_EDL933\_155864 Gly CCC:  
-GCGGGCGTAGTTCAAT--GGT--AGAACGAGAGCTTCCCAAGCTCTAT-----A-CGAGGGTTCGATTCCCTTCGCCCGCTCCA  
>tdbD00005176 Escherichia\_coli\_O157H7\_EDL933\_155864 Gly GCC:  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACGACCTTGCCAAGGTCGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005177 Escherichia\_coli\_O157H7\_EDL933\_155864 Gly TCC:  
-GCGGGCATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCGCTGCCCGCTCCA  
>tdbD00005541 Geobacter\_sulfurreducens\_PCA\_243231 Gly TCC  
-GCGGGAGTAGCTCAGTT--GGCT--AGAGCATCAGCCTTCCAAGCTGAGG-----GTCGCGGGTTCGAGTCCCGTTTCCCGCTCCA  
>tdbD00000845 Haemophilus\_influenzae\_727 Gly GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACGACCTTGCCAAGGTCGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005182 Haemophilus\_influenzae\_Rd\_KW20\_71421 Gly GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACGACCTTGCCAAGGTCGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005183 Haemophilus\_influenzae\_Rd\_KW20\_71421 Gly GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACGACCTTGCCAAGGTCGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005184 Haemophilus\_influenzae\_Rd\_KW20\_71421 Gly TCC  
-GCGGGCATCGTATAAT--GGCT--ATTACCTTAGCCTTCCAAGCTAATG-----A-TGCGGGTTCGATTCCCGCTGCCCGCTCCA  
>tdbD00005178 Helicobacter\_pylori\_26695\_85962 Gly GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACGACCTTGCCAAGGTCGGG-----GTCGCGGGTTCGATCCCGTTTCCCGCTCCA  
>tdbD00005179 Helicobacter\_pylori\_26695\_85962 Gly TCC  
-GCGGGAATAGCTCAGTT--GGCT--AGAGCATCAGCCTTCCAAGCTGAGG-----GTCGCGGGTTCGAGTCCCGTTTCCCGCTCCA  
>tdbD00005181 Helicobacter\_pylori\_J99\_85963 Gly TCC  
-GCGGGAATAGCTCAGTT--GGCT--AGAGCATCAGCCTTCCAAGCTGAGG-----GTCGCGGGTTCGAGTCCCGTTTCCCGCTCCA  
>tdbD00005448 Lactobacillus\_plantarum\_WCFS1\_220668 Gly GCC  
-GCGGAAGTAGTTTCAAT--GGT--AGAACATCACCTTGCCATGGTGGGG-----GTCGCGGGTTCGAATCCCGTCTTCCGCT---  
>tdbD00005547 Leifsonia\_xyli\_subsp\_xyli\_str\_CTCB07\_281090 Gly GCC  
-GCGGATGTAGCGCAGTT--GGT--AGCGCATCACCTTGCCAAGGTGAGG-----GTCGCGAGTTCGAGTCTCGTCATCCGCT---  
>tdbD00005223 Listeria\_monocytogenes\_EGD-e\_169963 Gly GCC  
-GCGGAAGTAGTTTCAAT--GGT--AGAACATCACCTTGCCAAGGTGAGG-----GTCGCGGGTTCGAACCCCGTCTTCCGCT---  
>tdbD00005225 Listeria\_monocytogenes\_EGD-e\_169963 Gly GCC  
-GCGGAAGTAGTTTCAAT--GGT--AGAACATCACCTTGCCAAGGTGAGG-----GTCGCGGGTTCGAACCCCGTCTTCCGCTCCA  
>tdbD00005226 Listeria\_monocytogenes\_EGD-e\_169963 Gly GCC  
-GCGGAAGTAGTTTCAAT--GGT--AGAACATCACCTTGCCAAGGTGAGG-----GTCGCGGGTTCGAACCCCGTCTTCCGCT---  
>tdbD00005224 Listeria\_monocytogenes\_EGD-e\_169963 Gly TCC  
-GCGGGTGTAGTTTCAAT--GGT--AAAACATCACCTTCCAAGCTGTTG-----T-CGTGGGTTTCGATTCCCATCACCCGCT---  
>tdbD00005575 Listeria\_monocytogenes\_str\_4b\_F2365\_265669 Gly GCC  
-GCGGAAGTAGTTTCAAT--GGT--AGAACATCACCTTGCCAAGGTGAGG-----GTCGCGGGTTCGAACCCCGTCTTCCGCT---  
>tdbD00005577 Listeria\_monocytogenes\_str\_4b\_F2365\_265669 Gly GCC  
-GCGGAAGTAGTTTCAAT--GGT--AGAACATCACCTTGCCAAGGTGAGG-----GTCGCGGGTTCGAACCCCGTCTTCCGCT---  
>tdbD00005576 Listeria\_monocytogenes\_str\_4b\_F2365\_265669 Gly TCC  
-GCGGGTGTAGTTTCAAT--GGT--AAAACATCACCTTCCAAGCTGTTG-----T-CGTGGGTTTCGATTCCCATCACCCGCT---  
>tdbD00005246 Mesorhizobium\_loti\_MAFF303099\_266835 Gly CCC  
-GCGGGTATGATGTAAT--GGT--AGCCTGTGAGCTTCCCAAGCTGAAAC-----G-CGCGGGTTCGATTCCCGTACCCGCTCCA  
>tdbD00005163 Mycobacterium\_leprae\_TN\_272631 Gly GCC  
-GCGGATGTAGCGCAGTT--GGT--AGCGCATCACCTTGCCAAGGTGAGG-----GTCGCGGGTTCGAATCCCGTCTTCCGCT---  
>tdbD00005150 Mycobacterium\_tuberculosis\_CDC1551\_83331 Gly GCC  
-GCGGATGTAGCGCAGTT--GGT--AGCGCATCACCTTGCCAAGGTGAGG-----GTCGCGGGTTCGAATCCCGTCTTCCGCT---  
>tdbD00005151 Mycobacterium\_tuberculosis\_CDC1551\_83331 Gly TCC  
-GCGGGCGTAGCTCAAT--GGT--AGAGCCCTAGTCTTCCAAGCTAGCG-----A-CGCGGGTTCGATTCCCGTTCGCCCGCT---  
>tdbD00005519 Mycobacterium\_tuberculosis\_H37Rv\_83332 Gly GCC  
-GCGGATGTAGCGCAGTT--GGT--AGCGCATCACCTTGCCAAGGTGAGG-----GTCGCGGGTTCGAATCCCGTCTTCCGCT---  
>tdbD00005518 Mycobacterium\_tuberculosis\_H37Rv\_83332 Gly TCC  
-GCGGGCGTAGCTCAAT--GGT--AGAGCCCTAGTCTTCCAAGCTAGCG-----A-CGCGGGTTCGATTCCCGTTCGCCCGCT---  
>tdbD00005196 Mycoplasma\_genitalium\_G37\_243273 Gly TCC  
-GCGAGTATAGTTTCAAT--GGT--AGAACATCACCTTCCAAGCTGATC-----G-TGTCGGTTCGATTCCGATTACTCGCTCCA  
>tdbD00005198 Mycoplasma\_pneumoniae\_M129\_272634 Gly TCC  
-GCGAGTATAGTTTCAAT--GGT--AGAACATCACCTTCCAAGCTGATC-----G-TGTCGGTTCGATTCCGATTACTCGCTCCA  
>tdbD00005154 Neisseria\_meningitidis\_Z2491\_122587 Gly GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCGCAACCTTGCCAAGGTTGAG-----GTCGCGAGTTCGAGACTCGTTTCCCGCTCCA

>tdbD00005155 *Neisseria meningitidis*\_Z2491\_122587\_Gly\_TCC  
-GCGGGTGTAGCTCAAT--GGT--AGAGCAGAAGCCTTCCAAGCTTACG-----G-TGAGGGTTCGATTCCCTTACCCGCTCCA  
>tdbD00005494 *Nitrosomonas europaea*\_ATCC\_19718\_228410\_Gly\_GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCGCAACCTTGCCAAGGTTGAG-----GTCGCGAGTTCGAGACTCGTTTCCCGCTCCA  
>tdbD00005419 *Oceanobacillus iheyensis*\_HTE831\_221109\_Gly\_GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAACCACACCTTGCCAAGGTGGG-----GTCGCGGGTTCGAATCCCGTCTTCCGCTCCA  
>tdbD00005200 *Pasteurella multocida*\_subsp.\_multocida\_str.\_Pm70\_272843\_Gly\_TCC  
-GCGGGCATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCGTCCCGCTCCA  
>tdbD00005522 *Photobacterium luminescens*\_subsp.\_laumondii\_TTO1\_243265\_Gly\_GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACACCTTGCCAAGGTTGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005524 *Photobacterium luminescens*\_subsp.\_laumondii\_TTO1\_243265\_Gly\_GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACACCTTGCCAAGGTTGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005525 *Photobacterium luminescens*\_subsp.\_laumondii\_TTO1\_243265\_Gly\_TCC  
-GCGGGCATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCGTCCCGCTCCA  
>tdbD00005204 *Pseudomonas aeruginosa*\_PAO1\_208964\_Gly\_GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACACCTTGCCAAGGTTGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005205 *Pseudomonas aeruginosa*\_PAO1\_208964\_Gly\_TCC  
-GCGGTATAGTTCAGT--GGT--AGAACCACACCTTGCCAAGGTTGGG-----A-TGCGGGTTCGATTCCCGTCCCGCTCCA  
>tdbD00000847 *Pseudomonas putida*\_303\_Gly\_GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACACCTTGCCAAGGTTGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005502 *Pseudomonas syringae*\_pv.\_tomato\_str.\_DC3000\_223283\_Gly\_GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACACCTTGCCAAGGTTGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005255 *Ralstonia solanacearum*\_GMI1000\_267608\_Gly\_TCC  
-GCGGGTGTAGCTCAAT--GGT--AGAGCAGAAGCCTTCCAAGCTTACG-----A-CGAGGGTTCGATTCCCTTACCCGCTCCA  
>tdbD00005528 *Rhodopseudomonas palustris*\_CGA009\_258594\_Gly\_GCC  
-GCGGGCGTAGTTCAAT--GGT--AGAACGCGAGCTTCCAAGCTGATG-----A-CGAGGGTTCGATTCCCTTCCCGCTCCA  
>tdbD00005526 *Rhodopseudomonas palustris*\_CGA009\_258594\_Gly\_GCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCACACCTTGCCAAGGTTGGG-----GTCGAGGGTTCGAATCCCTTCCCGCTCCA  
>tdbD00005527 *Rhodopseudomonas palustris*\_CGA009\_258594\_Gly\_TCC  
-GCGGGTGTAGCTCAAT--GGT--AGAGCAGCAGCTTCCAAGCTGAAT-----A-CGAGGGTTCGATTCCCTTACCCGCTCCA  
>tdbD00000842 *Rickettsia prowazekii*\_782\_Gly\_TCC  
-GCGGGTGTAGCTCAAT--GGT--AGAGTTCAGCCTTCCAAGCTGGCT-----G-TGTGGGTTTCGATTCCCATCACCCTCCA  
>tdbD00005370 *Rickettsia prowazekii*\_str.\_Madrid\_E\_272947\_Gly\_TCC  
-GCGGGTGTAGCTCAAT--GGT--AGAGTTCAGCCTTCCAAGCTGGCT-----G-TGTGGGTTTCGATTCCCATCACCCTCCA  
>tdbD00005553 *Rickettsia typhi*\_str.\_Wilmington\_257363\_Gly\_GCC  
-GCGGGTGTAGCTCAGG--GGT--AGAGCGTACCTTGCCAAGGTCGAA-----GTCGAGGGTTCGAATCCCTTACCCGCTCCA  
>tdbD00005266 *Salmonella enterica*\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341\_Gly\_GCC  
-GCGGGCGTAGTTCAAT--GGT--AGAACGAGAGCTTCCAAGCTCTAT-----A-CGAGGGTTCGATTCCCTTCCCGCTCCA  
>tdbD00005265 *Salmonella enterica*\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341\_Gly\_GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACACCTTGCCAAGGTTGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005267 *Salmonella enterica*\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341\_Gly\_TCC  
-GCGGGCATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCGTCCCGCTCCA  
>tdbD00005488 *Salmonella enterica*\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261\_Gly\_GCC  
-GCGGGCGTAGTTCAAT--GGT--AGAACGAGAGCTTCCAAGCTCTAT-----A-CGAGGGTTCGATTCCCTTCCCGCTCCA  
>tdbD00005487 *Salmonella enterica*\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261\_Gly\_GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACACCTTGCCAAGGTTGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005489 *Salmonella enterica*\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261\_Gly\_TCC  
-GCGGGCATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCGTCCCGCTCCA  
>tdbD00005251 *Salmonella typhimurium*\_LT2\_99287\_Gly\_GCC  
-GCGGGCGTAGTTCAAT--GGT--AGAACGAGAGCTTCCAAGCTCTAT-----A-CGAGGGTTCGATTCCCTTCCCGCTCCA  
>tdbD00005250 *Salmonella typhimurium*\_LT2\_99287\_Gly\_GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACACCTTGCCAAGGTTGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005252 *Salmonella typhimurium*\_LT2\_99287\_Gly\_TCC  
-GCGGGCATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCGTCCCGCTCCA  
>tdbD00005427 *Shigella flexneri*\_2a\_str.\_301\_198214\_Gly\_GCC  
-GCGGGCGTAGTTCAAT--GGT--AGAACGAGAGCTTCCAAGCTCTAT-----A-CGAGGGTTCGATTCCCTTCCCGCTCCA  
>tdbD00005428 *Shigella flexneri*\_2a\_str.\_301\_198214\_Gly\_GCC  
-GCGGGAATAGCTCAGTT--GGT--AGAGCACACCTTGCCAAGGTTGGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005426 *Shigella flexneri*\_2a\_str.\_301\_198214\_Gly\_TCC  
-GCGGGCATCGTATAAT--GGCT--ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCGTCCCGCTCCA  
>tdbD00005269 *Sinorhizobium meliloti*\_1021\_266834\_Gly\_TCC  
-GCGGGTATAGCTCAAT--GGT--AGAGCAGCAGCCTTCCAAGCTGAAT-----A-CGCGGGTTCGATTCCCGTACCCGCTCCA  
>tdbD00005376 *Staphylococcus aureus*\_subsp.\_aureus\_MW2\_196620\_Gly\_TCC  
-GCGGGTGTAGTTTAAAT--GGC--AAAACCTCAGCCTTCCAAGCTGATG-----T-TGTGGGTTTCGATTCCCATCACCCTCCA  
>tdbD00005160 *Staphylococcus aureus*\_subsp.\_aureus\_N315\_158879\_Gly\_TCC  
-GCGGGTGTAGTTTAAAT--GGC--AAAACCTCAGCCTTCCAAGCTGATG-----T-TGTGGGTTTCGATTCCCATCACCCTCCA  
>tdbD00005455 *Staphylococcus epidermidis*\_ATCC\_12228\_176280\_Gly\_GCC  
-GCGGAAGTAGTTCAGT--GGT--AGAACCACACCTTGCCAAGGTTGGG-----GTCGCGGGTTCGAATCCCGTCTTCCGCTCCA  
>tdbD00005451 *Staphylococcus epidermidis*\_ATCC\_12228\_176280\_Gly\_TCC  
-GCGGGTGTAGTTTAAAT--GGC--AAAACCTCAGCCTTCCAAGCTGATG-----T-TGTGGGTTTCGATTCCCATCACCCTCCA  
>tdbD00005379 *Streptococcus agalactiae*\_NEM316\_211110\_Gly\_GCC  
-GCCAAGTAGTTCAGT--GGT--AGAACATCACCTTGCCAAGGTTGAGG-----GTCGCGGGTTCGAACCCCGTCTTCCGCT---  
>tdbD00005380 *Streptococcus agalactiae*\_NEM316\_211110\_Gly\_TCC  
-GCGGGTGTAGTTTAAAT--GGT--AAAACCTCAGCCTTCCAAGCTGATG-----T-CGCGAGTTCGATTCTCGTACCCGCT---  
>tdbD00005433 *Streptococcus mutans*\_UA159\_210007\_Gly\_TCC

-GCGGGTGTAGTTTGTAGT--GGT--AAAACCACAGCCTTCCAAGCTGTTG-----T-CGCGAGTTCGATTCTCGTCACCCGCT---  
>tdbD00005435 Streptococcus\_mutans\_UA159 210007 Gly TCC  
-GCGGGTGTAGTTTGTAGT--GGT--AAAACACTACAGCCTTCCAAGCTGTTG-----T-CGCGAGTTCGATTCTCGTCACCCGCT---  
>tdbD00005234 Streptococcus\_pneumoniae\_TIGR4 170187 Gly TCC  
-GCGGGTGTAGTTTGTAGT--GGT--AAAACACTACAGCCTTCCAAGCTGTTG-----T-CGCGAGTTCGATTCTCGTCACCCGCT---  
>tdbD00005232 Streptococcus\_pyogenes\_M1\_GAS 160490 Gly GCC  
-GCGAACGTAGTTCAGT--GGT--AGAACATCACCTTGCCAAGGTGGGG-----GTCGCGGGTTCGAATCCCGTCGTTCCGCT---  
>tdbD00005233 Streptococcus\_pyogenes\_M1\_GAS 160490 Gly TCC  
-GCGGGTGTAGTTTGTAGT--GGT--AAAACACTACAGCCTTCCAAGCTGTTG-----T-CGCGAGTTCGATTCTCGTCACCCGCT---  
>tdbD00005381 Streptococcus\_pyogenes\_MGAS315 198466 Gly GCC  
-GCGAACGTAGTTCAGT--GGT--AGAACATCACCTTGCCAAGGTGGGG-----GTCGCGGGTTCGAATCCCGTCGTTCCGCT---  
>tdbD00005382 Streptococcus\_pyogenes\_MGAS315 198466 Gly TCC  
-GCGGGTGTAGTTTGTAGT--GGT--AAAACACTACAGCCTTCCAAGCTGTTG-----T-CGCGAGTTCGATTCTCGTCACCCGCT---  
>tdbD00005469 Streptococcus\_pyogenes\_SSI-1 193567 Gly GCC  
-GCGAACGTAGTTCAGT--GGT--AGAACATCACCTTGCCAAGGTGGGG-----GTCGCGGGTTCGAATCCCGTCGTTCCGCT---  
>tdbD00005470 Streptococcus\_pyogenes\_SSI-1 193567 Gly TCC  
-GCGGGTGTAGTTTGTAGT--GGT--AAAACACTACAGCCTTCCAAGCTGTTG-----T-CGCGAGTTCGATTCTCGTCACCCGCT---  
>tdbD00005422 Streptomyces\_coelicolor\_A3(2) 100226 Gly GCC  
-GCGGACGTAGCTCAGT--GGT--AGAGCGCAACCTTGCCAAGGTTGAG-----GTCGCGAGTTCGAGCCTCGTCGTCGCT---  
>tdbD00000820 Streptomyces\_lividans 1916 Gly GCC  
-GCGGACGTAGCTCAGT--GGT--AGAGCGCAACCTTGCCAAGGTTGAG-----GTCGCGAGTTCGAGCCTCGTCGTCGCT---  
>tdbD00005206 Synechocystis\_sp.\_PCC\_6803 1148 Gly CCC  
-GCGGGTATAGTTTGTAGT--GGT--AAAACGAAAGCCTCCCATGCTTTAG-----T-TGGGGTTCGATTCCCCCTACCCGCT---  
>tdbD00005207 Synechocystis\_sp.\_PCC\_6803 1148 Gly GCC  
-GCGGGTATAGCTCAGT--GGT--AGAGCGCAACCTTGCCAAGGTTGAG-----GTCGCGGGTTCGAATCCCGTTACCCGCT---  
>tdbD00005208 Synechocystis\_sp.\_PCC\_6803 1148 Gly TCC  
-GCGGGTGTAGTTTGTAGT--GGT--AAAACCTTAGCCTTCCAAGCTAATG-----A-TAGGGTTCGATTCCCCCTACCCGCT---  
>tdbD00005385 Thermosynechococcus\_elongatus\_BP-1 197221 Gly GCC  
-GCGGGTATAGCTCAGT--GGT--AGAGCGCAACCTTGCCAAGGTTGAG-----GTCGCGGGTTCGAATCCCGTTACCCGCT---  
>tdbD00005585 Thermus\_thermophilus\_HB27 262724 Gly GCC  
-GCGGGAGTAGCTCAGT--GGT--AGAGCAGACCTTGCCAAGGTGCGG-----GTCGCGGGTTCGAATCCCGTCTCCCGCTCCA  
>tdbD00005201 Treponema\_pallidum\_subsp.\_pallidum\_str.\_Nichols 243276 Gly GCC  
-GCGGGAATAGCTCAGT--GGT--AGAGCGCAACCTTGCCAAGGTGAG-----GTCGCGGGTTCGATCCCGTTTCCCGCT---  
>tdbD00005202 Treponema\_pallidum\_subsp.\_pallidum\_str.\_Nichols 243276 Gly TCC  
-GCGGATGTTGTATAAC--GGCT-ATTACCCAGCCTTCCAAGCTGAG-----A-CGTGGTTCGACTCCCATCATCCGCT---  
>tdbD00005460 Tropheryma\_whipplei\_TW08/27 218496 Gly CCC  
-GCGAGTGTAGTTCAAT--GGC--AGAACTTCAGCTTCCAAGCTGAG-----G-CGCGGGTTCGATTCCCGTCACTCGCT---  
>tdbD00005459 Tropheryma\_whipplei\_TW08/27 218496 Gly GCC  
-GCGGATGTGGCGCAGT--GGT--AGCGCATCACCTTGCCAAGGTGAGG-----GTCGCGAGTTCGAATCTCGTCATCCGCT---  
>tdbD00005157 Vibrio\_cholerae\_O1\_biovar\_El\_Tor\_str.\_N16961 243277 Gly TCC  
-GCGGGCATCGTATAAT--GGCT-ATTACCTCAGCCTTCCAAGCTGATG-----A-TGCGGGTTCGATTCCCGTCCCCGCTCCA  
>tdbD00005394 Xanthomonas\_campestris\_pv.\_campestris\_str.\_ATCC\_33913 190485 Gly CCC  
-GCGGGCAGTACTCAAT--GGT--AGAGCTGTAGCTTCCAAGCTACTG-----A-CGTGGTTCGATTCCCATCGCCCGCTCCA  
>tdbD00005393 Xanthomonas\_campestris\_pv.\_campestris\_str.\_ATCC\_33913 190485 Gly GCC  
-GCGGGAATAGCTCAGT--GGT--AGAGCGCAACCTTGCCAAGGTTGAG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005392 Xanthomonas\_campestris\_pv.\_campestris\_str.\_ATCC\_33913 190485 Gly TCC  
-GCGGGAGTAGTTCAAC--GGT--AGAACCACAGCCTTCCAAGCTGATG-----G-TGCGGGTTCGATTCCCGTCTCCCGCTCCA  
>tdbD00005214 Xylella\_fastidiosa\_9a5c 160492 Gly GCC  
-GCGGGAATAGCTCAGT--GGT--AGAGCGCAACCTTGCCAAGGTTGAG-----GTCGCGAGTTCGAGCCTCGTTTCCCGCTCCA  
>tdbD00005462 Xylella\_fastidiosa\_Temecula 183190 Gly CCC  
-GCGGGCAGTACTCAAT--GGT--AGAGCTGTAGCTTCCAAGCTACCG-----A-CGTGGTTCGATTCCCATCGCCCGCTCCA  
>tdbD00005461 Xylella\_fastidiosa\_Temecula 183190 Gly GCC  
-GCGGGAATAGCTCAGT--GGT--AGAGCGCAACCTTGCCAAGGTTGAG-----GTCGCGAGTTCGAGCCTCGTTTCCCGCTCCA  
>tdbD00005463 Xylella\_fastidiosa\_Temecula 183190 Gly TCC  
-GCGGGAGTAGTTCAAA--GGT--AGAACCACAGCCTTCCAAGCTGATG-----G-TGCGGGTTCGATTCCCGTCTCCCGCTCCA  
>tdbD00005559 Yersinia\_pestis\_biovar\_Microtus\_str.\_91001 229193 Gly GCC  
-GCGGGAATAGCTCAGT--GGT--AGAGCAGACCTTGCCAAGGTGCGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005248 Yersinia\_pestis\_CO92 214092 Gly CCC  
-GCGGGTGTAGTTCAAT--GGT--AGAACGAGAGCTTCCAAGCTCTAT-----A-CGAGGGTTCGATTCCCTTACCCGCTCCA  
>tdbD00005247 Yersinia\_pestis\_CO92 214092 Gly GCC  
-GCGGGAATAGCTCAGT--GGT--AGAGCAGACCTTGCCAAGGTGCGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005249 Yersinia\_pestis\_CO92 214092 Gly TCC  
-GCGGGCATCGTATAAT--GGCT-ATTACCTCAGCCTTCCAAGCTGATG-----A-TGTGGTTCGATTCCCACTGCCCCGCTCCA  
>tdbD00005403 Yersinia\_pestis\_KIM 187410 Gly CCC  
-GCGGGTGTAGTTCAAT--GGT--AGAACGAGAGCTTCCAAGCTCTAT-----A-CGAGGGTTCGATTCCCTTACCCGCTCCA  
>tdbD00005402 Yersinia\_pestis\_KIM 187410 Gly GCC  
-GCGGGAATAGCTCAGT--GGT--AGAGCAGACCTTGCCAAGGTGCGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005401 Yersinia\_pestis\_KIM 187410 Gly TCC  
-GCGGGCATCGTATAAT--GGCT-ATTACCTCAGCCTTCCAAGCTGATG-----A-TGTGGTTCGATTCCCACTGCCCCGCTCCA  
>tdbD00005564 Yersinia\_pseudotuberculosis\_IP\_32953 273123 Gly CCC  
-GCGGGTGTAGTTCAAT--GGT--AGAACGAGAGCTTCCAAGCTCTAT-----A-CGAGGGTTCGATTCCCTTACCCGCTCCA  
>tdbD00005563 Yersinia\_pseudotuberculosis\_IP\_32953 273123 Gly GCC  
-GCGGGAATAGCTCAGT--GGT--AGAGCAGACCTTGCCAAGGTGCGG-----GTCGCGAGTTCGAGTCTCGTTTCCCGCTCCA  
>tdbD00005562 Yersinia\_pseudotuberculosis\_IP\_32953 273123 Gly TCC  
-GCGGGCATCGTATAAT--GGCT-ATTACCTCAGCCTTCCAAGCTGATG-----A-TGTGGTTCGATTCCCACTGCCCCGCTCCA

>tdbD00005795 *Bacillus anthracis* str. *Sterne* 260799 His GTG  
GGCGGTTGTGGCGAAGT--GGTT--AACGCACCGGATTGTGGTCCGGCA-----TTCGTGGGTTTCGATTCCCATCAGTCGCCCA  
>tdbD00005808 *Bacillus cereus* ATCC 10987 222523 His GTG  
GGCGGTTGTGGCGAAGT--GGTT--AACGCACCGGATTGTGGTCCGGCA-----TTCGTGGGTTTCGATTCCCATCAGTCGCCCA  
>tdbD00005809 *Bacillus cereus* ATCC 10987 222523 His GTG  
GGCGGTTGTGGCGAAGT--GGTT--AACGCACCGGATTGTGGTCCGGCA-----TTCGTGGGTTTCGATTCCCATCAGTCGCCCA  
>tdbD00005774 *Bacillus cereus* ATCC 14579 226900 His GTG  
GGCGGTTGTGGCGAAGT--GGTT--AACGCACCGGATTGTGGTCCGGCA-----TTCGTGGGTTTCGATTCCCATCAGTCGCCCA  
>tdbD00005651 *Bacillus subtilis* subsp. *subtilis* str. 168 224308 His GTG  
GGCGGTTGTGGCGAAGT--GGTT--AACGCACCGATTGTGGTCTGGCA-----CTCGTGGGTTTCGATTCCCATCAATCGCCCA  
>tdbD00005652 *Bacillus subtilis* subsp. *subtilis* str. 168 224308 His GTG  
GGCGGTTGTGGCGAAGT--GGTT--AACGCACCGATTGTGGTCTGGCA-----TTCGTGGGTTTCGATTCCCATCAATCGCCCA  
>tdbD00005820 *Bacillus thuringiensis* serovar *konkukian* str. 97-27 281309 His GTG  
GGCGGTTGTGGCGAAGT--GGTT--AACGCACCGATTGTGGTCCGGCA-----TTCGTGGGTTTCGATTCCCATCAGTCGCCCA  
>tdbD00005669 *Borrelia burgdorferi* B31 224326 His GTG  
GGTGGTGTAGCTCAGTT-GGT--AGAGCGTCGGGTTGTGGTCCGAAT-----GTCGCGGGTTCAAGCCCGTCAATCACC--  
>tdbD00005796 *Borrelia garinii* PBI 290434 His GTG  
GGTGGTGTAGCTCAGTT-GGT--AGAGCGTCGGGTTGTGGTCCGAAT-----GTCGCGGGTTCAAGCCCGTCAATCACC--  
>tdbD00005649 *Chlamydia trachomatis* D/UW-3/CX 272561 His GTG  
GGCGAAGCTAGCTCAGTT-GGTT--AGAGCGTCGGGTTGTGGTCCGAAG-----GTCGCGGGTTCAAGCCCGTTCGTTCCGCC--  
>tdbD00005648 *Chlamydia pneumoniae* CWL029 115713 His GTG  
GGCGAAGCTAGCTCAGTT-GGTT--AGAGCGTCGGGTTGTGGTCCGAAG-----GTCGCGGGTTCAAGCCCGTTCGTTCCGCC--  
>tdbD00005662 *Chlamydia pneumoniae* J138 138677 His GTG  
GGCGAAGCTAGCTCAGTT-GGTT--AGAGCGTCGGGTTGTGGTCCGAAG-----GTCGCGGGTTCAAGCCCGTTCGTTCCGCC--  
>tdbD00005750 *Corynebacterium efficiens* YS-314 196164 His GTG  
GGTGGCTGTAGCTCAGTT-GGT--AGAGCACCGATTGTGATCCAGTT-----GTCGCGGGTTTCGAGCCCGTTCAGCCACC--  
>tdbD00005735 *Corynebacterium glutamicum* ATCC 13032 196627 His GTG  
GGTGGCTGTAGCTCAGTT-GGT--AGAGCACCGATTGTGATCCAGTT-----GTCGCGGGTTTCGAGCCCGTTCAGCCACC--  
>tdbD00005776 *Escherichia coli* CFT073 199310 His GTG  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGTGGGTTTCGAATCCCATTAGCCACCCCA  
>tdbD00005663 *Escherichia coli* K12 83333 His GTG  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGTGGGTTTCGAATCCCATTAGCCACCCCA  
>tdbD00005664 *Escherichia coli* O157H7 83334 His GTG:  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGTGGGTTTCGAATCCCATTAGCCACCCCA  
>tdbD00005665 *Escherichia coli* O157H7 EDL933 155864 His GTG:  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGTGGGTTTCGAATCCCATTAGCCACCCCA  
>tdbD00000992 *Haemophilus influenzae* 727 His GTG  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGTGGGTTTCGAATCCCATTAGCCACCCCA  
>tdbD00005668 *Haemophilus influenzae* Rd KW20 71421 His GTG  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGTGGGTTTCGAATCCCATTAGCCACCCCA  
>tdbD00005666 *Helicobacter pylori* 26695 85962 His GTG  
GGTGGGAGTAGCTCAGTC-GGTT--AGAGCATCAGATTGTGGTCCAGG-----GTCGTGGGTTTCGATTCCCATTCTCCACCCCA  
>tdbD00005667 *Helicobacter pylori* J99 85963 His GTG  
GGTGGGAGTAGCTCAGTC-GGTT--AGAGCATCAGATTGTGGTCCAGG-----GTCGTGGGTTTCGATTCCCATTCTCCACCCCA  
>tdbD00005684 *Listeria monocytogenes* EGD-e 169963 His GTG  
GGCGGATATGGCGAAGT--GGTT--AACGCACCTGATTGTGGTCCAGCA-----TTCGTGGGTTTCGATTCCCATTATCCGCC--  
>tdbD00005685 *Listeria monocytogenes* EGD-e 169963 His GTG  
GGCGGATATGGCGAAGT--GGTT--AACGCACCTGATTGTGGTCCAGCA-----TTCGTGGGTTTCGATTCCCATTATCCGCC--  
>tdbD00005811 *Listeria monocytogenes* str. 4b F2365 265669 His GTG  
GGCGGATATGGCGAAGT--GGTT--AACGCACCTGATTGTGGTCCAGCA-----TTCGTGGGTTTCGATTCCCATTATCCGCC--  
>tdbD00005812 *Listeria monocytogenes* str. 4b F2365 265669 His GTG  
GGCGGATATGGCGAAGT--GGTT--AACGCACCTGATTGTGGTCCAGCA-----TTCGTGGGTTTCGATTCCCATTATCCGCC--  
>tdbD00005660 *Mycobacterium leprae* TN 272631 His GTG  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGCGGGTTTCGAGTCCCGTCACTCACCCCA  
>tdbD00005674 *Mycobacterium tuberculosis* CDC1551 83331 His GTG  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGCGGGTTTCGAGTCCCGTCACTCACCCCA  
>tdbD00005789 *Mycobacterium tuberculosis* H37Rv 83332 His GTG  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGCGGGTTTCGAGTCCCGTCACTCACCCCA  
>tdbD00005674 *Mycobacterium tuberculosis* M129 272634 His GTG  
GGCGGATATGGCGAAGT--GGTT--AACGCACCTGATTGTGGATCAGGCA-----TTCGTGGGTTTCGATTCCCATTATCCGCC--  
>tdbD00005656 *Neisseria meningitidis* Z2491 122587 His GTG  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGCGGGTTTCGAGTCCCGTCACTCACCCCA  
>tdbD00005801 *Rickettsia typhi* str. *Wilmington* 257363 His GTG  
GGCGGATATGGCGAAGT--GGTT--AACGCACCTGATTGTGGATCAGGCA-----TTCGTGGGTTTCGATTCCCATTATCCGCC--  
>tdbD00005700 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. *CT18* 220341 His GTG  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGCGGGTTTCGAGTCCCGTCACTCACCCCA  
>tdbD00005778 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. *Ty2* 209261 His GTG  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGCGGGTTTCGAGTCCCGTCACTCACCCCA  
>tdbD00000989 *Salmonella typhimurium* 602 His GTG  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGCGGGTTTCGAGTCCCGTCACTCACCCCA  
>tdbD00005695 *Salmonella typhimurium* LT2 99287 His GTG  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGCGGGTTTCGAGTCCCGTCACTCACCCCA  
>tdbD00005756 *Shigella flexneri* 2a str. 301 198214 His GTG  
GGTGGCTATAGCTCAGTT-GGT--AGAGCCCTGGATTGTGATCCAGTT-----GTCGCGGGTTTCGAGTCCCGTCACTCACCCCA  
>tdbD00005794 *Staphylococcus aureus* subsp. *aureus* *MRSA252* 282458 His GTG



GGCGGCTGTGGTGAAGT--GGTT-AACACATCGGATTGTGGTTCGACA-----TTCGAGGGTTCGATCCCCTTCAGCCGCC---  
>tdbD00005736 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620\_His\_GTG  
GGCGGTTGTGGTGAAGT--GGTT-AACACATCGGATTGTGGTTCGACA-----TTCGAGGGTTCGATCCCCTTCAGCCGCCCA  
>tdbD00005737 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620\_His\_GTG  
GGCGGCTGTGGTGAAGT--GGTT-AACACATCGGATTGTGGTTCGACA-----TTCGAGGGTTCGATCCCCTTCAGCCGCC---  
>tdbD00005658 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879\_His\_GTG  
GGCGGCTGTGGTGAAGT--GGTT-AACACATCGGATTGTGGTTCGACA-----TTCGAGGGTTCGATCCCCTTCAGCCGCC---  
>tdbD00005659 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879\_His\_GTG  
GGCGGTTGTGGTGAAGT--GGTT-AACACATCGGATTGTGGTTCGACA-----TTCGAGGGTTCGATCCCCTTCAGCCGCCCA  
>tdbD00005738 Streptococcus\_agalactiae\_NEM316\_211110\_His\_GTG  
GGCGGTTGTGGTGAAGT--GGTT-AACACATCAGATTGTGGCTTGACA-----TTCGTGGGTTTCGATCCCATCACTCGCC---  
>tdbD00005689 Streptococcus\_pneumoniae\_TIGR4\_170187\_His\_GTG  
GGCGGTTGTGGTGAAGT--GGTT-AACACACCAGATTGTGGCTTGACA-----TTCGTGGGTTTCGATCCCATCACTCGCC---  
>tdbD00005688 Streptococcus\_pyogenes\_M1\_GAS\_160490\_His\_GTG  
GGCGGTTGTGGTGAAGT--GGTT-AACACATCAGATTGTGGCTTGACA-----TTCGTGGGTTTCGATCCCATCACTCGCC---  
>tdbD00005739 Streptococcus\_pyogenes\_MGAS315\_198466\_His\_GTG  
GGCGGTTGTGGTGAAGT--GGTT-AACACATCAGATTGTGGCTTGACA-----TTCGTGGGTTTCGATCCCATCACTCGCC---  
>tdbD00005772 Streptococcus\_pyogenes\_SSI-1\_193567\_His\_GTG  
GGCGGTTGTGGTGAAGT--GGTT-AACACATCAGATTGTGGCTTGACA-----TTCGTGGGTTTCGATCCCATCACTCGCC---  
>tdbD00005754 Streptomyces\_coelicolor\_A3(2)\_100226\_His\_GTG  
GGTGGGTTAGCTCAGCT--GGT--AGAGCACCTGGTGTGGTCCAGGAT-----GCCGCGGGTTCAGTCCCCTCACTCACC---  
>tdbD00005678 Xylella\_fastidiosa\_Temeculal\_183190\_His\_GTG  
GGCGAGCGTAGCCAAGG--GGTT-AAGGCAGAGGATTGTGGTTCCTCCA-----CTCGTGGGTTTCGAATCCCATCGTTCGCC---  
>tdbD00005676 Treponema\_pallidum\_subsp.\_pallidum\_str.\_Nichols\_243276\_His\_GTG  
GGTGGGTTAGTTCAGT--GGT--AGAGCGCCAGATTGTGGATTCGGTT-----GTCGTGGGTTTCGAATCCCATCACTCACC---  
>tdbD00005767 Tropheryma\_whipplei\_TW08/27\_218496\_His\_GTG  
GGTGGATATAGCTCAGCT--GGT--AGAGCACCTGGTGTGGTCCAGGAT-----GTCGCGGGTTCGAGTCCCCTTATCCACC---  
>tdbD00005743 Xanthomonas\_campestris\_pv.\_campestris\_str.\_ATCC\_33913\_190485\_His\_GTG  
GGTGGCTAGCTCAGCT--GGT--AGAGTACTGGATTGTGATTCCAGAT-----GTCGCGGGTTCGAGTCCCCTCAGCCACCCCA  
>tdbD00005768 Xylella\_fastidiosa\_Temeculal\_183190\_His\_GTG  
GGTGGCTAGCTCAGCT--GGT--AGAGTACTGGATTGTGATTCCAGTT-----GTCGCGGGTTCGAGTCCCCTCAGCCACCCCA  
>tdbD00005804 Yersinia\_pestis\_biovar\_Microtus\_str.\_91001\_229193\_His\_GTG  
GGTGGCTATAGCTCAGCT--GGT--AGAGCCCTGGATTGTGATTCCAGTT-----GTCGTGGGTTTCGAGTCCCATTAGCCACCCCA  
>tdbD00005694 Yersinia\_pestis\_C092\_214092\_His\_GTG  
GGTGGCTATAGCTCAGCT--GGT--AGAGCCCTGGATTGTGATTCCAGTT-----GTCGTGGGTTTCGAGTCCCATTAGCCACCCCA  
>tdbD00005746 Yersinia\_pestis\_KIM\_187410\_His\_GTG  
GGTGGCTATAGCTCAGCT--GGT--AGAGCCCTGGATTGTGATTCCAGTT-----GTCGTGGGTTTCGAGTCCCATTAGCCACCCCA  
>tdbD00005805 Yersinia\_pseudotuberculosis\_IP\_32953\_273123\_His\_GTG  
GGTGGCTATAGCTCAGCT--GGT--AGAGCCCTGGATTGTGATTCCAGTT-----GTCGTGGGTTTCGAGTCCCATTAGCCACCCCA  
>tdbD00004534 Bacillus\_anthraxis\_str.\_Ames\_198094\_Asp\_GTC  
-GGTCCCGTGGTGTAGT--GGTT-AACATGCCTGCCTGTACAGCAGGAG-----ATCGCCGGTTCGACCCCGGTCGGGACCGCCA  
>tdbD00004546 Bacillus\_anthraxis\_str.\_Sterne\_260799\_Asp\_GTC  
-GGTCCCGTGGTGTAGT--GGTT-AACATGCCTGCCTGTACAGCAGGAG-----ATCGCCGGTTCGACCCCGGTCGGGACCGCCA  
>tdbD00004561 Bacillus\_cereus\_ATCC\_10987\_222523\_Asp\_GTC  
-GGTCCCGTGGTGTAGT--GGTT-AACATGCCTGCCTGTACAGCAGGAG-----ATCGCCGGTTCGACCCCGGTCGGGACCGCCA  
>tdbD00004562 Bacillus\_cereus\_ATCC\_10987\_222523\_Asp\_GTC  
-GGTCCCGTGGTGTAGT--GGTT-AACATGCCTGCCTGTACAGCAGGAG-----ATCGCCGGTTCGACCCCGGTCGGGACCGCCA  
>tdbD00004524 Bacillus\_cereus\_ATCC\_14579\_226900\_Asp\_GTC  
-GGTCCCGTGGTGTAGT--GGTT-AACATGCCTGCCTGTACAGCAGGAG-----ATCGCCGGTTCGACCCCGGTCGGGACCGCCA  
>tdbD00000402 Bacillus\_subtilis\_1423\_Asp\_GTC  
-GGTCCCGTGGTGTAGT--GGTT-AGAATGCCTGCCTGTACAGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGGACCGCCA  
>tdbD00004382 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308\_Asp\_GTC  
-GGTCCCGTGGTGTAGT--GGTT-AGAATGCCTGCCTGTACAGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGGACCGCCA  
>tdbD00004574 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27\_281309\_Asp\_GTC  
-GGTCCCGTGGTGTAGT--GGTT-AACATGCCTGCCTGTACAGCAGGAG-----ATCGCCGGTTCGACCCCGGTCGGGACCGCCA  
>tdbD00004400 Borrelia\_burgdorferi\_B31\_224326\_Asp\_GTC  
-GGGGCGTAGTTCAGGT--GGTT-AGAACGCCTGCCTGTACAGCAGGAG-----GTCGCGGGTTCGAGACCCGTCGCTCCCG---  
>tdbD00004526 Escherichia\_coli\_CFT073\_199310\_Asp\_GTC  
-GGAGCGGTAGTTCAGTC--GGTT-AGAATACCTGCCTGTACAGCAGGGG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004393 Escherichia\_coli\_K12\_83333\_Asp\_GTC  
-GGAGCGGTAGTTCAGTC--GGTT-AGAATACCTGCCTGTACAGCAGGGG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004395 Escherichia\_coli\_O157H7\_83334\_Asp\_GTC:  
-GGAGCGGTAGTTCAGTC--GGTT-AGAATACCTGCCTGTACAGCAGGGG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004396 Escherichia\_coli\_O157H7\_EDL933\_155864\_Asp\_GTC:  
-GGAGCGGTAGTTCAGTC--GGTT-AGAATACCTGCCTGTACAGCAGGGG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004399 Haemophilus\_influenzae\_Rd\_KW20\_71421\_Asp\_GTC  
-GGAGTGGTAGTTCAGCT--GGTT-AGAATACCTGCCTGTACAGCAGGGG-----GTCGCGGGTTCGAGTCCCCTCCATTCCGCCA  
>tdbD00004397 Helicobacter\_pylori\_26695\_85962\_Asp\_GTC  
-GGAGCGGTAGTTCAGCT--GGTT-AGAATATCTGCCTGTACAGCAGGGG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004398 Helicobacter\_pylori\_J99\_85963\_Asp\_GTC  
-GGAGCGGTAGTTCAGCT--GGTT-AGAATATCTGCCTGTACAGCAGGGG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004513 Lactobacillus\_plantarum\_WCFS1\_220668\_Asp\_GTC  
-GGTCCGTTGGTCTAGT--GGTTTAGGACGCCTGCCTGTACAGCAGGAG-----ATCAGGATTCGAGTCTCGTACGGACCG---  
>tdbD00004418 Listeria\_monocytogenes\_EGD-e\_169963\_Asp\_GTC  
-GGTCCGTTGGTGTAGG--GGTT-AACATGCCTGCCTGTACAGCAGGAG-----ATCAGGATTCGAGTCTCGTACGGACCG---

>tdbD00004419 *Listeria monocytogenes* EGD-e 169963 Asp GTC  
-GGTTCGCGGGTTCAATCCCCTCGGGACCGCCA  
>tdbD00004565 *Listeria monocytogenes* str. 4b\_F2365 265669 Asp GTC  
-GGTTCGCGGGTTCAATCCCCTCGGGACCG---  
>tdbD00004566 *Listeria monocytogenes* str. 4b\_F2365 265669 Asp GTC  
-GGTTCGCGGGTTCAATCCCCTCGGGACCGCCA  
>tdbD00004406 *Mycoplasma pneumoniae* M129 272634 Asp GTC  
-GGTTCATGTGTAGT--GAT--AACATATCTCCCTGTCACGAGGGG-----T-TGCGGGTTTGATTCCCCTGGAACCGCCA  
>tdbD00004530 *Nitrosomonas europaea* ATCC 19718 228410 Asp GTC  
-GGAGTGGTAGTTCAGTT-GGTT-AGAATACCGCCTGTCACGCCGGGG-----GTCGCGGGTTCGAGTCCCCTCCACTCCGCCA  
>tdbD00004500 *Oceanobacillus iheyensis* HTE831 221109 Asp GTC  
-GGTCCGGTAGTTCAGTT-GGTT-AGAATGCCTGCCTGTCACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGACCGCCA  
>tdbD00004407 *Pasteurella multocida* subsp. *multocida* str. Pm70 272843 Asp GTC  
-GGAGTGGTAGTTCAGTT-GGTT-AGAATACCTGCCTGTCACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCATTCCGCCA  
>tdbD00004432 *Ralstonia solanacearum* GMI1000 267608 Asp GTC  
-GGAGCGGTAGTTCAGTC-GGTT-AGAATACCGCCTGTCACGCCGGGG-----GTCGCGGGTTCGAGTCCCCTCCGCTCCGCCA  
>tdbD00004528 *Salmonella enterica* subsp. *enterica* serovar *Typhi* str. Ty2 209261 Asp GTC  
-GGAGCGGTAGTTCAGTT-GGTT-AGAATACCTGCCTGTCACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004430 *Salmonella typhimurium* LT2 99287 Asp GTC  
-GGAGCGGTAGTTCAGTT-GGTT-AGAATACCTGCCTGTCACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004503 *Shigella flexneri* 2a\_str. 301 198214 Asp GTC  
-GGAGCGGTAGTTCAGTT-GGTT-AGAATACCTGCCTGTCACGCAGGAG-----GTCGCGGGTTCGAGTCCCCTCCGTTCCGCCA  
>tdbD00004545 *Staphylococcus aureus* subsp. *aureus* MRSA252 282458 Asp GTC  
-GGTCTCGTAGTGTAGC--GGTT-AACACGCCTGCCTGTCACGCAGGAG-----ATCGCGGGTTCGATTCCCCTCGAGACCGCCA  
>tdbD00004479 *Staphylococcus aureus* subsp. *aureus* MW2 196620 Asp GTC  
-GGTCTCGTAGTGTAGC--GGTT-AACACGCCTGCCTGTCACGCAGGAG-----ATCGCGGGTTCGATTCCCCTCGAGACCG---  
>tdbD00004480 *Staphylococcus aureus* subsp. *aureus* MW2 196620 Asp GTC  
-GGTCTCGTAGTGTAGC--GGTT-AACACGCCTGCCTGTCACGCAGGAG-----ATCGCGGGTTCGATTCCCCTCGAGACCGCCA  
>tdbD00004388 *Staphylococcus aureus* subsp. *aureus* N315 158879 Asp GTC  
-GGTCTCGTAGTGTAGC--GGTT-AACACGCCTGCCTGTCACGCAGGAG-----ATCGCGGGTTCGATTCCCCTCGAGACCG---  
>tdbD00004389 *Staphylococcus aureus* subsp. *aureus* N315 158879 Asp GTC  
-GGTCTCGTAGTGTAGC--GGTT-AACACGCCTGCCTGTCACGCAGGAG-----ATCGCGGGTTCGATTCCCCTCGAGACCGCCA  
>tdbD00004515 *Staphylococcus epidermidis* ATCC 12228 176280 Asp GTC  
-GGTCTCGTAGTGTAGC--GGTT-AACACGCCTGCCTGTCACGCAGGAG-----ATCGCGGGTTCGATTCCCCTCGAGACCGCCA  
>tdbD00004481 *Streptococcus agalactiae* NEM316 211110 Asp GTC  
-GGTCCCGTAGTGTAGC--GGTT-ATCACGTCGCCCTGTCACGGCGAAG-----ATCGCGGGTTCGATTCCCCTCGGGACCG---  
>tdbD00004423 *Streptococcus pneumoniae* TIGR4 170187 Asp GTC  
-GGTCCCGTAGTGTAGC--GGTT-ATCACGTCGCCCTGTCACGGCGAAG-----ATCGCGGGTTCGATTCCCCTCGGGACCG---  
>tdbD00004422 *Streptococcus pyogenes* M1 GAS 160490 Asp GTC  
-GGTCCCGTAGTGTAGC--GGTT-ATCACGTCGCCCTGTCACGGCGAAG-----ATCGCGGGTTCGATTCCCCTCGGGACCG---  
>tdbD00004482 *Streptococcus pyogenes* MGAS315 198466 Asp GTC  
-GGTCCCGTAGTGTAGC--GGTT-ATCACGTCGCCCTGTCACGGCGAAG-----ATCGCGGGTTCGATTCCCCTCGGGACCG---  
>tdbD00004522 *Streptococcus pyogenes* SSI-1 193567 Asp GTC  
-GGTCCCGTAGTGTAGC--GGTT-ATCACGTCGCCCTGTCACGGCGAAG-----ATCGCGGGTTCGATTCCCCTCGGGACCG---  
>tdbD00004412 *Synechocystis* sp. PCC 6803 1148 Asp GTC  
-GGTCTGTAGTTCATT--GTT-AGAGCACCGCCTGTCACGGCGGAA-----GTTGCGGGTTCGAGCCCCGTCAGACCG---  
>tdbD00004409 *Treponema pallidum* subsp. *pallidum* str. Nichols 243276 Asp GTC  
-GGGGCGTAGCGAAGTT-GGTT-ATCGCGCCAGCCTGTCACGCCGAG-----ATCGCGGGTTCGAGCCCCGTCGCTCCCG---  
>tdbD00004387 *Vibrio cholerae* O1 biovar El Tor str. N16961 243277 Asp GTC  
-GGAGCGGTAGTTCAGT-GGTT-AGAATACCGCCTGTCACGCCGGG-----GTCGCGGGTTCGAGTCCCCTCCGCTCCGCCA  
>tdbD00004487 *Xanthomonas campestris* pv. *campestris* str. ATCC 33913 190485 Asp GTC  
-GGAGCGGTAGTTCAGT-GGTT-AGAATGTGGCCTGTCACGCCGAG-----GTCGCGGGTTCGAGTCCCCTCCGCTCCGCCA  
>tdbD00004414 *Xylella fastidiosa* 9a5c 160492 Asp GTC  
-GGAGCGGTAGTTCAGT-GGTT-AGAATGTGGCCTGTCACGCCGAG-----GTCGCGGGTTCGAGTCCCCTCCGCTCCGCCA  
>tdbD00004519 *Xylella fastidiosa* Temeculal 183190 Asp GTC  
-GGAGCGGTAGTTCAGT-GGTT-AGAATGTGGCCTGTCACGCCGAG-----GTCGCGGGTTCGAGTCCCCTCCGCTCCGCCA  
>tdbD00004556 *Yersinia pestis* biovar *Microtus* str. 91001 229193 Asp GTC  
-GGTGGGTAGTTCAGTC-GGTT-AGAATACCGCCTGTCACGCCGGG-----GTCGCGGGTTCGAGTCCCCTCCGACCGCCA  
>tdbD00004428 *Yersinia pestis* CO92 214092 Asp GTC  
-GGAGCGGTAGTTCAGTT-GGTT-AGAATACCTGCCTGTCACGCAGGAG-----GTCGCGGGTTCGAGCCCCGTCGTTCCGCCA  
>tdbD00004429 *Yersinia pestis* CO92 214092 Asp GTC  
-GGTGGGTAGTTCAGTC-GGTT-AGAATACCGCCTGTCACGCCGGG-----GTCGCGGGTTCGAGTCCCCTCCGACCGCCA  
>tdbD00004490 *Yersinia pestis* KIM 187410 Asp GTC  
-GGAGCGGTAGTTCAGTT-GGTT-AGAATACCTGCCTGTCACGCAGGAG-----GTCGCGGGTTCGAGCCCCGTCGTTCCGCCA  
>tdbD00004491 *Yersinia pestis* KIM 187410 Asp GTC  
-GGTGGGTAGTTCAGTC-GGTT-AGAATACCGCCTGTCACGCCGGG-----GTCGCGGGTTCGAGTCCCCTCCGACCGCCA  
>tdbD00004492 *Yersinia pestis* KIM 187410 Asp GTC  
-GGAGCGGTAGTTCAGTT-GGTT-AGAATACCTGCCTGTCACGCAGGAG-----GTCGCGGGTTCGAGCCCCGTCGTTCCGCCA  
>tdbD00004558 *Yersinia pseudotuberculosis* IP 32953 273123 Asp GTC  
-GGAGCGGTAGTTCAGTT-GGTT-AGAATACCTGCCTGTCACGCAGGAG-----GTCGCGGGTTCGAGCCCCGTCGTTCCGCCA  
>tdbD00004559 *Yersinia pseudotuberculosis* IP 32953 273123 Asp GTC  
-GGTGGGTAGTTCAGTC-GGTT-AGAATACCGCCTGTCACGCCGGG-----GTCGCGGGTTCGAGTCCCCTCCGACCGCCA  
>tdbD00006324 *Bacillus anthracis* str. Ames 198094 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAG-----GTCGAAGGTTTCGAGTCCCTTCATGGCTACCA  
>tdbD00006342 *Bacillus anthracis* str. Sterne 260799 Lys TTT

-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGAAGGTTTCGAGTCCTTCATGGCTCACCA  
>tdbD00006343 Bacillus\_anthraxis\_str.\_Sterne\_260799 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGAAGGTTTCGAGTCCTTCATGGCTCA---  
>tdbD00006362 Bacillus\_cereus\_ATCC\_10987\_222523 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGAAGGTTTCGAGTCCTTCATGGCTCACCA  
>tdbD00006363 Bacillus\_cereus\_ATCC\_10987\_222523 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGAAGGTTTCGAGTCCTTCATGGCTCA---  
>tdbD00006364 Bacillus\_cereus\_ATCC\_10987\_222523 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGAAGGTTTCGAGTCCTTCATGGCTCACCA  
>tdbD00006306 Bacillus\_cereus\_ATCC\_14579\_226900 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGAAGGTTTCGAGTCCTTCATGGCTCACCA  
>tdbD00006307 Bacillus\_cereus\_ATCC\_14579\_226900 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGAAGGTTTCGAGTCCTTCATGGCTCA---  
>tdbD00006308 Bacillus\_cereus\_ATCC\_14579\_226900 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGAAGGTTTCGAGTCCTTCATGGCTCA---  
>tdbD00006279 Bacillus\_halodurans\_C-125\_272558 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGAAGGTTTCGAGTCCTTCATGGCTCACCA  
>tdbD00001357 Bacillus\_subtilis\_1423 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGAAGGTTTCGAGTCCTTCATGGCTCACCA  
>tdbD00006069 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168\_224308 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGAAGGTTTCGAGTCCTTCATGGCTCACCA  
>tdbD00006380 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27\_281309 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGAAGGTTTCGAGTCCTTCATGGCTCA---  
>tdbD00006381 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27\_281309 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGAAGGTTTCGAGTCCTTCATGGCTCACCA  
>tdbD00006344 Borrelia\_garinii\_PBi\_290434 Lys TTT  
-GGGTCATAGCTCAGGT-GGT--AGAGCAGCGCCCTTTTAAGCGTGT-----GTCGTAGGTTTCGAGTCCTACTGAGCTCA---  
>tdbD00006261 Brucella\_suis\_1330\_204722 Lys TTT  
-GAGCGGTAGCTCAGCC--AGAGCAACTGACTTTTAATCAGTAG-----GTCCAGGGTTTCGAATCCCTGCGCGCTCACCA  
>tdbD00006309 Buchnera\_aphidicola\_str.\_Bp\_(Baizongia\_pistaciae)\_224915 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAATCAATTG-----GTCGCAGGTTTCAAATCCTGCACGACCCCA---  
>tdbD00006066 Chlamydomydia\_pneumoniae\_CWL029\_115713 Lys TTT  
-GGGTCGTTAGCTCAGC--GGT--AGAGCACCTCACTTTTAATGAGGGG-----GTCGAAGGTTTCAAATCCTTCAAGACCCCA---  
>tdbD00006084 Chlamydomydia\_pneumoniae\_J138\_138677 Lys TTT  
-GGGTCGTTAGCTCAGC--GGT--AGAGCACCTCACTTTTAATGAGGGG-----GTCGAAGGTTTCAAATCCTTCAAGACCCCA---  
>tdbD00006310 Escherichia\_coli\_CFT073\_199310 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAATCAATTG-----GTCGCAGGTTTCGAATCCTGCACGACCCACCA  
>tdbD00006085 Escherichia\_coli\_K12\_83333 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAATCAATTG-----GTCGCAGGTTTCGAATCCTGCACGACCCACCA  
>tdbD00006086 Escherichia\_coli\_O157H7\_83334 Lys TTT:  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAATCAATTG-----GTCGCAGGTTTCGAATCCTGCACGACCCACCA  
>tdbD00006087 Escherichia\_coli\_O157H7\_EDL933\_155864 Lys TTT:  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAATCAATTG-----GTCGCAGGTTTCGAATCCTGCACGACCCACCA  
>tdbD00006091 Haemophilus\_influenzae\_Rd\_KW20\_71421 Lys TTT  
-GGGTCGTTAGCTCAGTC--GGT--AGAGCAGCGGACTTTTAATCCGTTG-----GTCGAAGGTTTCGAATCCTTCAAGACCCCA  
>tdbD00006088 Helicobacter\_pylori\_26695\_85962 Lys TTT  
-GACCCGTTAGCTCAGCT-GGT--AGAGCAATTCCCTTTTAAGGAATGG-----GCCGTTGGTTTCAAATCCAACACGGGTCACCA  
>tdbD00006089 Helicobacter\_pylori\_J99\_85963 Lys TTT  
-GACCCGTTAGCTCAGCT-GGT--AGAGCAATTCCCTTTTAAGGAATGG-----GCCGTTGGTTTCAAATCCAACACGGGTCACCA  
>tdbD00006119 Listeria\_monocytogenes\_EGD-e\_169963 Lys TTT  
-GAGCCGTTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGCTGGTTTCGAACCCAGCAGCGGCTCA---  
>tdbD00006368 Listeria\_monocytogenes\_str.\_4b\_F2365\_265669 Lys TTT  
-GAGCCGTTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGCTGGTTTCGAACCCAGCAGCGGCTCA---  
>tdbD00006369 Listeria\_monocytogenes\_str.\_4b\_F2365\_265669 Lys TTT  
-GAGCCGTTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAATCAGAGG-----GTCGCTGGTTTCGAACCCAGCAGCGGCTCA---  
>tdbD00006072 Mycobacterium\_tuberculosis\_CDC1551\_83331 Lys TTT  
-GCCCCATAGCTCAGTT-GGT--AGAGCTACGGACTTTTAATCCGCAG-----GTCCCAGGTTTCGAGTCCTGGTGGGGGCA---  
>tdbD00006332 Mycobacterium\_tuberculosis\_H37Rv\_83332 Lys TTT  
-GCCCCATAGCTCAGTT-GGT--AGAGCTACGGACTTTTAATCCGCAG-----GTCCCAGGTTTCGAGTCCTGGTGGGGGCA---  
>tdbD00006102 Mycoplasma\_pneumoniae\_M129\_272634 Lys TTT  
-GACTCACTAGCTCAGC--GGT--AGAGCATTTGACTTTTAATCAAAGG-----GTCCCAGGTTTCGATCCTCGGGTGGAGTCACCA  
>tdbD00001347 Mycoplasma\_sp.\_PG50\_2126 Lys TTT  
-GACTCGTTAGCTCAGCC--GGT--AGAGCAACTGGCTTTTAACCAAGTGG-----GTCCGGGGTTTCGAATCCCGACGAGTCACCA  
>tdbD00006075 Neisseria\_meningitidis\_Z2491\_122587 Lys TTT  
-GGGTCGTTAGCTCAGTC--GGT--AGAGCAGCGGACTTTTAATCCGTTG-----GTCGAGCGGTTTCGAATCCTGCACGACCCACCA  
>tdbD00006103 Pasteurella\_multocida\_subsp.\_multocida\_str.\_Pm70\_272843 Lys TTT  
-GGGTCGTTAGCTCAGTC--GGT--AGAGCAGCGGACTTTTAATCCGTTG-----GTCGAGCGGTTTCGAATCCTGCACGACCCACCA  
>tdbD00006148 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAATCAATTG-----GTCGCAGGTTTCGAATCCTGCACGACCCACCA  
>tdbD00006314 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAATCAATTG-----GTCGCAGGTTTCGAATCCTGCACGACCCACCA  
>tdbD00006136 Salmonella\_typhimurium\_LT2\_99287 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAATCAATTG-----GTCGCAGGTTTCGAATCCTGCACGACCCACCA  
>tdbD00006137 Salmonella\_typhimurium\_LT2\_99287 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAATCAATTG-----GTCGCAGGTTTCGAATCCTGCACGACCCACCA

>tdbD00006138 Salmonella\_typhimurium LT2 99287 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAAATCAATTG-----GTCGCAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00006273 Shigella\_flexneri\_2a\_str\_301 198214 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAAATCAATTG-----GTCGCAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00006149 Sinorhizobium\_meliloti\_1021 266834 Lys TTT  
-GAGCGGTAGCTCAGCC-GGT--AGAGCAACTGACTTTTAAATCAGTAG-----GTCAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00006340 Staphylococcus\_aureus\_subsp.\_aureus\_MRSA252 282458 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCAGAGGTTTGAATCCTCTATGGCTCACCA  
>tdbD00006237 Staphylococcus\_aureus\_subsp.\_aureus\_MW2 196620 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCAGAGGTTTGAATCCTCTATGGCTCA---  
>tdbD00006238 Staphylococcus\_aureus\_subsp.\_aureus\_MW2 196620 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCAGAGGTTTGAATCCTCTATGGCTCACCA  
>tdbD00006077 Staphylococcus\_aureus\_subsp.\_aureus\_N315 158879 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCAGAGGTTTGAATCCTCTATGGCTCA---  
>tdbD00006079 Staphylococcus\_aureus\_subsp.\_aureus\_N315 158879 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCAGAGGTTTGAATCCTCTATGGCTCACCA  
>tdbD00006288 Staphylococcus\_epidermidis\_ATCC\_12228 176280 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCAGAGGTTTGAATCCTCTATGGCTCACCA  
>tdbD00006289 Staphylococcus\_epidermidis\_ATCC\_12228 176280 Lys TTT  
-GAGCCATTAGCTCAGTT-GGT--AGAGCATCTGACTTTTAAATCAGAGG-----GTCAGAGGTTTGAATCCTCTATGGCTCA---  
>tdbD00006240 Streptococcus\_agalactiae\_NEM316 211110 Lys TTT  
-GACTCGTTAGCTCAGTT-GGT--AGAGCAATTGACTTTTAAATCAATGG-----GTCAGGTTTGAATCCTCTATGGCTCA---  
>tdbD00006126 Streptococcus\_pneumoniae\_TIGR4 170187 Lys TTT  
-GACTCGTTAGCTCAGTT-GGT--AGAGCAATTGACTTTTAAATCAATGG-----GTCAGGTTTGAATCCTCTATGGCTCA---  
>tdbD00006123 Streptococcus\_pyogenes\_M1\_GAS 160490 Lys TTT  
-GACTCGTTAGCTCAGTT-GGT--AGAGCAATTGACTTTTAAATCAATGG-----GTCAGGTTTGAATCCTCTATGGCTCA---  
>tdbD00006243 Streptococcus\_pyogenes\_MGAS315 198466 Lys TTT  
-GACTCGTTAGCTCAGTT-GGT--AGAGCAATTGACTTTTAAATCAATGG-----GTCAGGTTTGAATCCTCTATGGCTCA---  
>tdbD00006301 Streptococcus\_pyogenes\_SSI-1 193567 Lys TTT  
-GACTCGTTAGCTCAGTT-GGT--AGAGCAATTGACTTTTAAATCAATGG-----GTCAGGTTTGAATCCTCTATGGCTCA---  
>tdbD00006107 Synechocystis\_sp.\_PCC\_6803 1148 Lys TTT  
-GGGTCGTTAGCTCAGC--GGT--AGAGCACTCGGCTTTTAAACCGATTG-----GTCCTGGGTTTGAATCCCAGGCGACCCA---  
>tdbD00006244 Thermosynechococcus\_elongatus\_BP-1 197221 Lys TTT  
-GGGTCGTTAGCTCAGC--GGT--AGAGCACTCGGCTTTTAAACCGATTG-----GTCCTGGGTTTGAATCCCAGGCGACCCA---  
>tdbD00006105 Treponema\_pallidum\_subsp.\_pallidum\_str.\_Nichols 243276 Lys TTT  
-GGGCTATTAGCTCAGCT-GGT--AGAGCAACGCCCTTTTAAAGCGTGG-----GTCGATGGTTTGAATCCATCATGGCTCA---  
>tdbD00006293 Tropheryma\_whipplei\_TW08/27 218496 Lys TTT  
-GGGCTGTAGCTCAGT-GGA--AGAGCACTCGGACTTTTAAATCCGCTG-----GTCGTTGGGTTTGAATCCCAGGCGACCCA---  
>tdbD00006251 Xanthomonas\_campestris\_pv.\_campestris\_str.\_ATCC\_33913 190485 Lys TTT  
-GGGCGTTAGCTCAGTC-GGT--AGAGCAGAAGACTTTTAAATCTTTTG-----GTCGATGGTTTGAATCCATCAGGCGCCACCA  
>tdbD00006113 Xylella\_fastidiosa\_9a5c 160492 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAAATCAATTG-----GTCGCAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00006294 Xylella\_fastidiosa\_Temecula 183190 Lys TTT  
-GGGCGTTAGCTCAGTC-GGT--AGAGCATCGGACTTTTAAATCCGCTG-----GTCGTTGGGTTTGAATCCCAGGCGACCCA---  
>tdbD00006134 Yersinia\_pestis\_CO92 214092 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAAATCAATTG-----GTCGCAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00006256 Yersinia\_pestis\_KIM 187410 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAAATCAATTG-----GTCGCAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00006358 Yersinia\_pseudotuberculosis\_IP\_32953 273123 Lys TTT  
-GGGTCGTTAGCTCAGTT-GGT--AGAGCAGTTGACTTTTAAATCAATTG-----GTCGCAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00007995 Bacillus\_anthraxis\_str.\_Sterne\_260799 Asn GTT  
-TCCGCAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAACCGATCG-----GTCGTTAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00007996 Bacillus\_anthraxis\_str.\_Sterne\_260799 Asn GTT  
-TCCGCAGTAGCTCAGC--GGT--AGAGCTATCGGCTGTTAACCGATCG-----GTCGTTAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00008011 Bacillus\_cereus\_ATCC\_10987 222523 Asn GTT  
-TCCGCAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAACCGATCG-----GTCGTTAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00008012 Bacillus\_cereus\_ATCC\_10987 222523 Asn GTT  
-TCCGCAGTAGCTCAGC--GGT--AGAGCTATCGGCTGTTAACCGATCG-----GTCGTTAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00007971 Bacillus\_cereus\_ATCC\_14579 226900 Asn GTT  
-TCCGCAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAACCGATCG-----GTCGTTAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00007972 Bacillus\_cereus\_ATCC\_14579 226900 Asn GTT  
-TCCGCAGTAGCTCAGC--GGT--AGAGCTATCGGCTGTTAACCGATCG-----GTCGTTAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00007799 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168 224308 Asn GTT  
-TCCGCAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAACCGATCG-----GTCGTTAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00007800 Bacillus\_subtilis\_subsp.\_subtilis\_str.\_168 224308 Asn GTT  
-TCCACAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAACCGATCG-----GTCGAGGTTTGAATCCTGCCTGTGGAGCCA  
>tdbD00008026 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27 281309 Asn GTT  
-TCCGCAGTAGCTCAGC--GGT--AGAGCTATCGGCTGTTAACCGATCG-----GTCGTTAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00008027 Bacillus\_thuringiensis\_serovar\_konkukian\_str.\_97-27 281309 Asn GTT  
-TCCGCAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAACCGATCG-----GTCGTTAGGTTTGAATCCTGCACGACCCACCA  
>tdbD00008029 Bartonella\_quintana\_str.\_Toulouse 283165 Asn GTT  
-TCCCGGTAGCTCAGT--GGT--AGAGCAACCGGCTGTTAACCGGTTG-----GTCGTTGGTTCGAATCCGCGCCGGGAGCCA  
>tdbD00007821 Borrelia\_burgdorferi\_B31 224326 Asn GTT  
-TCCCTATAGCTCAGT--GGT--AGAGCGGTTGGCTGTTAACCCTAG-----GTCGAGGTTTCAAGTCTTCTGGGGGAG---  
>tdbD00007997 Borrelia\_garinii\_PBi 290434 Asn GTT

-TCCCCTATAGCTCAGT--GGT--AGAGCGGGTGGCTGTTAACCCACTAG-----GTCGGAGGTTCAAGTCTTCTGGGGGAG---  
>tdbD00007939 Brucella\_suis\_1330\_204722 Asn GTT  
-TCCCCGGTAGCTCAGC--GGT--AGAGCAACCGGCTGTTAACCGGTTG-----GTCGCTGGTTCGAATCCGGCCCGGGAGGCCA  
>tdbD00007797 Chlamydia\_trachomatis\_D/UW-3/CX\_272561 Asn GTT  
-TCCGGAGTAGCTCAGC--GGT--AGAGCAGTGGACTGTTAATCCATTG-----GTCGTTGGTTCGAACCCATCCTCCGGAG---  
>tdbD00007795 Chlamydomphila\_pneumoniae\_AR39\_115711 Asn GTT  
-TCCGGAGTAGCTCAGC--GGT--AGAGCAGTGGACTGTTAATCCATTG-----GTCGTTGGTTCGAACCCATCCTCCGGAG---  
>tdbD00007796 Chlamydomphila\_pneumoniae\_CWL029\_115713 Asn GTT  
-TCCGGAGTAGCTCAGC--GGT--AGAGCAGTGGACTGTTAATCCATTG-----GTCGTTGGTTCGAACCCATCCTCCGGAG---  
>tdbD00007812 Chlamydomphila\_pneumoniae\_J138\_138677 Asn GTT  
-TCCGGAGTAGCTCAGC--GGT--AGAGCAGTGGACTGTTAATCCATTG-----GTCGTTGGTTCGAACCCATCCTCCGGAG---  
>tdbD00007841 Clostridium\_perfringens\_str.\_13\_195102 Asn GTT  
-TCCTCGGTAGCTCAAT--GGT--GGAGCACTCGGCTGTTAACCGATAG-----GTTGGAGGTTTCGAGTCTCTCCGAGGAGGCCA  
>tdbD00007974 Escherichia\_coli\_CFT073\_199310 Asn GTT  
-TCCTCTGTAGTTCAGTC--GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00007813 Escherichia\_coli\_K12\_83333 Asn GTT  
-TCCTCTGTAGTTCAGTC--GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00007814 Escherichia\_coli\_O157H7\_83334 Asn GTT:  
-TCCTCTGTAGTTCAGTC--GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00007816 Escherichia\_coli\_O157H7\_EDL933\_155864 Asn GTT:  
-TCCTCTGTAGTTCAGTC--GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00007819 Haemophilus\_influenzae\_Rd\_KW20\_71421 Asn GTT  
-TCCTCCTTAGTTCAGTC--GGT--AGAACGGTGGACTGTTAATCCATAT-----GTCGCAGGTTTCGAGTCCCGCAGGAGGCCA  
>tdbD00007820 Haemophilus\_influenzae\_Rd\_KW20\_71421 Asn GTT  
-TCCTCCTTAGTTCAGTC--GGT--AGAACGGTGGACTGTTAATCCATAT-----GTCGCAGGTTTCGAGTCCCGCAGGAGGCCA  
>tdbD00001944 Klebsiella\_aerogenes\_28451 Asn GTT  
-TCCTCTGTAGTTCAGTC--GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00001951 Listeria\_ivanovii\_1638 Asn GTT  
-TCCACAGTAGCTCAGTT--GGT--AGAGCAATCGGCTGTTAACCGATCG-----GTCGCAGGTTTCGAGTCCCTGCCTGTGGAGGCCA  
>tdbD00001952 Listeria\_monocytogenes\_1639 Asn GTT  
-TCCACAGTAGCTCAGTT--GGT--AGAGCAATCGGCTGTTAACCGATCG-----GTCGCAGGTTTCGAGTCCCTGCCTGTGGAGGCCA  
>tdbD00007837 Listeria\_monocytogenes\_EGD-e\_169963 Asn GTT  
-TCCACAGTAGCTCAGTT--GGT--AGAGCAATCGGCTGTTAACCGATCG-----GTCGCAGGTTTCGAGTCCCTGCCTGTGGAG---  
>tdbD00007838 Listeria\_monocytogenes\_EGD-e\_169963 Asn GTT  
-TCCACAGTAGCTCAGTT--GGT--AGAGCAATCGGCTGTTAACCGATCG-----GTCGCAGGTTTCGAGTCCCTGCCTGTGGAGGCCA  
>tdbD00008014 Listeria\_monocytogenes\_str.\_4b\_F2365\_265669 Asn GTT  
-TCCACAGTAGCTCAGTT--GGT--AGAGCAATCGGCTGTTAACCGATCG-----GTCGCAGGTTTCGAGTCCCTGCCTGTGGAG---  
>tdbD00008015 Listeria\_monocytogenes\_str.\_4b\_F2365\_265669 Asn GTT  
-TCCACAGTAGCTCAGTT--GGT--AGAGCAATCGGCTGTTAACCGATCG-----GTCGCAGGTTTCGAGTCCCTGCCTGTGGAGGCCA  
>tdbD00007850 Mesorhizobium\_loti\_MAFF303099\_266835 Asn GTT  
-TCCCCGGTAGCTCAGT--GGT--AGAGCAACCGGCTGTTAACCGGTTG-----GTCGCTGGTTCGAATCCGGCCCGGGAGGCCA  
>tdbD00007803 Mycobacterium\_tuberculosis\_CDC1551\_83331 Asn GTT  
-TCCCCTGTAGCTCAATT--GGC--AGAGCGTTCGGCTGTTAACCGAAGG-----GTTGGAGGTTTCGAGTCCCTCCCGGGGGAG---  
>tdbD00007989 Mycobacterium\_tuberculosis\_H37Rv\_83332 Asn GTT  
-TCCCCTGTAGCTCAATT--GGC--AGAGCGTTCGGCTGTTAACCGAAGG-----GTTGGAGGTTTCGAGTCCCTCCCGGGGGAG---  
>tdbD00001937 Mycoplasma\_mycooides\_2102 Asn GTT  
-GGCTTTTTAGCTCAGCA--GGT--AGAGCAACCGGCTGTTAACCGGTTT-----GTCACAGGTTTCGAGCCCTGTAAAAGCCGCCA  
>tdbD00001938 Mycoplasma\_pneumoniae\_2104 Asn GTT  
-GGCCACATAGCTCAGC--GGT--AGAGCAACCGGCTGTTAACCGGTTG-----GTCACAGGTTTCGATCCCTGTGTGGCCGCCA  
>tdbD00007826 Mycoplasma\_pneumoniae\_M129\_272634 Asn GTT  
-GGCCACATAGCTCAGC--GGT--AGAGCAACCGGCTGTTAACCGGTTG-----GTCACAGGTTTCGATCCCTGTGTGGCCGCCA  
>tdbD00007805 Neisseria\_meningitidis\_MC58\_122586 Asn GTT  
-TCCCCGATAGCTCAGTC--GGT--AGAGCGACGGACTGTTAATCCGCAG-----GTCCTTGGTTCGAGCCAGGTCGGGGAGGCCA  
>tdbD00008004 Rickettsia\_typhi\_str.\_Wilmington\_257363 Asn GTT  
-TCCTCGGTAGCTCAGT--GGT--AGAGCAACCGGCTGTTAACCGTTCG-----GTCGCTGGTTCGAGTCCGGCCCGGGAGGCCA  
>tdbD00007860 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341 Asn GTT  
-TCCTCTGTAGTTCAGTC--GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00007976 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261 Asn GTT  
-TCCTCTGTAGTTCAGTC--GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00007852 Salmonella\_typhimurium\_LT2\_99287 Asn GTT  
-TCCTCTGTAGTTCAGTC--GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00007853 Salmonella\_typhimurium\_LT2\_99287 Asn GTT  
-TCCTCTGTAGTTCAGTC--GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00007947 Shigella\_flexneri\_2a\_str.\_301\_198214 Asn GTT  
-TCCTCTGTAGTTCAGTC--GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCACTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00007921 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620 Asn GTT  
-TCCACAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAACCGATCG-----GTCGTAGGTTTCGAGTCCCTACCTGTGGAGGCCA  
>tdbD00007809 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879 Asn GTT  
-TCCACAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAACCGATCG-----GTCGTAGGTTTCGAGTCCCTACCTGTGGAGGCCA  
>tdbD00007960 Staphylococcus\_epidermidis\_ATCC\_12228\_176280 Asn GTT  
-TCCGAGTAGCTCAGT--GGT--AGAGCTATCGGCTGTTAACCGATCG-----GTCGTAGGTTTCGAATCCTACCTGCGGAGGCCA  
>tdbD00007922 Streptococcus\_agalactiae\_NEM316\_211110 Asn GTT  
-TCCGCCATAGCTCAGTT--GGTA--GTAGCGCATGACTGTTAATCATGAT-----GTCGTAGGTTTCGAGTCCCTACTGGCGGAG---  
>tdbD00007923 Streptococcus\_agalactiae\_NEM316\_211110 Asn GTT  
-TCCGCCATAGCTCAGTT--GGTA--GTAGCGCATGACTGTTAATCATGAT-----GTCGCAGGTTTCGAGTCCCTGCCTGCCGGAG---

>tdbD00007950 Streptococcus\_mutans\_UA159\_210007\_Asn\_GTT  
-TCCGGCATAGCTCAGTT-GGTA-GTAGCGCATGACTGTTAATCATGAT-----GTCGTAGGTTTCGAGTCTACTGCCGGAG---  
>tdbD00007845 Streptococcus\_pneumoniae\_TIGR4\_170187\_Asn\_GTT  
-TCCGGCATAGCTCAGTT-GGTA-GTAGCGCATGACTGTTAATCATGAT-----GTCGTAGGTTTCGAGTCTACTGCCGGAG---  
>tdbD00007843 Streptococcus\_pyogenes\_M1\_GAS\_160490\_Asn\_GTT  
-TCCGGCATAGCTCAGTT-GGTA-GTAGCGCATGACTGTTAATCATGAT-----GTCGTAGGTTTCGAGTCTACTGCCGGAG---  
>tdbD00007844 Streptococcus\_pyogenes\_M1\_GAS\_160490\_Asn\_GTT  
-TCCGGCATAGCTCAGTT-GGTA-GTAGCGCATGACTGTTAATCATGAT-----GTCGTAGGTTTCGAGTCTACTGCCGGAG---  
>tdbD00007924 Streptococcus\_pyogenes\_MGAS315\_198466\_Asn\_GTT  
-TCCGGCATAGCTCAGTT-GGTA-GTAGCGCATGACTGTTAATCATGAT-----GTCGTAGGTTTCGAGTCTACTGCCGGAG---  
>tdbD00007925 Streptococcus\_pyogenes\_MGAS315\_198466\_Asn\_GTT  
-TCCGGCATAGCTCAGTT-GGTA-GTAGCGCATGACTGTTAATCATGAT-----GTCGTAGGTTTCGAGTCTACTGCCGGAG---  
>tdbD00007968 Streptococcus\_pyogenes\_SSI-1\_193567\_Asn\_GTT  
-TCCGGCATAGCTCAGTT-GGTA-GTAGCGCATGACTGTTAATCATGAT-----GTCGTAGGTTTCGAGTCTACTGCCGGAG---  
>tdbD00007969 Streptococcus\_pyogenes\_SSI-1\_193567\_Asn\_GTT  
-TCCGGCATAGCTCAGTT-GGTA-GTAGCGCATGACTGTTAATCATGAT-----GTCGTAGGTTTCGAGTCTACTGCCGGAG---  
>tdbD00007943 Streptomyces\_coelicolor\_A3(2)\_100226\_Asn\_GTT  
-TCCCTCGTAGCTCAATT-GGC--AGAGCAGCCGGCTGTTAACCGGGAG-----GTTACTGGTTCGAGTCCAGTCCGGGGGAG---  
>tdbD00001942 Streptomyces\_lividans\_1916\_Asn\_GTT  
-TCCTCGTAGCTCAATT-GGC--AGAGCAGCCGGCTGTTAACCGGGAG-----GTTACTGGTTCGAGTCCAGTCCGGGGGAG---  
>tdbD00001943 Streptomyces\_lividans\_1916\_Asn\_GTT  
-TCCTCGTAGCTCAATT-GGC--AGAGCAGCCGGCTGTTAACCGGGAG-----GTTACTGGTTCGAGTCCAGTCCGGGGGAG---  
>tdbD00007830 Synechocystis\_sp.\_PCC\_6803\_1148\_Asn\_GTT  
-TCCTCGTAGCTCAGT--GGT--AGAGCGGTCGGCTGTTAACCGATTG-----GTCGTAGGTTTCGAATCCTACCCGGGGAG---  
>tdbD00007828 Treponema\_pallidum\_subsp.\_pallidum\_str.\_Nichols\_243276\_Asn\_GTT  
-TCCCTGTAGCTCAGTT-GGT--AGAGCAATGGCTGTTAACCATGG-----GTCGTGGTTCGAGCCCGCGGGGGGAG---  
>tdbD00007963 Tropheryma\_whipplei\_TW08/27\_218496\_Asn\_GTT  
-TCCTCGTAGCTCAATT-GGC--AGAGCAGCCGGCTGTTAACCGGGAG-----GTTCTGGTTCGAGTCCAAGTCCGGGGAG---  
>tdbD00007930 Xanthomonas\_campestris\_pv.\_campestris\_str.\_ATCC\_33913\_190485\_Asn\_GTT  
-GCCCGAATAGCTCAGCC-GGTT-AGAGCACTTGACTGTTAATCAGGGG-----GTCGTGGTTCGAGTCCAACCTCGGGCGCCA  
>tdbD00007832 Xylella\_fastidiosa\_9a5c\_160492\_Asn\_GTT  
-GCCCGAATAGCTCAGCC-GGTT-AGAGCACTTGACTGTTAATCAGGGG-----GTCGTGGTTCGAGTCCAACCTCGGGCGCCA  
>tdbD00007964 Xylella\_fastidiosa\_Temecula\_183190\_Asn\_GTT  
-GCCCGAATAGCTCAGCC-GGTT-AGAGCACTTGACTGTTAATCAGGGG-----GTCGTGGTTCGAGTCCAACCTCGGGCGCCA  
>tdbD00008006 Yersinia\_pestis\_biovar\_Microtus\_str.\_91001\_229193\_Asn\_GTT  
-TCCTCTGTAGTTCAGTC-GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCCTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00007851 Yersinia\_pestis\_CO92\_214092\_Asn\_GTT  
-TCCTCTGTAGTTCAGTC-GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCCTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00007934 Yersinia\_pestis\_KIM\_187410\_Asn\_GTT  
-TCCTCTGTAGTTCAGTC-GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCCTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00002078 Yersinia\_pseudotuberculosis\_633\_Asn\_GTT  
-TCCTCTGTAGTTCAGTC-GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCCTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00008007 Yersinia\_pseudotuberculosis\_IP\_32953\_273123\_Asn\_GTT  
-TCCTCTGTAGTTCAGTC-GGT--AGAACGGCGGACTGTTAATCCGTAT-----GTCCTGGTTCGAGTCCAGTCCAGGAGGCCA  
>tdbD00005060 Escherichia\_coli\_CFT073\_199310\_Phe\_GAA  
-GCCCGGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTGGTTCGATCCGAGTCCGGGCACCA  
>tdbD00004934 Escherichia\_coli\_K12\_83333\_Phe\_GAA  
-GCCCGGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTGGTTCGATCCGAGTCCGGGCACCA  
>tdbD00004936 Escherichia\_coli\_O157H7\_83334\_Phe\_GAA:  
-GCCCGGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTGGTTCGATCCGAGTCCGGGCACCA  
>tdbD00004937 Escherichia\_coli\_O157H7\_EDL933\_155864\_Phe\_GAA:  
-GCCCGGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTGGTTCGATCCGAGTCCGGGCACCA  
>tdbD00004938 Escherichia\_coli\_O157H7\_EDL933\_155864\_Phe\_GAA:  
-GCCCGGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTGGTTCGATCCGAGTCCGGGCACCA  
>tdbD00004941 Haemophilus\_influenzae\_Rd\_KW20\_71421\_Phe\_GAA  
-GCCTCGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCGGTGGTTCGATCCGCCTCGAGGCACCA  
>tdbD00004949 Pasteurella\_multocida\_subsp.\_multocida\_str.\_Pm70\_272843\_Phe\_GAA  
-GCCTCGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCGGTGGTTCGATCCGCCTCGAGGCACCA  
>tdbD00004975 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341\_Phe\_GAA  
-GCCCGGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTGGTTCGATCCGAGTCCGGGCACCA  
>tdbD00005062 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261\_Phe\_GAA  
-GCCCGGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTGGTTCGATCCGAGTCCGGGCACCA  
>tdbD00004968 Salmonella\_typhimurium\_LT2\_99287\_Phe\_GAA  
-GCCCGGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTGGTTCGATCCGAGTCCGGGCACCA  
>tdbD00005038 Shigella\_flexneri\_2a\_str.\_301\_198214\_Phe\_GAA  
-GCCCGGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTGGTTCGATCCGAGTCCGGGCACCA  
>tdbD00005027 Xanthomonas\_campestris\_pv.\_campestris\_str.\_ATCC\_33913\_190485\_Phe\_GAA  
-GGCCGAGTAGCTCAGTT-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCGGCGGTTTCGATCCGCTCCTCGGCCACCA  
>tdbD00004955 Xylella\_fastidiosa\_9a5c\_160492\_Phe\_GAA  
-GCCCGGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTGGTTCGATCCGAGTCCGGGCACCA  
>tdbD00005092 Yersinia\_pestis\_biovar\_Microtus\_str.\_91001\_229193\_Phe\_GAA  
-GCCCGGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTGGTTCGATCCGAGTCCGGGCACCA  
>tdbD00004967 Yersinia\_pestis\_CO92\_214092\_Phe\_GAA  
-GCCCGGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAATCCCCGT-----GTCCTGGTTCGATCCGAGTCCGGGCACCA  
>tdbD00005030 Yersinia\_pestis\_KIM\_187410\_Phe\_GAA

-GCCCCGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAAATCCCCGT-----GTCCTTGGTTTCGATCCCGAGTCCGGGCACCA  
>tdbD00005093 *Yersinia pseudotuberculosis* IP\_32953 273123 Phe GAA  
-GCCCCGATAGCTCAGTC-GGT--AGAGCAGGGGATTGAAAAATCCCCGT-----GTCCTTGGTTTCGATCCCGAGTCCGGGCACCA  
>tdbD00004030 *Bacillus anthracis*\_str.\_Sterne 260799 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00004031 *Bacillus anthracis*\_str.\_Sterne 260799 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00004032 *Bacillus anthracis*\_str.\_Sterne 260799 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00004058 *Bacillus cereus*\_ATCC\_10987 222523 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00004059 *Bacillus cereus*\_ATCC\_10987 222523 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00004060 *Bacillus cereus*\_ATCC\_10987 222523 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00003988 *Bacillus cereus*\_ATCC\_14579 226900 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00003989 *Bacillus cereus*\_ATCC\_14579 226900 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00000057 *Bacillus subtilis* 1423 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00003692 *Bacillus subtilis*\_subsp.\_subtilis\_str.\_168 224308 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00003693 *Bacillus subtilis*\_subsp.\_subtilis\_str.\_168 224308 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00004079 *Bacillus thuringiensis*\_serovar\_konkukian\_str.\_97-27 281309 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00004080 *Bacillus thuringiensis*\_serovar\_konkukian\_str.\_97-27 281309 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00004013 *Bartonella henselae*\_str.\_Houston-1 283166 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCACCA  
>tdbD00004014 *Bartonella henselae*\_str.\_Houston-1 283166 Ala TGC  
-GGGGCCGTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCGTCGGTTTCGATCCCGTCCGGCTCCACCA  
>tdbD00000026 *Bartonella quintana* 803 Ala TGC  
-GGGGCCGTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCGTCGGTTTCGATCCCGTCCGGCTCCACCA  
>tdbD00004085 *Bartonella quintana*\_str.\_Toulouse 283165 Ala TGC  
-GGGGCCGTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCGTCGGTTTCGATCCCGTCCGGCTCCACCA  
>tdbD00000084 *Brucella abortus* 235 Ala TGC  
-GGGGCCGTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCGTCGGTTTCGATCCCGTCCGGCTCCACCA  
>tdbD00000082 *Brucella melitensis* 29459 Ala TGC  
-GGGGCCGTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCGTCGGTTTCGATCCCGTCCGGCTCCACCA  
>tdbD00003770 *Brucella melitensis*\_16M 224914 Ala TGC  
-GGGGCCGTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCGTCGGTTTCGATCCCGTCCGGCTCCACCA  
>tdbD00003940 *Brucella suis*\_1330 204722 Ala CGC  
-GGGGCTGTAGCTCAGCT-GGG--AGAGCGCGTTCGTCGCAATGACGAG-----GTCAGGGGTTTCGATCCCCCTCAGCTCCACCA  
>tdbD00003939 *Brucella suis*\_1330 204722 Ala TGC  
-GGGGCCGTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCGTCGGTTTCGATCCCGTCCGGCTCCACCA  
>tdbD00003903 *Buchnera aphidicola*\_str.\_Sg\_(Schizaphis\_graminum) 198804 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCA---  
>tdbD00000073 *Burkholderia cepacia* 292 Ala TGC  
-GGGGCATAAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----T-CGTCGGTTTCGATCCCGTCTGCCTCCACCA  
>tdbD00000075 *Burkholderia gladioli* 28095 Ala TGC  
-GGGGCATAAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----T-CGTCGGTTTCGATCCCGTCTGCCTCCACCA  
>tdbD00000077 *Burkholderia mallei* 13373 Ala TGC  
-GGGGCATAAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----T-CGTCGGTTTCGATCCCGTCTGCCTCCACCA  
>tdbD00003987 *Coxiella burnetii*\_RSA\_493 227377 Ala TGC  
-GGGGCATAAGCTCAGTT-GGG--AGAGCATCTGCCTTGCACGCAGGAG-----GTCGCGGTTTCGACTCCGCCTGGCTCCACCA  
>tdbD00003967 *Enterococcus faecalis*\_V583 226185 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00000048 *Enterococcus hirae* 1354 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00000067 *Escherichia coli* 562 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCACCA  
>tdbD00000066 *Escherichia coli* 562 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCTGCGGTTTCGATCCCGCATAGCTCCACCA  
>tdbD00003993 *Escherichia coli*\_CFT073 199310 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCACCA  
>tdbD00003994 *Escherichia coli*\_CFT073 199310 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCTGCGGTTTCGATCCCGCATAGCTCCACCA  
>tdbD00003715 *Escherichia coli*\_K12 83333 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCACCA  
>tdbD00003716 *Escherichia coli*\_K12 83333 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCCTGCCTTGCACGCAGGAG-----GTCTGCGGTTTCGATCCCGCATAGCTCCACCA  
>tdbD00003717 *Escherichia coli*\_O157H7 83334 Ala GGC:  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCACCA

>tdbD00003718 *Escherichia coli*\_O157H7\_83334 Ala TGC:  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCTGCGGTTTCGATCCCGCATAGCTCCACCA  
>tdbD00003719 *Escherichia coli*\_O157H7\_EDL933\_155864 Ala GGC:  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCACCA  
>tdbD00003720 *Escherichia coli*\_O157H7\_EDL933\_155864 Ala TGC:  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCTGCGGTTTCGATCCCGCATAGCTCCACCA  
>tdbD00000032 *Gluconacetobacter hansenii*\_436 Ala TGC  
-GGGGCGTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCGTGCGGTTTCGATCCCGTCCCGCTCCACCA  
>tdbD00000038 *Gluconacetobacter xylinus*\_28448 Ala TGC  
-GGGGCGTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCGTGCGGTTTCGATCCCGTCCCGCTCCACCA  
>tdbD00000047 *Gluconobacter oxydans*\_442 Ala TGC  
-GGGGCATAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCGTGCGGTTTCGATCCCGTCCCGCTCCACCA  
>tdbD00003725 *Haemophilus influenzae*\_Rd\_KW20\_71421 Ala GGC  
-GGGGATATAGCTCAGCT-GGG--AGAGCGCTTGAATGGCATTCAAGAG-----GTCGTGCGGTTTCGATCCCGATTATCTCCACCA  
>tdbD00003682 *Haemophilus influenzae*\_Rd\_KW20\_71421 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00003721 *Helicobacter pylori*\_26695\_85962 Ala GGC  
-GGGGTGTAGCTCAGCT-GGG--AGAGCGCAACGCTGGCAGCGTTGAG-----GTCAGGGGTTTCGATCCCGCTTACTCCACCA  
>tdbD00003722 *Helicobacter pylori*\_26695\_85962 Ala TGC  
-GGGGAATTAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTATTCTCCACCA  
>tdbD00003723 *Helicobacter pylori*\_J99\_85963 Ala GGC  
-GGGGTGTAGCTCAGCT-GGG--AGAGCGCAACGCTGGCAGCGTTGAG-----GTCAGGGGTTTCGATCCCGCTTACTCCACCA  
>tdbD00003724 *Helicobacter pylori*\_J99\_85963 Ala TGC  
-GGGGAATTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTATTCTCCACCA  
>tdbD00000062 *Lactobacillus curvatus*\_28038 Ala TGC  
-GGGGATATAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCATCGGTTTCGATCCCGTTATCTCCCA---  
>tdbD00000064 *Lactobacillus helveticus*\_1587 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGAG-----GTCATCGGTTTCGATCCCGTTAGCTCCA---  
>tdbD00000054 *Lactococcus lactis*\_1358 Ala TGC  
-GGGGCGTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCGTGCGGTTTCGATCCCGTCCCGCTCCACCA  
>tdbD00000055 *Lactococcus lactis*\_1358 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00000065 *Leuconostoc lactis*\_1246 Ala TGC  
-GGGGAATTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCAGCGGTTTCGATCCCGCTATTCTCCCA---  
>tdbD00000068 *Leuconostoc mesenteroides*\_1245 Ala TGC  
-GGGGAATTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCAGCGGTTTCGATCCCGCTATTCTCCCA---  
>tdbD00003756 *Listeria innocua*\_Cliph1262\_272626 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00003757 *Listeria innocua*\_Cliph1262\_272626 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00003758 *Listeria innocua*\_Cliph1262\_272626 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00003759 *Listeria monocytogenes*\_EGD-e\_169963 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00003760 *Listeria monocytogenes*\_EGD-e\_169963 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00004064 *Listeria monocytogenes*\_str.\_4b\_F2365\_265669 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00004065 *Listeria monocytogenes*\_str.\_4b\_F2365\_265669 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00003946 *Oceanobacillus iheyensis*\_HTE831\_221109 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCACCA  
>tdbD00003947 *Oceanobacillus iheyensis*\_HTE831\_221109 Ala TGC  
-GGGGCCTTAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTAGGCTCCA---  
>tdbD00003739 *Pasteurella multocida*\_subsp.\_multocida\_str.\_Pm70\_272843 Ala TGC  
-GGGGATATAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGCGGTTTCGATCCCGCTATTCTCCACCA  
>tdbD00004025 *Photobacterium luminescens*\_subsp.\_laumondii\_TTO1\_243265 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCACCA  
>tdbD000000072 *Prevotella ruminicola*\_839 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCTGCGGTTTCGATCCCGCATAGCTCCACCA  
>tdbD00003744 *Pseudomonas aeruginosa*\_PAO1\_208964 Ala TGC  
-GGGGCCATAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCAGGAGTTTCGATCCTCCTTGCTCCACCA  
>tdbD000000087 *Pseudomonas pseudoalcaligenes*\_330 Ala TGC  
-GGGGCATAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----T-CGTGCGGTTTCGATCCCGTCTGCCTCCACCA  
>tdbD00003778 *Ralstonia solanacearum*\_GMI1000\_267608 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCACCA  
>tdbD00004026 *Rhodopseudomonas palustris*\_CGA009\_258594 Ala GGC  
-GGGGCCATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCGGCGGTTTCGATCCCGCTGGCTCCACCA  
>tdbD00004028 *Rhodopseudomonas palustris*\_CGA009\_258594 Ala TGC  
-GGGGCCATAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCGTGCGGTTTCGATCCCGTCTGGCTCCACCA  
>tdbD00003789 *Salmonella enterica*\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCGCTTAGCTCCACCA  
>tdbD00003790 *Salmonella enterica*\_subsp.\_enterica\_serovar\_Typhi\_str.\_CT18\_220341 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTGCTTTGCAAGCAGGAG-----GTCTGCGGTTTCGATCCCGCATAGCTCCACCA  
>tdbD00003998 *Salmonella enterica*\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261 Ala GGC



-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003999 Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhi\_str.\_Ty2\_209261 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003776 Salmonella\_typhimurium\_LT2\_99287 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003777 Salmonella\_typhimurium\_LT2\_99287 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003954 Shewanella\_oneidensis\_MR-1\_211586 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003957 Shigella\_flexneri\_2a\_str.\_301\_198214 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003956 Shigella\_flexneri\_2a\_str.\_301\_198214 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003792 Sinorhizobium\_meliloti\_1021\_266834 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003791 Sinorhizobium\_meliloti\_1021\_266834 Ala TGC  
-GGGGCTGTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00004029 Staphylococcus\_aureus\_subsp.\_aureus\_MRSA252\_282458 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003909 Staphylococcus\_aureus\_subsp.\_aureus\_MW2\_196620 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003708 Staphylococcus\_aureus\_subsp.\_aureus\_N315\_158879 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003970 Staphylococcus\_epidermidis\_ATCC\_12228\_176280 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003958 Streptococcus\_agalactiae\_2603V/R\_208435 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003910 Streptococcus\_agalactiae\_NEM316\_211110 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003959 Streptococcus\_mutans\_UA159\_210007 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00000096 Streptococcus\_pneumoniae\_1313 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003765 Streptococcus\_pneumoniae\_TIGR4\_170187 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003764 Streptococcus\_pyogenes\_M1\_GAS\_160490 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003911 Streptococcus\_pyogenes\_MGAS315\_198466 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003985 Streptococcus\_pyogenes\_SSI-1\_193567 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003922 Xanthomonas\_campestris\_pv.\_campestris\_str.\_ATCC\_33913\_190485 Ala GGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003921 Xanthomonas\_campestris\_pv.\_campestris\_str.\_ATCC\_33913\_190485 Ala GGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003923 Xanthomonas\_campestris\_pv.\_campestris\_str.\_ATCC\_33913\_190485 Ala TGC  
-GGGGCTTAGCTCAGCT-GGG--AGAGCACCTGCTTTGCAAGCAGGGG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00004053 Yersinia\_pestis\_biovar\_Microtus\_str.\_91001\_229193 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00004052 Yersinia\_pestis\_biovar\_Microtus\_str.\_91001\_229193 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003774 Yersinia\_pestis\_CO92\_214092 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003775 Yersinia\_pestis\_CO92\_214092 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003932 Yersinia\_pestis\_KIM\_187410 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00003933 Yersinia\_pestis\_KIM\_187410 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00004055 Yersinia\_pseudotuberculosis\_IP\_32953\_273123 Ala GGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA  
>tdbD00004054 Yersinia\_pseudotuberculosis\_IP\_32953\_273123 Ala TGC  
-GGGGCTATAGCTCAGCT-GGG--AGAGCGCTTGCATGGCATGCAAGAG-----GTCAGCGGTTTCGATCCCCTTAGCTCCACCA

Eukaryota - non redundant

>tdbD00003250 Arabidopsis\_thaliana 3702 Val AAC  
-GGTTTCGTTGGTGTAGT--GGTT-ATCACGTGAGTCTAACACACTGAAG-----GTCTCCGGTTTCGAACCCGGGCGAAGCCA---  
>tdbD00003252 Caenorhabditis\_elegans 6239 Val AAC  
-GGTTCGTTGGTGTAGT--GGTT-ATCACATCTGCTTAACACACAGAAG-----GTCGGTGGTTTCGAGCCC GCCCGAGATCA---  
>tdbD00011008 Caenorhabditis\_elegans 6239 Val AAC  
-GGTTTCGTTGGTGTAGT--GGTT-ATCACATCTGCTTAACACACAGAAG-----GTCGGTGGTTTCGAGCCC GCCCGAGATCA---  
>tdbD00011010 Caenorhabditis\_elegans 6239 Val AAC  
-GGTTCGTTGGTGTAGT--GGTT-ATCACATCTGCTTAACACACAGAAG-----GTCGGGCGTTTCGATCCC GCCCGAGATCA---  
>tdbD00011203 Candida\_glabrata CBS\_138 284593 Val AAC  
-GGTTTCGTTGGTCTAGTC--GGTT-ATGGCATCTGCTTAACACGCGAAG-----GTCCCAGTTTCGATCCTGGGCGAAATCA---  
>tdbD00011204 Candida\_glabrata CBS\_138 284593 Val CAC  
-GTTCCAATGGTGTAGT--GGTT-ATCACGTGCTTACACGCGCAAAG-----GTCCCAGTTTCGAACCTCGTTTGGAAACA---  
>tdbD00011205 Candida\_glabrata CBS\_138 284593 Val TAC  
-GGTCCAATAGTCCAGT--GGTTTAAGACGTCGCTTTACACGCGCAAAG-----ATCCCAGTTTCGAACCTCGTTTGGATCA---  
>tdbD00011206 Candida\_glabrata CBS\_138 284593 Val TAC  
-GGTCCAATAGTCCAGT--GGTTTAAGACGTCGCTTTACACGCGCAAAG-----ATCCCAGTTTCGAACCTCGTTTGGATCA---  
>tdbD00003243 Dictyostelium\_discoideum 44689 Val AAC  
-GTTCCGATGGTGTAGTC--GGTT-ATCACGAATCCTTAACACGGATTAG-----GTCGTGGGTTTCGATCCCCTCTGAATA---  
>tdbD00003244 Dictyostelium\_discoideum 44689 Val TAC  
-GGTCCGATGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGCAAAG-----GTCCTCGAGTTTCGATCCTCGTCCGATCA---  
>tdbD00003254 Drosophila\_melanogaster 7227 Val AAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACATCCGCTAACACGCGGAAG-----GCCCCGGTTCAATCCCGGGCGGAAACA---  
>tdbD00003255 Drosophila\_melanogaster 7227 Val CAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTGCTTACACGCGCAAAG-----GTCCCAGTTTCGAACCCGGGCGGAAACA---  
>tdbD00011065 Encephalitozoon\_cuniculi\_GB-M1 284813 Val AAC  
-GTGACCTTAGTGTAGT--GGTT-ATCACGTTGCTTACACGCGGAAG-----GTCCCAGTTTCGAGCCTGGGAGGTCGCA---  
>tdbD00011066 Encephalitozoon\_cuniculi\_GB-M1 284813 Val CAC  
-GCTTTGTAGTGTAGT--GGTT-ATCACGTATCCTTACACGCGGATGAG-----GTCCTCGGTTTCGAACCCGAGCAAAGCA---  
>tdbD00011064 Encephalitozoon\_cuniculi\_GB-M1 284813 Val TAC  
-GCCCTGTAGTGTAGT--GGTT-ATCACGCATCCTTACACGCGGATGAG-----GTCCTTGGTTTCGATCCCAGCGGGGCA---  
>tdbD00011238 Gallus\_gallus 9031 Val AAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTCGCTAACACGCGAAAG-----GTCCCAGTTTCGAACCCGGGCGGAAACA---  
>tdbD00011239 Gallus\_gallus 9031 Val AAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACATTCGCTAACACGCGAAAG-----GTCCCTGGTTTCGAACCCAGGCGGAAACA---  
>tdbD00011240 Gallus\_gallus 9031 Val AAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCAGTTTCGAACCCGGGCGGAAACA---  
>tdbD00011241 Gallus\_gallus 9031 Val AAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCTGGTTTCGAACCCAGGCGGAAACA---  
>tdbD00011242 Gallus\_gallus 9031 Val AAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCAGTTTCGAACCCGGGCGGAAACA---  
>tdbD00011244 Gallus\_gallus 9031 Val CAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCAGTTTCGAACCCGGGCGGAAACA---  
>tdbD00011245 Gallus\_gallus 9031 Val CAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCTGGTTTCGATCCCAGGTTGAAACA---  
>tdbD00011246 Gallus\_gallus 9031 Val CAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCAGTTTCGATCCCAGGTTGAAACA---  
>tdbD00011247 Gallus\_gallus 9031 Val CAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCAGTTTCGAACCCGGGCGGAAACA---  
>tdbD00011248 Gallus\_gallus 9031 Val TAC  
-GGTTCATAGTGTAGT--GGTT-ATCACGTTGCTTACACGTTAGAAG-----GTCCTGGGTTTCGAGCCCAGTGAACCA---  
>tdbD00011249 Gallus\_gallus 9031 Val TAC  
-GGTTCATAGTGTAGT--GGTT-ATCACATCTGCTTACACGCGAAAG-----GTCCTGAGTTTCGATCCTCAGTGAACCA---  
>tdbD00011250 Gallus\_gallus 9031 Val TAC  
-GGTTCATAGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCTGGGTTTCGAGCCCAGTGAACCA---  
>tdbD00003261 Homo\_sapiens 9606 Val AAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCAGTTTCGAACCCGGGCGGAAACA---  
>tdbD00003262 Homo\_sapiens 9606 Val AAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCTGGATCAAACCAGGCGGAAACA---  
>tdbD00003260 Homo\_sapiens 9606 Val CAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCAGTTTCGAACCCGGGCGGAAACA---  
>tdbD00003263 Homo\_sapiens 9606 Val CAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCAGTTTCGAACCCGGGCGGAAACA---  
>tdbD00003264 Homo\_sapiens 9606 Val CAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCAGTTTCGATCCCAGGTTGAAACA---  
>tdbD00010987 Homo\_sapiens 9606 Val AAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCAGTTTCGAACCCGGGCGGAAACA---  
>tdbD00010988 Homo\_sapiens 9606 Val AAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCAGTTTCGAACCCGGGCGGAAACA---  
>tdbD00010998 Homo\_sapiens 9606 Val CAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCAGTTTCGAACCCGGGCGGAAACA---  
>tdbD00010999 Homo\_sapiens 9606 Val CAC  
-GTTTCGTTGGTGTAGT--GGTT-ATCACGTTGCTTACACGCGAAAG-----GTCCCAGTTTCGAACCTGGGCGGAAACA---  
>tdbD00003242 Leishmania\_tarentolae 5689 Val TAC

-GCGTGGGTGATCTAGT--GGTT-ATGATGTCTGCTTTACACGCAGAAAC-----GTCGCGGGTTCGAAACCCCGCCCGCGTA---  
>tdbD00011265 Pan\_troglodytes 9598 Val AAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCGCGTTCGCCTAACACGCGAAAG-----GTTCTGGTTCGAAACCCAGGCGGAAACA---  
>tdbD00011266 Pan\_troglodytes 9598 Val AAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCACGTTTCGCCTAACACGCGAAAG-----GTCCCCAGTTCGAAACCCGGGCGGAAACA---  
>tdbD00011267 Pan\_troglodytes 9598 Val AAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCACGTTTCGCCTAACACGCGAAAG-----GTCCCCGGTTCGAAACCCGGGCGGAAACA---  
>tdbD00011273 Pan\_troglodytes 9598 Val CAC  
-GTTTCCGTAGTGTAGT--GGTT-ATTACGTTAGCCTACACGCGAAAA-----GTCCCCGGTTCAAAACCCGGGCGGGAACA---  
>tdbD00011275 Pan\_troglodytes 9598 Val CAC  
-GTTTCTGTAGTGTAGG--GGTT-ATCACGTTTCGCCTACACGCGAAAG-----GTCCCCGGTTCGAAACCCGGGCGAGAAGCA---  
>tdbD00011276 Pan\_troglodytes 9598 Val CAC  
-GTTTCCGTAGTGTAGC--GGTT-ATCACGTTTCGCCTACACGCGAAAG-----GTCTCCGGTTCGATCCCGGGCGGAAACA---  
>tdbD00011278 Pan\_troglodytes 9598 Val CAC  
-GTTTCCGTGGTGTAGT--GGTT-ATCACGTTTCGCCTACACGCGAAAG-----GTCCCCGGTTCGAAACCCGGGCGGAAACA---  
>tdbD00011281 Pan\_troglodytes 9598 Val TAC  
-GGTCCATAGTGTAGT--GGTT-ATCACGTTTCGCTTTACACGCGAGAAG-----GACCTGGGTTTCGAGCCCCAGTGAACCA---  
>tdbD00011282 Pan\_troglodytes 9598 Val TAC  
-GGTCCATAGTGTAGT--GGTT-ATCACATCTGCTTTACACGCGAGAAG-----GTCCTGGGTTCAAGCCCCAGTGAACCA---  
>tdbD00011283 Pan\_troglodytes 9598 Val TAC  
-GGTCCATAGTGTAGC--GGTT-ATCACGTTTCGCTTTACACGCGAGAAG-----GTCCTGGGTTTCGAGCCCCAGTGAACCA---  
>tdbD00011285 Pan\_troglodytes 9598 Val TAC  
-GCTCCAGTGGCTCAATC--GGTT-AGCGCTTGGTACTTACAATGCCAAG-----GTTGTGAGTTCGACCCTCACCTGGAGCA---  
>tdbD00003239 Plasmodium\_falciparum 5833 Val TAC  
-AAGTAATTAACCTTAGA--GGT--AAAGTTTCTGCTTTACATACAGAAG-----ACCATTGGTTCGAATCCAATATTACTTA---  
>tdbD00011231 Plasmodium\_falciparum\_3D7\_36329 Val AAC  
-GCGGGCATGGTCTAGT--GGCT-ATGACGCCTGCCTAACACGCGAGGAG-----ATCCCGAGTTCGATCCTCGGTGCCCGTA---  
>tdbD00011232 Plasmodium\_falciparum\_3D7\_36329 Val CAC  
-GCGAGCATGGTCTAGT--GGCT-ATGACGTTTCGCCTACACGCGAAAG-----ATCCCGAGTTCGATCCTCGGTGCTCGTA---  
>tdbD00011233 Plasmodium\_falciparum\_3D7\_36329 Val TAC  
-GCGGGCATGGTCTAGT--GGCT-ATGACGCCTGCCTTACACGCGAGGAG-----ATCCCGAGTTCGATCCTCGGTGCCCGTA---  
>tdbD00003247 Saccharomyces\_cerevisiae 4932 Val TAC  
-GGTCCAATGGTCCAGT--GGTTCAAGACGTCGCCTTTACACGGCGAAG-----ATCCCGAGTTCGAACCTCGGTTGGATCA---  
>tdbD00003248 Schizosaccharomyces\_pombe 4896 Val AAC  
-GGTCGTGTGGTTTAGAT--GGTT-ATAATTTCTGCTTAACACGCGAGCG-----GTCCCAAGTTCGAGTCTTGCCACGATCA---  
>tdbD00011251 Takifugu\_rubripes 31033 Val AAC  
-GTTTCATAGTGTAGT--GGTT-ATCACGTTTCGCCTAACACGCGAGAAG-----GTCCCCGGTTCGAAACCCGGGTGTAACA---  
>tdbD00011252 Takifugu\_rubripes 31033 Val AAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCACGTTTCGCCTAACACGCGAAAG-----GTCCCCGGTTCGAGACCCGGGCGGGAACA---  
>tdbD00011253 Takifugu\_rubripes 31033 Val AAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCACGTTTCGCCTAACACGCGAAAG-----GTCCCCGGTTCGAGACCCGGGCGGAAACA---  
>tdbD00011254 Takifugu\_rubripes 31033 Val AAC  
-GTTTCCATAGTGTAGT--GGTT-ATCACGTTTCGCCTAACACGCGAGAAG-----GTCCCCGGTTCGAAACCCGGGTGAAACA---  
>tdbD00011257 Takifugu\_rubripes 31033 Val CAC  
-GTTTCCGTAGTGCAGT--GGTT-ATCACGTTTCGCCTACACGCGAAAG-----GTCCCCGGTTCGAAACCCGGGCGGAAACA---  
>tdbD00011259 Takifugu\_rubripes 31033 Val TAC  
-GGTCCATAGTGTAGA--GGTC-ATCACGTTTCGCTTTACACGCGAGAAG-----GACCTGGGTTCAATTCAGTGGAGCCA---  
>tdbD00011260 Takifugu\_rubripes 31033 Val TAC  
-GGTTCATAGTGTAGC--GGTT-ATCATGTCTGCTTTACACGCGAGGAG-----GTCCTGGGTTTCGAGCCCCAGTGAACCA---  
>tdbD00011261 Takifugu\_rubripes 31033 Val TAC  
-GGTTCGTAGTGTAGC--GGTT-ATCACGTTTCGCTTTACACGCGAGAAG-----GTCCTGGGTTTCGAGCCCCAGTAGAACA---  
>tdbD00011262 Takifugu\_rubripes 31033 Val TAC  
-GGTCCATAGTGTAGA--GGTC-ATCATGTCTGCTTTACACGCGAGAAG-----GTCCTGGGTTTCGATTCCAGTGAACCA---  
>tdbD00003241 Trypanosoma\_brucei 5691 Val CAC  
-GCGATGGTCTAGT--GGTT-AGGACATTCGCCTACACGCGAGAG-----ATCGCGGGTTCGATCCCCGCCCGTCGTA---  
>tdbD00003256 Xenopus\_laevis 8355 Val CAC  
-GTTTCTGTAGTGTAGC--GGTT-ATCACGTTTCGCCTACATGCGAAAG-----GTCCCCGGTTCGAAACCCGGGCGGAAACA---  
>tdbD00005924 Arabidopsis\_thaliana 3702 Ile AAT  
-GGCCTATTAGCTCAGTT--GGTT-AGAGCGTTCGTGCTAATAACGCGAAG-----GTCACAGGTTTCGATCCTGTATAGGCC---  
>tdbD00005925 Arabidopsis\_thaliana 3702 Ile AAT  
-GGCCATTAGCTCAGTT--GGTT-AGAGCGTTCGTGCTAATAACGCGAAG-----GTCGCGAGTTCGAAACCTGCATGGGCC---  
>tdbD00005926 Arabidopsis\_thaliana 3702 Ile TAT  
-GCTCCCGTAGCTCAGTT--GGTT-AGAGCGTTGGTCTTATGAGCCGAAG-----GTCGCGGGTTCGAGCCCCGCCGGAAGC---  
>tdbD00005927 Arabidopsis\_thaliana 3702 Ile TAT  
-GGTCCCGTAGCTCAGTT--GGTT-AGAGCGTTGGTCTTATGAGCCGAAG-----GTCGCGGGTTCGAGCCCCGCCGGGACC---  
>tdbD00005928 Caenorhabditis\_elegans 6239 Ile AAT  
-GCCGCCATAGCTCAGTC--GGTT-AGAGCGTGGGCTAATAAGCCCAAG-----GTCGCGAGTTCGACCCTGTGGCGGC---  
>tdbD00005929 Caenorhabditis\_elegans 6239 Ile AAT  
-GCCGCCATAGCTCAGTC--GGTT-AGAGCGTGGGCTAATAAGCCCAAG-----GTCGCGAGTTCGACCCTGTGGCGGC---  
>tdbD00005930 Caenorhabditis\_elegans 6239 Ile TAT  
-GCCCGGTGGCCGAGC--GGTTCGAAGCGTGGGCTTATGATCTCTATTGGGT----TAA-----ACCAGTTCGCGGGTTCGAATCCCGCCCGGGGC---  
>tdbD00005931 Caenorhabditis\_elegans 6239 Ile TAT  
-GCCCATGGCGCAGTC--GGTT-AGCGCGTGGTACTTATAATGCCAAG-----GTCGCGAGTTCGAGCCTGGCATGGGGCA---  
>tdbD00005932 Caenorhabditis\_elegans 6239 Ile TAT  
-GCCCATGGCGCAGTC--GGTT-AGCGCGTGGTACTTATAATGCCAAG-----GTCGCGAGTTCGAGCCTGGCATGGGGC---

>tdbD00001319 *Candida albicans* 5476 Ile AAT  
-GGTCCTTGGCCAGTT-GGTT-AAGGCGTGGTGCATAATAAGTTTAAATTTGTT---ACGC---CAAGAT-CAGCAGTTTCGATCCTGCTAGGGACCA---  
>tdbD00006024 *Candida glabrata* CBS\_138 284593 Ile AAT  
-GGTCTCTGGCCAGTT-GGTT-AAGGCACCGTGCATAATAACGCGGGG-----ATCAGCGGTTTCGATCCCGCTAGAGACCA---  
>tdbD00001323 *Crithidia fasciculata* 5656 Ile AAT  
-GCTCTCATAGCTCAGTC-GGTT-AGAGCGTGGTCTAATAAGCCCAAG-----GTCACAGGTTTCGACCCCTGTGGGAGCA---  
>tdbD00001197 *Cyanophora paradoxa* 2762 Ile GAT  
-GGGCTATTAGCTCAGTT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GCCCTGTGTTTCAATCCAGGATGGCCCA---  
>tdbD00001328 *Drosophila melanogaster* 7227 Ile AAT  
-GGCCGATTAGCTCAGTT-GGTT-AGAGCGTGGTGCATAATAACGCGAAG-----GTCGCGGGTTTCGATCCCTCATGGGCCA---  
>tdbD00005938 *Drosophila melanogaster* 7227 Ile TAT  
-GCTCCAGTGGCGCAATT-GGTT-AGCGCACGGTACTTATAATGCGGGG-----GTTGTGAGTTTCGAGCCTCACCTGGAGC---  
>tdbD00005958 *Encephalitozoon cuniculi*\_GB-M1 284813 Ile AAT  
-GTTCTGGTAGCTCAGTC-GGTC-AGAGCGTGGTGCATAATAACGCGAAG-----GTCCAGGGTTTCGAGCCCTGTGCGGAACA---  
>tdbD00005959 *Encephalitozoon cuniculi*\_GB-M1 284813 Ile TAT  
-GCCCCGTAGCTCAGTC-GGTC-AGAGCGTGGTACTTATAATGCCAAG-----GTCGCGGGTTTCGAGCCCGTGGAGGCA---  
>tdbD00006041 *Gallus gallus* 9031 Ile AAT  
-GGCCGTTAGCTCAGTT-GGTT-AGAGCGTGGTGCATAATAACGCGAAG-----GTCGCGGGTTTCGATCCCGTACGGGCCA---  
>tdbD00006042 *Gallus gallus* 9031 Ile TAT  
-GCTCCAGTGGCGCAATC-GGTT-AGCGCGCGGTACTTATAATGCGGAG-----GTTGTGAGTTTCGAGCCTCACCTGGAGCA---  
>tdbD00005912 *Homo sapiens* 9606 Ile AAT  
-GGCTGGTTAGCTCAGTT-GGTT-AGAGCGTGGTGCATAATAACGCGAAG-----GTCGTGGGTTTCGATCCCATATCGGCC---  
>tdbD00005913 *Homo sapiens* 9606 Ile AAT  
-GGCCGTTAGCTCAGTC-GGCT-AGAGCGTGGTGCATAATAACGCGAAG-----GTCGCGGGTTTCGATCCCGTACGGGCCA---  
>tdbD00005914 *Homo sapiens* 9606 Ile AAT  
-GGCCGTTAGCTCAGTT-GGTT-AGAGCGTGGTGCATAATAACGCTAAG-----GTCGCGGGTTTCGATACCCGTTACTGGCC---  
>tdbD00005915 *Homo sapiens* 9606 Ile AAT  
-GGCCGTTAGCTCAGTT-GGTC-AGAGCGTGGTGCATAATAACGCGAAG-----GTCGCGGGTTTCGATCCCGTACGGGCCA---  
>tdbD00005917 *Homo sapiens* 9606 Ile AAT  
-GGCTGGTTAGCTCAGTT-GGTT-AGAGCGTGGTGCATAATAACGCGAAG-----GTCGCGGGTTTCGATCCCGTACTGGCCA---  
>tdbD00005918 *Homo sapiens* 9606 Ile AAT  
-GGCCGTTAGCTCAGTT-GGTT-AGAGCGTGGTGCATAATAACGCGAAG-----GTCGCGGGTTTCGATCCCGTACTGGCCA---  
>tdbD00005919 *Homo sapiens* 9606 Ile GAT  
-GGCCGTTAGCTCAGTT-GGTA-AGAGCGTGGTGCATAAACACCAAG-----GTCGCGGGCTCGACTCCCGCACC GGCC---  
>tdbD00005920 *Homo sapiens* 9606 Ile TAT  
-GCTCCAGTGGCGCAATC-GGTT-AGCGCGCGGTACTTATAATGCGGAG-----GTTGTGAGTTTCGAGCCTCACCTGGAGC---  
>tdbD00005921 *Homo sapiens* 9606 Ile TAT  
-GCTCCAGTGGCGCAATC-GGTT-AGCGCGCGGTACTTATAATGCGGAG-----GTTGTGAGTTCAAGCCTCACCTGGAGC---  
>tdbD00005923 *Homo sapiens* 9606 Ile TAT  
-GCTCCAGTGGCGCAATC-GGTT-AGCGCGCGGTACTTATAATGCGGAG-----GTTGTGAGTTTCGATCCTCACCTGGAGC---  
>tdbD00001318 *Leishmania tarentolae* 5689 Ile TAT  
-GCTCCGTTAGCTCAGTT-GGTT-AGGACGCTGGTCTTATGAACCGGAT-----GTCGCGGGTTTCGAGCCCGCGGGGAGCA---  
>tdbD00001326 *Mantoniella squamata* 13608 Ile GAT  
-GGGCTATTAGCTCAGTT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GTCTCTGGTTCAAGTCCAGAATAGCCCA---  
>tdbD00006056 *Pan troglodytes* 9598 Ile AAT  
-GGCCGTTAGCTCAGTT-GGCT-AGAGCGTGGTGCATAATAACGCGAAG-----GTCGCGGGTTTCGATCCCGTACGGGCCA---  
>tdbD00006059 *Pan troglodytes* 9598 Ile AAT  
-GGCCGTTAGCTCAGTT-GGTT-AGAGCGTGGTGCATAATAACGCGAAG-----GTCGCGGGTTTCGATCCCGTACGGGCCA---  
>tdbD00006061 *Pan troglodytes* 9598 Ile GAT  
-GGCCGTTAGCTCAGTT-GGTT-AGAGCGTGGTGCATAAACACCAAG-----GTCGCGGGCTCGACTCCCGCACTGGCCA---  
>tdbD00006063 *Pan troglodytes* 9598 Ile TAT  
-GCTCCAGTGGCGCAATC-GGTT-AGCGCGCGGTACTTATAATGCGGAG-----GTTGTGAGTTCAAGCCTCACCTGGAGCA---  
>tdbD00006064 *Pan troglodytes* 9598 Ile TAT  
-GCTCCAGTGGCGCAATC-GGTT-AGCGCGCGGTACTTATAATGCGGAG-----GTTGTGAGTTTCGATCCTCACCTGGAGCA---  
>tdbD00001317 *Plasmodium falciparum* 5833 Ile GAT  
-AGGTTTTTAGTTTAAAT--GGTT-AAAACATACTCTTGATAAGGGTAAA-----A-TTTTAGTTCAATCTAAAAAACCTA---  
>tdbD00006036 *Plasmodium falciparum* 3D7 36329 Ile AAT  
-GGTCTATAGCTCAGTT-GGTT-AGAGCGTACGGCTAATAACCGTAAG-----GTCGCGGGTTTCGAGACCGCCTGGGACCA---  
>tdbD00006037 *Plasmodium falciparum* 3D7 36329 Ile TAT  
-GATCCATTAGCTCAGT--GGTT-AGAGCGTGGTCTTATGTACCGAAG-----GTCGTGGGTTTCGAAACCCACATGGATCA---  
>tdbD00001198 *Pylaiella littoralis* 2885 Ile GAT  
-GGGCTATTAGCTCAGTT-GGTT-AGAGCGCACCCCTGATAAGGGTGAG-----GGCCCTGGTTCAAATCCAGGATGGCCCA---  
>tdbD00001321 *Saccharomyces cerevisiae* 4932 Ile TAT  
-GCTCGTAGCTCAGT--GGTT-AGAGCTTCGTGCTTATAACGCGACC-----GTCGTGGGTTCAATCCACCTCGAGCA---  
>tdbD00005936 *Saccharomyces cerevisiae* 4932 Ile TAT  
-GCTCGTAGCTCAGT--GGTT-AGAGCTTCGTGCTTATAACGCGACC-----GTCGTGGGTTCAAACCCACCTCGAGCA---  
>tdbD00001322 *Schizosaccharomyces pombe* 4896 Ile AAT  
-GGTCGCAT-ATGTAGTC-GGTT-ATCATGTCGATCTAATAAGTCAAT-----GTCGCGGGTTTCGAACCCGGCTGTGACCA---  
>tdbD00005940 *Schizosaccharomyces pombe* 4896 Ile AAT  
-GGTCGCATGATGTAGTC-GGTT-ATCATGTCGATCTAATAAGTCAAT-----GTCGCCAGTTTCGAACCTGGCTGTGACC---  
>tdbD00005941 *Schizosaccharomyces pombe* 4896 Ile AAT  
-GGTCGCATGATGTAGTC-GGTT-ATCATGTCGATCTAATAAGTCAAT-----GTCGCGGGTTTCGAACCCGGCTGTGACC---  
>tdbD00005942 *Schizosaccharomyces pombe* 4896 Ile TAT  
-GTCCTCGTGGCCAAAGCT-GGTT-AAGGCCTCATGCTTATAACGTGGAA-----ATCGCGAGTTTCGATCCTCGCCGGGAGC---  
>tdbD00006044 *Takifugu rubripes* 31033 Ile AAT

-GGCCGGTTAGCTCAGAT-GGTT-AGAGTGTGTGCTAATAATGCTAAG-----GTCATAGGTTCAACCCCATACTGGCCA---  
>tdbD00006045 Takifugu\_rubripes 31033 Ile AAT  
-GGCCGGTTAGCTCAGTT-GGTT-AGAGCGTGGTGCTAATAACGCCAAG-----GTCGCGGGTTCGATCCCCGTANNNNNNN---  
>tdbD00006046 Takifugu\_rubripes 31033 Ile AAT  
-GGCCGGTTAGCTCAGTT-GGTT-AGAGCGGGTGCTAATAACGCCAAG-----GTCGCGGGTTCGATCCCCGTACGGGCCA---  
>tdbD00006047 Takifugu\_rubripes 31033 Ile AAT  
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>tdbD00006048 Takifugu\_rubripes 31033 Ile AAT  
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>tdbD00006051 Takifugu\_rubripes 31033 Ile TAT  
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>tdbD00006053 Takifugu\_rubripes 31033 Ile TAT  
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>tdbD00006763 Arabidopsis\_thaliana 3702 Leu CAA  
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>tdbD00006764 Arabidopsis\_thaliana 3702 Leu CAA  
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>tdbD00006768 Arabidopsis\_thaliana 3702 Leu CAA  
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>tdbD00001763 Caenorhabditis\_elegans 6239 Leu AAG  
-GGAGAGATGGCCGAGC--GGTCTAAGGCGTGGTTAAGGCACCAGTCCCT----TCG----GGGG--CGTGGGTTCGAATCCCCTCTCTTCA---  
>tdbD00001764 Caenorhabditis\_elegans 6239 Leu CAG  
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>tdbD00001766 Caenorhabditis\_elegans 6239 Leu TAA  
-AGCACGATGGCCGAGT--GGTT-AAGGCGTGGACTTAAGTTCCAATGGTGG----ATA----ACACCTCGTGGGTTCGAACCCCACTCGTGCTA---  
>tdbD00001768 Caenorhabditis\_elegans 6239 Leu TAG  
-GGTGAGATGGCCGAGT--GGTCTAAGGCGTGGTTTATAGGCACCAGTCCCT----CCG----GGGG--CGTGGGTTCGAATCCCCTCTCATCA---  
>tdbD00006779 Caenorhabditis\_elegans 6239 Leu AAG  
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>tdbD00006781 Caenorhabditis\_elegans 6239 Leu AAG  
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>tdbD00006790 Caenorhabditis\_elegans 6239 Leu CAG  
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>tdbD00006793 Caenorhabditis\_elegans 6239 Leu TAA  
-AGCACGATGGCCGAGT--GGTT-AAGGCGTGGCCTTAAGTTCCAATGGTGG----ATA----ACACCGCGTGGGTTCGAACCCCACTCGTGCTA---  
>tdbD00007168 Candida\_glabrata CBS\_138 284593 Leu GAG  
-GGTACTCTGGCCGAGT--GGTCTAAGGCGCCAGGTCGAGGTCCTGGTCTC----TTCG----GAGGCGCGGGTTCGAACCCCGCGGGTATCA---  
>tdbD00007167 Candida\_glabrata CBS\_138 284593 Leu TAA  
-GGAGGGTTGGCCGAGT--GGTCTAAGGCGCCAGACTTAAGATCTGTGGAC----GGTT----GTCCGCGCAGGTTCGAACCTCGCATCCTTCA---  
>tdbD00007169 Candida\_glabrata CBS\_138 284593 Leu TAG  
-GGGAGGTTGGCCGAGT--GGTTTAAAGGCGTCAGATTTAGGTTCTGATATC----TTCG----GATGCAAGGGTTTCGAATCCCCTTATCTCTCA---  
>tdbD00001769 Drosophila\_melanogaster 7227 Leu CAA  
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>tdbD00001770 Drosophila\_melanogaster 7227 Leu CAG  
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>tdbD00006808 Drosophila\_melanogaster 7227 Leu CAA  
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>tdbD00006889 Encephalitozoon\_cuniculi\_GB-M1 284813 Leu AAG  
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>tdbD00006890 Encephalitozoon\_cuniculi\_GB-M1 284813 Leu CAA  
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>tdbD00006892 Encephalitozoon\_cuniculi\_GB-M1 284813 Leu CAG  
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>tdbD00006891 Encephalitozoon\_cuniculi\_GB-M1 284813 Leu TAA  
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>tdbD00006893 Encephalitozoon\_cuniculi\_GB-M1 284813 Leu TAG  
-GGTACAATGGCCGAGC--GGTCTAAGGCGTGGAAATTAGGCTCCAGTCTC----ATT----GAGGCGGGGTTTCGAATCCCCTTGTGCCA---  
>tdbD00007234 Gallus\_gallus 9031 Leu AAG  
-GGTAGCGTGGCCGAGC--GGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCT----TCG----GGGG--CGTGGGTTTCGAATCCCACCGCTGCCA---  
>tdbD00007235 Gallus\_gallus 9031 Leu AAG  
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>tdbD00007236 Gallus\_gallus 9031 Leu CAA  
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>tdbD00007237 Gallus\_gallus 9031 Leu CAA  
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>tdbD00007240 Gallus\_gallus 9031 Leu CAG  
-GTCAGGATGGCCGAGC--GGTCTAAGGCGTGCCTCAGGTCGCAGTCTCC----CCT----GGAGGCGTGGGTTTCGAATCCCCTTCTGACA---  
>tdbD00007241 Gallus\_gallus 9031 Leu CAG  
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>tdbD00007242 Gallus\_gallus 9031 Leu CAG  
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>tdbD00007243 Gallus\_gallus 9031 Leu TAA  
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>tdbD00007244 Gallus\_gallus 9031 Leu TAA  
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>tdbD00007246 Gallus\_gallus 9031 Leu TAG  
-GGTAGCGTGGCCGAGT--GGTCTAAGGCGCTGGATTAGGCTCCAGTCTCAT-----TTCG-----ATGGCGTGGGTTTCAATCCCACCGCTGCCA---  
>tdbD00001761 Helianthus\_annuus 4232 Leu AAG  
-GTCAGGATGGCCGAGT--GGTCTAAGGCGCCAGATTAAGGTTCTGGTCC-----GAAA-----GGGCGTGGGTTTCAATCCCACCTTCTAACA---  
>tdbD00001776 Homo\_sapiens 9606 Leu TAG  
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>tdbD00006740 Homo\_sapiens 9606 Leu AAG  
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>tdbD00006742 Homo\_sapiens 9606 Leu AAG  
-GGTAGCGTGGCCGAGC--GGTCTAAGGCGCTGGATTAGGCTCCAGTCTC-----TTCG-----GAGGCGTGGGTTTCAATCCCACCGCTGCCA---  
>tdbD00001750 Leishmania\_tarentolae 5689 Leu CAG  
-GTCAGGATGGCCGAGT--GGTCTAAGGCGCTCAGTTCAGGTCGTGATCTCC-----CCT-----GGAGGCGTGGGTTTCAACCCCACTCTTGTC---  
>tdbD00001752 Neurospora\_crassa 5141 Leu AAG  
-GGCAGATGGCCGAGC--GGTCTAAGGCGCCAGTTCAGGCGTGGTCC-----GAAA-----GGGCGTGGGTTTCAATCCCACCTCTTGTC---  
>tdbD00007271 Pan\_troglodytes 9598 Leu CAA  
-GTCAGGATGGCCGAGT--GGTCTAAGGCGCCAGACTCAAGTCTGGTCTCC-----GGAT-----GGAGGCGTGGGTTTCAATCCCACCTCTGACA---  
>tdbD00007272 Pan\_troglodytes 9598 Leu CAA  
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>tdbD00007273 Pan\_troglodytes 9598 Leu CAA  
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>tdbD00007274 Pan\_troglodytes 9598 Leu CAA  
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>tdbD00007276 Pan\_troglodytes 9598 Leu CAG  
-GTCAGGATGGCCGAGT--GGTCTAAGGCGCTGCGTTCAGGTCGCGAGTCTCC-----CCCT-----GGAGGCGTGGGTTTCAATCCCACCTCTGACA---  
>tdbD00007283 Pan\_troglodytes 9598 Leu TAA  
-ACCGGGATGGCTGAGT--GGTT-AAGACGTTGGACTTAAGATCCAATGGAC-----AGGT-----GTCCGCGTGGGTTTCAACCCCACTCCCGGTA---  
>tdbD00007284 Pan\_troglodytes 9598 Leu TAA  
-ACCAGAATGGCCGAGT--GGTT-AAGGCGTTGGACTTAAGATCCAATGGAT-----TCAT-----ATCCGCGTGGGTTTCAACCCCACTCTGGTA---  
>tdbD00007285 Pan\_troglodytes 9598 Leu TAA  
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>tdbD00007286 Pan\_troglodytes 9598 Leu TAA  
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>tdbD00007288 Pan\_troglodytes 9598 Leu TAG  
-GGTAGTGTGGCCGAGC--GGTCTAAGGCGCTGGATTAGGCTCCAGTCTCT-----TCG-----GGGG-CGTGGGTTTCAATCCCACCACTGCCA---  
>tdbD00001760 Phaseolus\_vulgaris 3885 Leu CAA  
-GTCAGGATGGCCGAGT--GGTCTAAGGCGCCAGACTCAAGTCTGGTCTTC-----GAGA-----GAGGCGTGGGTTTCAATCCCACCTCTGACA---  
>tdbD00007219 Plasmodium\_falci-parum 3D7 36329 Leu AAG  
-GACAGAATGGCCGAGT--GGTCTAAGGCGCAACGTTAAGGCCGTTGTC-----GAAA-----GGGCGTGGGTTTCAACCCCACTCTGTCA---  
>tdbD00007220 Plasmodium\_falci-parum 3D7 36329 Leu CAA  
-GCACGGATGGCTGAGT--GGTCTAAGGCGCTCAGACTCAAGATCTGATGAAC-----GTAA-----GTTTCGATGGGTTTCAACCCCATTTCTGCA---  
>tdbD00007222 Plasmodium\_falci-parum 3D7 36329 Leu TAA  
-GCACGGGTGCCCCGAGT--GGTT-AAGGGGTTGGACTTAAGATCCTCTGGTC-----ACTA-----GACCGCGTGGGTTTCAACCCCACTCTGCA---  
>tdbD00007223 Plasmodium\_falci-parum 3D7 36329 Leu TAG  
-GTCAGGATGGCCGAGT--GGTCTAAGGCGCAGCGTTTAGGCCGCTGTCC-----GTAA-----GGGCGTGGGTTTCAACCCCACTCTGACA---  
>tdbD00001773 Rattus\_norvegicus 10116 Leu CAG  
-GTCAGGATGGCCGAGC--GGTCTAAGGCGCTGCGTTCAGGTCGAGTCTCCC-----CTA-----GAGAGGCGTGGGTTTCAATCCCACCTCTGACA---  
>tdbD00001774 Rattus\_norvegicus 10116 Leu CAG  
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>tdbD00001754 Saccharomyces\_cerevisiae 4932 Leu CAA  
-GGTTGTTTGGCCGAGC--GGTCTAAGGCGCTGATTCAGGCTCAGGTATC-----GTAA-----GATGCAAGGTTTCAATCTCTTAGCAACCA---  
>tdbD00001755 Saccharomyces\_cerevisiae 4932 Leu TAA  
-GGAGGTTTGGCCGAGC--GGTCTAAGGCGGCGAGACTTAAGATCTGTTGGAC-----GGTT-----GTCCGCGGAGTTTCAACCTCGCATCTTCA---  
>tdbD00007247 Takifugu\_rubripes 31033 Leu AAG  
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>tdbD00007248 Takifugu\_rubripes 31033 Leu AAG  
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>tdbD00007249 Takifugu\_rubripes 31033 Leu AAG  
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>tdbD00007250 Takifugu\_rubripes 31033 Leu AAG  
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>tdbD00007256 Takifugu\_rubripes 31033 Leu CAG  
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>tdbD00007259 Takifugu\_rubripes 31033 Leu TAA  
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>tdbD00007260 Takifugu\_rubripes 31033 Leu TAA  
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>tdbD00007261 Takifugu\_rubripes 31033 Leu TAA  
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>tdbD00007263 Takifugu\_rubripes 31033 Leu TAG  
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>tdbD00007264 Takifugu\_rubripes 31033 Leu TAG  
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>tdbD00007266 Takifugu\_rubripes 31033 Leu TAG

-GTCAGGATGGCCGAGC--GGTCGAAGGCGCTGTGTTTAGGTCGAGTCTCC-----TTT-----GGAGGCGTGGGTTTCGAATCCCACCTTCTGACA---  
>tdbD00001922 Arabidopsis thaliana 3702 Met CAT  
-GGGGTGGTGGCGCAGTT-GGCT-AGCGCGTAGGTCTCATAATCCTGAG-----GTCGAGAGTTTCGAGCCTCTCTCACCCCA---  
>tdbD00007461 Arabidopsis thaliana 3702 Met CAT  
-GGGCTTATAGTTTAAATT-GGTT-GAAACGTACCGCTCATAACGGTTAT-----ATTGTAGGTTTCGAGCCCTACTAAGCCTA---  
>tdbD00007463 Arabidopsis thaliana 3702 Met CAT  
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>tdbD00007716 Candida glabrata CBS\_138 284593 Met CAT  
-GCTTCTGTAGCTCAGTC-GGA--AGAGCGTCAGTCTCATAATCTGAAG-----GTCGAGAGTTTCGAACCTCCCAGGAGCA---  
>tdbD00001918 Dictyostelium discoideum 44689 Met CAT  
-AGTCTCTTAAGTACAGG--GGT--AGAGTGGCAGGCCCATACCTCGAG-----GTCCTAGGATCGAAACCTAGAGAAGCTA---  
>tdbD00001924 Drosophila melanogaster 7227 Met CAT  
-AGCAGAGTGGCGCAGT--GGA--AGCGTGGTGGTCCCATACCCAGAG-----GTCCGAGGATCGAAACCTTGGCTCTGCTA---  
>tdbD00007475 Drosophila melanogaster 7227 Met CAT  
-AGCAGAGTGGCGCAGT--GGA--AGCGTGGTGGGCCCATACCTCAGAG-----GTCCGAGGATCGAAACCTTGGCTCTGCTA---  
>tdbD00007476 Drosophila melanogaster 7227 Met CAT  
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>tdbD00007526 Encephalitozoon cuniculi GB-M1 284813 Met CAT  
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-GTGACATTGGCGCAATA-GGT--AGCGCGTGGTCTCATAATCCAGAG-----GTTGCGAGTTTCGAGTCTCGCATGTCGCA---  
>tdbD00007757 Gallus gallus 9031 Met CAT  
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>tdbD00007758 Gallus gallus 9031 Met CAT  
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>tdbD00007759 Gallus gallus 9031 Met CAT  
-AGCAGAGTGGCGCAGC--GGA--AGCGTGGTGGGCCCATACCCAGAG-----GTCGATGGATCGAAACCATCCTCTGCTA---  
>tdbD00007760 Gallus gallus 9031 Met CAT  
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>tdbD00007761 Gallus gallus 9031 Met CAT  
-GCCCTCTTAGCGCAGCC-GGC--AGCGCGTCAGTCTCATAATCTGAAG-----GTCCTGAGTTTCGAGCCTCAGAGAGGGCA---  
>tdbD00007762 Gallus gallus 9031 Met CAT  
-GCCTCGTTAGCGCAGTA-GGT--AGCGCGTCAGTCTCATAATCTGAAG-----GTCGTGAGTTTCGAGCCTCACACGGGGCA---  
>tdbD00007763 Gallus gallus 9031 Met CAT  
-GCCTCGTTAGCGCAGTA-GGT--AGCGCGTCAGTCTCATAATCTGAAG-----GTCGTGAGTTTCGATCCTCACACGGGGCA---  
>tdbD00001923 Glycine max 3847 Met CAT  
-GGGGTGGTGGCGCAGTT-GGGC-AGCGCGTAGGTCTCATAATCCTGAG-----GTCGAGAGTTTCGAGCCTCTCTCACCCCA---  
>tdbD00007783 Pan\_troglodytes 9598 Met CAT  
-GCCTCCTTAGTGCAGTA-GGT--AGTGCCTCAGTCTCATAAATCCGAA-----G-----GTCCTGAGTTTCGAGCCTCAGAGGGGGCA---  
>tdbD00007785 Pan\_troglodytes 9598 Met CAT  
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>tdbD00007786 Pan\_troglodytes 9598 Met CAT  
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>tdbD00007788 Pan\_troglodytes 9598 Met CAT  
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>tdbD00007789 Pan\_troglodytes 9598 Met CAT  
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-GCCCTCCTTAGCGCAGCT-GGC--AGCGCGTCAGTCTCATAATCTGAAG-----GTCCTGAGTTCAAGCCTCAGAGAGGGCA---  
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-GCCTCCTTAGCGCAGTA-GGC--AGCGCGTCAGTCTCATAATCTGAAG-----GTCCTGAGTTTCGAACCTCAGAGGGGGCA---  
>tdbD00007794 Pan\_troglodytes 9598 Met CAT  
-GCCCTCCTTAGCGCAGTG-GGC--AGCGCGTCAGTCTCATAATCTGAAG-----GTCCTGAGTTTCGAGCCTCAGAGAGGGCA---  
>tdbD00001917 Plasmodium falciparum 5833 Met CAT  
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>tdbD00007747 Plasmodium falciparum\_3D7 36329 Met CAT  
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>tdbD00007748 Plasmodium falciparum\_3D7 36329 Met CAT  
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>tdbD00001919 Saccharomyces cerevisiae 4932 Met CAT  
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>tdbD00001920 Saccharomyces cerevisiae 4932 Met CAT  
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>tdbD00007474 Saccharomyces cerevisiae 4932 Met CAT  
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>tdbD00001925 *Salmo salar* 8030 Met CAT  
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>tdbD00001926 *Salmo salar* 8030 Met CAT  
AAGCAGAGTGGCGCAGC--GGA--AGCATGTGGGCCCCATAACCCAAAG-----GTCGATGGATCGAAACCATCCTCTGCTA---  
>tdbD00001927 *Salmo salar* 8030 Met CAT  
AAGCAGAGTGGCGCAGC--GGA--AGCGTGCTGGGCCCCATAACCCAGAG-----GTCGATGGATCGATAACCATCCTCTGCTA---  
>tdbD00007768 *Takifugu rubripes* 31033 Met CAT  
-AGCAGAGTGGCGCAGA--GGA--AGCGTGCTGGGCCCCATAACCCAGAG-----GTCAATGGATCGAAACCATCCTCTGCTA---  
>tdbD00007769 *Takifugu rubripes* 31033 Met CAT  
-AGCAGAGTGGCGCAGC--GGA--AGCGTGCTGGGCCCCATAACCCAGAG-----GACGATGGATCGAAACCATCCTCTGCTA---  
>tdbD00007770 *Takifugu rubripes* 31033 Met CAT  
-AGCAGAGTGGCGCAGC--GGG--AGCGTGCTGGGCCCCATAACCCAGAG-----GGCGATGGATCGAAACCATCCTCTGCTA---  
>tdbD00007771 *Takifugu rubripes* 31033 Met CAT  
-AGCAGAGTGGCGCAGC--GGG--AGCGTGCTGGGCCCCATAACCCAGAG-----GCCGATGGATCGAAACCATCCTCTGCTA---  
>tdbD00007772 *Takifugu rubripes* 31033 Met CAT  
-AGCAGAGTGGCGCAGC--GGA--AGCGTGCTGGGCCCCATAACCCAGAG-----GTCAGTGGATCGAAACCATTCTCTGCTA---  
>tdbD00007773 *Takifugu rubripes* 31033 Met CAT  
-AGCAGAGTGGCGCAGC--GGG--AGCGTGCTGGGCCCCATAACCCAGAG-----GTCGATGGATCGAAACCATCCTCTGCTA---  
>tdbD00007775 *Takifugu rubripes* 31033 Met CAT  
-AGCAGAGTGGCGCAGA--GGA--AGCGTGCTGGGCCCCATAACCCAGAG-----GTCGATGGATCGAAACCATCCTCTGCTA---  
>tdbD00007776 *Takifugu rubripes* 31033 Met CAT  
-AGCAGAGTGGCGCAGC--GGG--AGCGTGCTGGGCCCCATAACCCAGAG-----GTCGATGGATCGAAACCATCCTCTGCTA---  
>tdbD00007778 *Takifugu rubripes* 31033 Met CAT  
-GTCTCGTTGGCGCAGTA--GGC--AGCGCGTCAGTCTCATAATCTGAAG-----GTCGTGAGTTCGAGCCTCACACGGGGCA---  
>tdbD00007779 *Takifugu rubripes* 31033 Met CAT  
-GCCTTGTGGCGCAGCA--GGC--AGCGCGTCAGTCTCATAATCTGAAG-----GTCGTGAGTTCGAGCCTCACACAGGGCA---  
>tdbD00007780 *Takifugu rubripes* 31033 Met CAT  
-GCCTCGTTGGCGCAGTA--GGC--AGCGCGTCAGTCTCATAATCTGAAG-----GTCGTGAGTTCGAGCCTCACACGGGGCA---  
>tdbD00000374 *Arabidopsis thaliana* 3702 Cys GCA  
-GGTCCATAGCTCAGT--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCACCGGTTTCAACCCGGTTGGGCCCT---  
>tdbD00004233 *Arabidopsis thaliana* 3702 Cys GCA  
-GGCTAGGTAACATAAT--GGA--AATGTATCGACTGCAATCCTGTA-----A-TGACGGTTCGACTCCGTCCTTGGCCT---  
>tdbD00004241 *Arabidopsis thaliana* 3702 Cys GCA  
-GGTCCATAGCTCAGT--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCACCGGTTTCAACCCGGTAGGGCCCT---  
>tdbD00004243 *Arabidopsis thaliana* 3702 Cys GCA  
-GGTCCATAGCTCAGT--GGT--AGAGCAATTTGACTGCAGATCAATAG-----GTCACCGGTTTCAACCCGGTTGGGCCCT---  
>tdbD00004331 *Candida glabrata* CBS 138 284593 Cys GCA  
-GCTCGTATGGCGCAGT--GGT--AGCGCAGCAGATTGCAAAATCTGTG-----GTCCTTAGTTTCAACCTGAGTGCAGGCT---  
>tdbD00000377 *Cyanidium caldarium* 2771 Cys GCA  
-GGCGGATGGCCAAGT--GGT--AAGCAGAGGATTGCAAAATCCTTTA-----TCCCCAGTTTCAACCTGGGTGCCGCT---  
>tdbD00004251 *Drosophila melanogaster* 7227 Cys GCA  
-GGGATATAGCTCAGT--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCACCGGTTTCAACCCGGGTGCCCT---  
>tdbD00004270 *Encephalitozoon cuniculi* GB-M1 284813 Cys GCA  
-GGTCCGATAGCTCAGC--GGT--AGAGCAATTTGATTGCAGATCAATCG-----GTCACAGGTTTCAATCCTGTCGTGCCCT---  
>tdbD00000381 *Euplotes octocarinatus* 5937 Cys GCA  
-GGTCAATAGCTCAGT--GGT--AGAGCAGCAGATTGCAGATCTGTAG-----GTCACCGGTTTCAATCCTGTCGTGCCCT---  
>tdbD00004348 *Gallus gallus* 9031 Cys GCA  
-GGGGTATAGCTCAGT--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCACCGGTTTCAACTCCAGGTGCCCT---  
>tdbD00004349 *Gallus gallus* 9031 Cys GCA  
-GGGGTATAGCTCAGG--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCACCGGTTTCAACTCCAGGTGCCCT---  
>tdbD00004350 *Gallus gallus* 9031 Cys GCA  
-GGGGTATAGCTCAGT--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCCTTGGTTTCAACTCCAGGTGCCCT---  
>tdbD00004351 *Gallus gallus* 9031 Cys GCA  
-GGGGTATAGCTCAGT--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCACCGGTTTCAACTCCAGGTGCCCT---  
>tdbD00004216 *Homo sapiens* 9606 Cys GCA  
-GGGGTATAGTTTCAAG--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCCTTGGTTTCAACTCCAGGTGCCCT---  
>tdbD00004219 *Homo sapiens* 9606 Cys GCA  
-GGGGTATAGCTCAGG--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCCTTGGTTTCAACTCCAGGTGCCCT---  
>tdbD00004225 *Homo sapiens* 9606 Cys GCA  
-GGGGTATAGCTCAGG--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCCTTGGTTTCAACTCCAGGTGCCCT---  
>tdbD00004228 *Homo sapiens* 9606 Cys GCA  
-GGGGTGTAGCTCAGT--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCCTTGGTTTCAACTCCAGGTGCCCT---  
>tdbD00004229 *Homo sapiens* 9606 Cys GCA  
-GGGGTATAGCTCAGT--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCCTTGGTTTCAACTCCAGGTGCCCT---  
>tdbD00004230 *Homo sapiens* 9606 Cys GCA  
-GGGGTATAGCTCAGG--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCCTTGGTTTCAACTCCAGGTGCCCT---  
>tdbD00004232 *Homo sapiens* 9606 Cys GCA  
-GGGGCATAGCTCAGT--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCCTTGGTTTCAACTCCAGGTGCCCT---  
>tdbD00004359 *Pan troglodytes* 9598 Cys ACA  
-GGGGTATAGCTCAGG--GGT--AGAGCAATTTGACCACAGATCAAGAG-----GAGCCCGGTTTCAAGTCCGGGTGCCCT---  
>tdbD00004362 *Pan troglodytes* 9598 Cys GCA  
-GGGCGTATAGCTCAGG--GGT--AGAGCAATTTGACTGCAGATCAAGAG-----GTCACCGGTTTCAACTCTGGGTGCCCT---  
>tdbD00004363 *Pan troglodytes* 9598 Cys GCA  
-GGGGTATAGCTCAGG--GGT--AGAGCAATTTGACTGCAGATCAAGAA-----GTCCTTGGTTTCAACTCCAGGTGCCCT---  
>tdbD00004365 *Pan troglodytes* 9598 Cys GCA



-GGGGGTGTAGCTCAGG--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCCCGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00004366 Pan\_troglodytes 9598 Cys GCA  
-GGGGGTATAGCTCAGG--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCCCAGTTCAAATCTGGGTGCCCCCT---  
>tdbD00004367 Pan\_troglodytes 9598 Cys GCA  
-GGGGGTATAGCTCAGG--GGT--AGAGCATTGACTGCAGATCAAGAA-----GTCCCCGGTTCAAATCCGGGTACCCCT---  
>tdbD00004368 Pan\_troglodytes 9598 Cys GCA  
-GGGGGTATAGCTCAGG--GGT--AGAGCATTGACTGCAGATCAAAAG-----GTCCCTGGTTCAAATCCAGGTGCCCCCT---  
>tdbD00004371 Pan\_troglodytes 9598 Cys GCA  
-GGGGGTATAGCTCAGG--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCCCGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00004373 Pan\_troglodytes 9598 Cys GCA  
-GGGGGTATAGCTCAGC--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCCCGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00004374 Pan\_troglodytes 9598 Cys GCA  
-GGGGGTATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCCTGGTTCAAATCCGGGTGTCCCT---  
>tdbD00004376 Pan\_troglodytes 9598 Cys GCA  
-GGGGGTATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCCTGGTTCAAATCCAGGTGCCCCCT---  
>tdbD00000378 Podocoryne\_carnea 6096 Cys GCA  
-GGGGATATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCGAGAG-----GTCCCTGGTTCAAACCCGGGTGTCCCT---  
>tdbD00000372 Saccharomyces\_cerevisiae 4932 Cys GCA  
-GCTCGTATGGCGCAGT--GGT--AGCGCAGCAGATTGCAAATCTGTTG-----GTCCTTAGTTCGATCCTGAGTGCAGCT---  
>tdbD00000373 Schizosaccharomyces\_pombe 4896 Cys GCA  
-GGGGTCATAGCTCAGT--GGT--AGAGTGAGGGATTGCAGATCCCCAG-----GTCGCTGGTTCAAATCCGGGTGTCCCT---  
>tdbD000004252 Schizosaccharomyces\_pombe 4896 Cys GCA  
-GGGGTCATAGCTCAGT--GGT--AGAGTGAGGGATTGCAGATCCCCAG-----GTCCTGGTTCAAATCCGGTGTCCCT---  
>tdbD00004352 Takifugu\_rubripes 31033 Cys GCA  
-GGGGGTATAGCTCAGC--GGC--AGAGCATTGACTGCAGATCAAGAG-----GTCCCCAGTTCAAATCTGGGTGCCCCCT---  
>tdbD00004353 Takifugu\_rubripes 31033 Cys GCA  
-GGGGGTATATCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCTCTGGTTCAAATCCAGGTGCCCCCT---  
>tdbD00004354 Takifugu\_rubripes 31033 Cys GCA  
-GGGGGTATAGCTCAGC--GGC--AGAGCATTGACTGCAGATCAAGAG-----GTCCCCAGTTCAAATCTGGGTGCCCCCT---  
>tdbD00004355 Takifugu\_rubripes 31033 Cys GCA  
-GGGGGTATAGCTCAGT--GGC--AGAGCATTGACTGCAGATCAAGAG-----GTCCCCAGTTCAAATCTGGGTGCCCCCT---  
>tdbD00004356 Takifugu\_rubripes 31033 Cys GCA  
-GGGGGTATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCTCTGGTTCAAATCCAGATGCCCCCT---  
>tdbD00004357 Takifugu\_rubripes 31033 Cys GCA  
-GGGGGTATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCTCGGTTCAAATCCGGATGCCCCCT---  
>tdbD00003657 Arabidopsis\_thaliana 3702 Tyr GTA  
-CCGACCTTAGCTCAGTT--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCCTGGTTCGAATCCGGTAGGTCGGA---  
>tdbD00003658 Arabidopsis\_thaliana 3702 Tyr GTA  
-CCGACCTTAGCTCAGTT--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCATTTGGTTCGAATCCGCTAGGTCGGA---  
>tdbD00003660 Arabidopsis\_thaliana 3702 Tyr GTA  
-CCGACCTTAGCTCAGTT--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCCTGGTTCGAATCTGGTAGGTTTGA---  
>tdbD00011656 Arabidopsis\_thaliana 3702 Tyr GTA  
-CCGACCTTAGCTCAGTT--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCATTTGGTTCGAATCCGGTAGGTCGGA---  
>tdbD00011666 Caenorhabditis\_elegans 6239 Tyr GTA  
-CCGTCGATAGCTCAGTT--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCCTGGTTCGAATCCGGTTCGACGGA---  
>tdbD00011668 Caenorhabditis\_elegans 6239 Tyr GTA  
-CCGTCGATAGCTCAGTT--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCCTGGTTCGAATCCGGTTCGACGGA---  
>tdbD00011670 Caenorhabditis\_elegans 6239 Tyr GTA  
-CCGTCGATAGCTCAGTT--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTTCGAATCCGGTTCGACGGA---  
>tdbD00011671 Caenorhabditis\_elegans 6239 Tyr GTA  
-CCGTCGATAGCTCAGTT--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCCTGGTTTCGAATCCGGTTCGACGGA---  
>tdbD00011675 Caenorhabditis\_elegans 6239 Tyr GTA  
-CAGTCGATAGCTCAGTT--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTTCGAATCCGGTTCGACGGA---  
>tdbD00011771 Candida\_glabrata\_CBS\_138 284593 Tyr GTA  
-CTCTCGTAGCCCAAGTT--GGT--AGAGCGGAGGACTGTAAATCTTGTAG-----ATCGGGGTTTCGAATCCGCCCGGGAGA---  
>tdbD00003653 Dictyostelium\_discoideum 44689 Tyr GTA  
-CCGGCTTTGGCGCAAT--GGT--AGCGCGATTGACTGTAGATCAATCG-----GTTGCTAGTTTCGAATCTGGCAAGCCGGA---  
>tdbD00003666 Drosophila\_melanogaster 7227 Tyr GTA  
-CCTTCGATAGCTCAGTT--GGT--AGAGCGGTGGACTGTAGATCCATAG-----GTCGCTGGTTCAAATCCGGTTCGAAGGA---  
>tdbD00011679 Drosophila\_melanogaster 7227 Tyr GTA  
-CCTTCGATAGCTCAGTT--GGT--AGAGCGGTGGACTGTAGATCCATAG-----GTCGCTGGTTCAAAGTCCGGTTCGAAGGA---  
>tdbD00011707 Encephalitozoon\_cuniculi\_GB-M1 284813 Tyr GTA  
-CTCTCAATAGCTCAGT--GGT--AGAGCATTGACTGTAGATCGAATG-----GCCGCTGGTTTCGACTCCAGCTTGGGAGA---  
>tdbD00011786 Gallus\_gallus 9031 Tyr GTA  
-CCTTCGATAGCTCAGTT--GGT--AGAGTGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTCAAATCCGGTTCGAAGGA---  
>tdbD00011787 Gallus\_gallus 9031 Tyr GTA  
-CCTTCGATAGCTCAGCT--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTCAAATCCGGTTCGAAGGA---  
>tdbD00011788 Gallus\_gallus 9031 Tyr GTA  
-CCTTCGATAGCTCAGCT--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTTCGATTCGGTTCGAAGGA---  
>tdbD00011789 Gallus\_gallus 9031 Tyr GTA  
-CCTTCGATAGCTCAGC--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTCAAATCCGGTTCGAAGGA---  
>tdbD00011790 Gallus\_gallus 9031 Tyr GTA  
-CCTTCGATAGCTCAGCT--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTCAAATCCGGTTCGAAGGA---  
>tdbD00011638 Homo\_sapiens 9606 Tyr GTA  
-CCTTCGATAGCTCAGCT--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTTCGATTCAGTTCGAAGGA---

>tdbD00011642 Homo\_sapiens 9606 Tyr GTA  
-CCTTCGATAGCTCAGTT-GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTTCGATTCCGGCTCGAAGGA---  
>tdbD00011643 Homo\_sapiens 9606 Tyr GTA  
-CCTTCGATAGCTCAGTT-GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTTCGAATCCGGCTCGGAGGA---  
>tdbD00011644 Homo\_sapiens 9606 Tyr GTA  
-CTTTCGATAGCTCAGTT-GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTTCGAATCCGGCTCGAAGGA---  
>tdbD00011645 Homo\_sapiens 9606 Tyr GTA  
-CCTTCGATAGCTCAGTT-GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTTCGAATCCGGCTCGAAGGA---  
>tdbD00003656 Leishmania\_donovani 5661 Tyr GTA  
-CCTTCGTAGCTCAATT-GGT--AGAGCATGTGACTGTAAATCACAGG-----GTCGCTGGTTTCGATTCCGGCCGAAGGA---  
>tdbD00003662 Nicotiana\_rustica 4093 Tyr GTA  
-CCGACCTTAGCTCAGTT-GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTTCGAATCCGGCAGGTCGGA---  
>tdbD00011804 Pan\_troglodytes 9598 Tyr GTA  
-CTTTCGATAGCTCAGTT-GGT--AGAGTGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTTCGAATCCGGCTGAAGGA---  
>tdbD00011805 Pan\_troglodytes 9598 Tyr GTA  
-CCTTCGATAGCTCAGTT-GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTCAAATCCGGCTCGGAGGA---  
>tdbD00011806 Pan\_troglodytes 9598 Tyr GTA  
-CCTTCGATAGCTCAGTT-GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTTCGAATCCGGCTCGGAGGA---  
>tdbD00011783 Plasmodium\_falciparum\_3D7\_36329 Tyr GTA  
-CCGATGATAGCTCAGTT-GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCACCGGTTTCGATTCCGGTTCATCGGA---  
>tdbD00003654 Saccharomyces\_cerevisiae 4932 Tyr GTA  
-CTCTCGGTAGCTCAAGTT-GGT--AGAGCGGAGGACTGTAAATCCTTAG-----ATCGGGCGTTTCGACTCGCCCCGGGAGA---  
>tdbD00003655 Saccharomyces\_cerevisiae 4932 Tyr GTA  
-CTCTCGGTAGCTCAAGTT-GGT--AGAGCGGAGGACTGTAAATCCTTAG-----ATCGGGCGTTTCGACTCGCCCCGGGAGA---  
>tdbD00011791 Takifugu\_rubripes 31033 Tyr GTA  
-CCTTCGATAGCTCAGTT-GGT--AGAGCGGAGGACTGTAGCTGTCTAGCGGA--AAT--CCTTAGGTCGCTGGTTCAAATCCGGCTCGAAGGA---  
>tdbD00011792 Takifugu\_rubripes 31033 Tyr GTA  
-CCTTCGATAACTCAGTT-GGT--AGAGTGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTCAAATCCGGCTCGAAGGA---  
>tdbD00011793 Takifugu\_rubripes 31033 Tyr GTA  
-CCTTGTAGCTCAGTT-GGC--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTTCGACTCCGGCTCGAAGGA---  
>tdbD00011796 Takifugu\_rubripes 31033 Tyr GTA  
-CCTTCGGTAGCTCAGC--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTCAAATCCGGCTCGAAGGA---  
>tdbD00011797 Takifugu\_rubripes 31033 Tyr GTA  
-CCTTCGATAGCTCAGC--GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTCAAATCCGGCTCGAAGGA---  
>tdbD00003652 Tetrahymena\_thermophila 5911 Tyr GTA  
-CCGAACCTTAGCTCAGTT-GGA--AGAGCATCGGACTGTAAATCCGGTG-----GTCCCGGTTTCGAACCCGGGAGTTCGGACCA  
>tdbD00003664 Triticum\_aestivum 4565 Tyr GTA  
-CCGATCTTAGCTCAGTT-GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCACTGGTTTCGAATCCGGTAGGTCGGA---  
>tdbD00003667 Xenopus\_laevis 8355 Tyr GTA  
-CCTTCGATAGCTCAGCT-GGT--AGAGCGGAGGACTGTAAATCCTTAG-----GTCGCTGGTTTCGATTCCGGCTCGAAGGA---  
>tdbD00003408 Arabidopsis\_thaliana 3702 Trp CCA  
-GGATCCGTGGCGCAAT--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCGATTACAGTCGGGTTACCA  
>tdbD00003409 Arabidopsis\_thaliana 3702 Trp CCA  
-GGATTCGTGGCGCAAT--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCGATTACAGTCGGGTTACCA  
>tdbD00011357 Arabidopsis\_thaliana 3702 Trp CCA  
-GCGCTCTTAGTTCAGTTCGGT--AGAACGTGGGTCTCCAAACCCAAT-----GTCGTAGTTCAAATCCTACAGAGCGTG---  
>tdbD00011358 Arabidopsis\_thaliana 3702 Trp CCA  
-GGATTCGTGGCGCAAT--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCGATTACAGTCGGGTTACCA  
>tdbD00011359 Arabidopsis\_thaliana 3702 Trp CCA  
-GGATCCGTGGCGCAAT--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCGATTACAGTCGGGTTACCA  
>tdbD00003410 Caenorhabditis\_elegans 6239 Trp CCA  
-GACTGCTTGGCGCAAT--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGGGCGTTTCGATCCGCTCAGTGGTCA---  
>tdbD00011361 Caenorhabditis\_elegans 6239 Trp CCA  
-GACTGCTTGGCGCAAT--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----ATTGGGCGTTTCGATCCGCTCAGTGGTCA---  
>tdbD00011363 Caenorhabditis\_elegans 6239 Trp CCA  
-GGTGTGTTGGCCGAGC--GGTCTAAGGCGCTGATCCAGCTCACGTATC-----GTAA-----GATGCAAGGTTTCGAATCTCTTAGCAACCA---  
>tdbD00011450 Candida\_glabrata\_CBS\_138\_284593 Trp CCA  
-GAAGCGGTGGCTCAAT--GGT--AGAGCTTTCGACTCCAAATCGAAG-----GTTGCAGGTTCAATCTCTGTCCGTTTCA---  
>tdbD00003402 Dictyostelium\_discoideum 44689 Trp CCA  
-GACTCCTTAGCATAGT--GGTTTATTGTAATTGTCTCCAAAGCAGTTG-----GTCCAGGTTTCAACTCCCTGAGGGGTCT---  
>tdbD00011365 Drosophila\_melanogaster 7227 Trp CCA  
-GACTCCGTGGCGCAAC--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----G-----TTGCGGTGTTCAAATCACGTCGGGGTTC---  
>tdbD00011366 Drosophila\_melanogaster 7227 Trp CCA  
-GACTCCGTGGCGCAAC--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCGAATCACGTCGGGGTTC---  
>tdbD00011367 Drosophila\_melanogaster 7227 Trp CCA  
-GACTCCGTGGCGCAAC--GGT--AGCGCGTCCGACTCCAGATCAGAAG-----GTTGCGTGTTCGAATCACGTCGGGGTTC---  
>tdbD00011383 Encephalitozoon\_cuniculi\_GB-M1\_284813 Trp CCA  
-GACGGTGTGGCGCAAC--GGT--AGCGCGTCCGATTCCAGTCCCGAAG-----GTTCTAGGTTCAAATCCTGGCTCCGTCA---  
>tdbD00003411 Gallus\_gallus 9031 Trp CCA  
-GACCTCGTGGCGCAAC--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GCTGCGTGTTCGAATCACGTCGGGGTCA---  
>tdbD00011468 Gallus\_gallus 9031 Trp CCA  
-GACCTCGTGGCGCAAG--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTATGTGTTCAAATCACATCGGGGTCA---  
>tdbD00011469 Gallus\_gallus 9031 Trp CCA  
-GACCTCGTGGCGCAAT--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GCTGTGTGTTCAAATCACACCGGGGTCA---  
>tdbD00011351 Homo\_sapiens 9606 Trp CCA

-GACCTCGTGGCGCAAC--GGC--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCAAATCACGTCGGGGTTC----  
>tdbD00011353 Homo\_sapiens 9606 Trp CCA  
-GACCTCGTGGCGCAAC--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCAAATCACGTCGGGGTTC----  
>tdbD00011354 Homo\_sapiens 9606 Trp CCA  
-GACCTCGTGGCGCAAT--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCAAAGTCACGTCGGGGTTC----  
>tdbD00003401 Leishmania\_tarentolae 5689 Trp CCA  
-GGGGGCTTAGCTCAGT--GGT--AGAGCATTGGATTCCAAATCCAGGG-----GTCGTAGGTTCAATCCCTGCAGCTCTCA--  
>tdbD00011482 Pan\_troglodytes 9598 Trp CCA  
-GGCCTCGTGGCGCAAC--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCAAATCACGTCGGGGTTC----  
>tdbD00011464 Plasmodium\_falciiparum\_3D7 36329 Trp CCA  
-AGGGGTATAGCTCAATT--GGC--AGAGCGTCGGTCTCCAAAACCGAAG-----GTTGTAGGTTTCGATTCTACTGCCCTG--  
>tdbD00003405 Schizosaccharomyces\_pombe 4896 Trp CCA  
-GGCCCTTAAGTCAAGT--GGT--AGAGTGTGAGATTCCAAATCTCAAAA-----GTCAAGTGTTCAAAGTCACTTAGGGGTTC----  
>tdbD00011470 Takifugu\_rubripes 31033 Trp CCA  
-GGCCTTGTGGTGCAAT--GGG--ATCACATCTGACCCAGATCGGATG-----TTTGTGCGTTCAACTCACGTCAGGGGCT--  
>tdbD00011472 Takifugu\_rubripes 31033 Trp CCA  
-GACCTCGTGGCGCAAC--GGT--AGCGCATCTGACTCCAGATCAGAAG-----GCTGCGTGTTCAAATCACGTCGGGGTTC----  
>tdbD00011473 Takifugu\_rubripes 31033 Trp CCA  
-GACCTTGTGGCGCAAC--GGT--AGCGCATCTGACTCCAGATCAGAAG-----GTTGCGTGTTCAAATCACGTCGGGGTTC----  
>tdbD00011474 Takifugu\_rubripes 31033 Trp CCA  
-GACCTTGTGGCGCAAT--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCAAATCACGTCGGGGTTC----  
>tdbD00011476 Takifugu\_rubripes 31033 Trp CCA  
-GACCTTGTGGCGCAAT--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCAAATCACGTCAGGGTTC----  
>tdbD00011477 Takifugu\_rubripes 31033 Trp CCA  
-GACCTCGTGGCGCAAT--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCAAATCACGTCGAGGTTC----  
>tdbD00003406 Toxoplasma\_gondii 5811 Trp CCA  
-ACGTTTTTAGTTTAAAT--GGT--AGAATAAAGGTCTCCAAAATCTAAG-----G-TGAAAGTTCAACTCTTTCAAACGTC--  
>tdbD00000649 Arabidopsis\_thaliana 3702 Glu CTC  
-TCCGTTGTAGTCTAGCT--GGTC--AGGATACTCGGCTCTCACCCGAGAG-----A-CCCGGGTTCGAGTCCCGGCAACGGAG--  
>tdbD00004703 Arabidopsis\_thaliana 3702 Glu CTC  
-TCCGTTGTAGTCTAGCT--GGTC--AGGATACTCGGCTCTCACCCGAGAG-----A-CCCGGGTTCGAGTCCCGGCAACGGAG--  
>tdbD00004705 Arabidopsis\_thaliana 3702 Glu CTC  
-TCCGTTGTAGTCTAGCT--GGTT--AGGATACTCGGCTCTCACCCGAGAG-----A-CCCGGGTTCGAGTCCCGGCAACGGAG--  
>tdbD00004706 Arabidopsis\_thaliana 3702 Glu CTC  
-TCCGTCGTAGTCTAGCT--GGTT--AGGATACTCGGCTCTCACCCGAGAG-----A-CCCGGGTTCGAGTCCCGGCGACGGAG--  
>tdbD00004707 Arabidopsis\_thaliana 3702 Glu TTC  
-GTCCCTTTCGTCAGT--GGTT--AGGACATCGTCTTTTCATGTGCGAAG-----A-CACGGGTTTCGATTCCCGTAAGGGATA--  
>tdbD00004708 Arabidopsis\_thaliana 3702 Glu TTC  
-TCCGTTATCGTCCAGC--GGTT--AGGATATCTGGCTTTCACCCAGGAG-----A-CCCGGGTTCGATTCCCGGTAACGGAA--  
>tdbD00004709 Arabidopsis\_thaliana 3702 Glu TTC  
-TCCGATGTGCTCCAGC--GGTT--AGGATATCTGGCTTTCACCCAGGAG-----A-CCCGGGTTCGATTCCCGGCATCGGA--  
>tdbD00004710 Arabidopsis\_thaliana 3702 Glu TTC  
-TCCGTTGTGCTCCAGC--GGTT--AGGATATCTGGCTTTCACCCAGGAG-----A-CCCGGGTTCGATTCCCGGCAACGGAA--  
>tdbD00004711 Arabidopsis\_thaliana 3702 Glu TTC  
-TCCATTGTGCTCCAGC--GGTT--AGGATATCTGGCTTTCACCCAGGAG-----A-CCCGGGTTCGATTCCCGGCAATGGA--  
>tdbD00000652 Bombyx\_mori 7091 Glu TTC  
-TCCCGTATGGTCTAGT--GGTT--AGGATACCTGGCTTTCACCCAGGAG-----G-CTCGGGTTCGATTCCCGGTACGGGAA--  
>tdbD00000650 Caenorhabditis\_elegans 6239 Glu CTC  
-TCCGTTGTGCTTAGT--GGTT--AGGATTTATGGCTCTCACCCATAAG-----G-CCGGGGTTCGATTCCCGGCAACGGAA--  
>tdbD00000651 Caenorhabditis\_elegans 6239 Glu TTC  
-TCCCATGTGCTTAGT--GGTT--AGGATTCGTGGTTTTCACCCACGCG-----G-CCCGGGTTCGATTCCCGGCATGGGAA--  
>tdbD00004712 Caenorhabditis\_elegans 6239 Glu CTC  
-TCCGTTGTGCTTAGT--GGTT--AGGATTTATGGCTCTCACCCATAAG-----G-CCGGGGTTCGATTCCCGGCAACAAA--  
>tdbD00004714 Caenorhabditis\_elegans 6239 Glu CTC  
-TCCGTTGTGCTTAGT--GGTT--AGGATTTATGGCTCTCACCCATAAG-----G-CCGGGGTTCGATTCCCGGCAACGAAA--  
>tdbD00004715 Caenorhabditis\_elegans 6239 Glu CTC  
-TCCGTTGTGCTTAGT--GGTT--AGGATTTATGGCTCTCACTCATAAG-----G-CCGGGGTTCGATTCCCGGCAACGGAA--  
>tdbD00004717 Caenorhabditis\_elegans 6239 Glu TTC  
-TCCCATGTGCTTAGT--GGTT--AGGATTCGTGGTTTTCACCCACGCG-----GCCGGGTTTCGATTCCCGGCATGGGA--  
>tdbD00004718 Caenorhabditis\_elegans 6239 Glu TTC  
-TCCCATGTGCTTAGT--GGTT--AGGATTCGTGGTTTTCACCCACGCG-----G-CCCGGGTTCGATTCCCGGCATGGGAA--  
>tdbD00004854 Candida\_glabrata\_CBS\_138 284593 Glu CTC  
-TCCGATGTAGTGAAC--GGCT--ATCACATCACGCTCTCACCCGAGAG-----A-CCGGGGTTCGACTCCCGCTTCGGAG--  
>tdbD00004855 Candida\_glabrata\_CBS\_138 284593 Glu TTC  
-TCCGATATAGTGAAC--GGCT--ATCACATCACGCTTTCACCCGAGAG-----A-CCGGGGTTCGACTCCCGTATCGGAG--  
>tdbD00000643 Dictyostelium\_discoideum 44689 Glu TTC  
-TCCTCATTTGTTAGTTC--GGT--AACACTCTAGTCTTTCACACTGGTA-----C-CTCGGGTTCGATTCCCGAATGGGGAG--  
>tdbD00000653 Drosophila\_melanogaster 7227 Glu CTC  
-TCCTATATTGCTTAGT--GGTT--AGGATATCCGGCTCTCACCCGAGAG-----G-CCCGGGTTCAAATCCCGGTATGGGAA--  
>tdbD00000654 Drosophila\_melanogaster 7227 Glu CTC  
-TCCATATTTGCTTAGT--GGTT--AGGATATCCGGCTCTCACCCGAGAG-----G-CCCGGGTTCAAATCCCGGTATGGGAA--  
>tdbD00000655 Drosophila\_melanogaster 7227 Glu TTC  
-TCCATATTTGCTTAGT--GGCT--AGGATATCTGGCTTTCACCCAGAG-----G-CCCGGGTTCGATTCCCGGTATGGGAA--  
>tdbD00004724 Drosophila\_melanogaster 7227 Glu CTC  
-TCCCATATTTGCTTAGT--GGTT--AGGATACCCGGCTCTCACCCGAGAG-----G-CCCGGGTTCAAATCCCGGTATGGGAA--

>tdbD00004752 *Encephalitozoon\_cuniculi*\_GB-M1\_284813\_Glu\_CTC  
-TCCTTGGTGGTCCAGT--GGTT-AGGATAGCTGCCCTCAGCAGCAG-----G-CTCGGGTTCGATTCCCGGACGAGGAA---  
>tdbD00004753 *Encephalitozoon\_cuniculi*\_GB-M1\_284813\_Glu\_TTC  
-TTCCTACTGGTCTAGC--GGTT-AGGATGTCTGCCCTTCAAGCAGGAG-----G-TGGGGGTTTCGATTCCCGGTCAGGGAA---  
>tdbD00004879 *Gallus\_gallus*\_9031\_Glu\_CTC  
-TCCCTGGTGGTCTAGT--GGTT-AGGATTCGGCGCTCTCACCGCCGCG-----G-CCCGGGTTCGATTCCCGGTCAGGGAA---  
>tdbD00004881 *Gallus\_gallus*\_9031\_Glu\_TTC  
-TCCCTGGTGGTCTAGT--GGTT-AGGATCCGGCGCTTTCACCTCCAAG-----G-CCCGGGTTCGATTCCCGGTCAGGGAA---  
>tdbD00004882 *Gallus\_gallus*\_9031\_Glu\_TTC  
-TCCCTGGTGGTCTAGT--GGCT-AGGATTCGGCGCTTTCACCGCCGCG-----G-CCCGGGTTCGATTCCCGGTCAGGGAA---  
>tdbD00004884 *Gallus\_gallus*\_9031\_Glu\_TTC  
-TCCCACATGGTCTAGC--GGTT-AGGATTTCTGGTTTTACCCAGGCA-----G-CCCGGGTTCGACTCCCGGTGTGGGAA---  
>tdbD00004885 *Gallus\_gallus*\_9031\_Glu\_TTC  
-TCCCATATGGTCTAGC--GGTT-AGGATTCGGTTTTACCCAGGCG-----G-CCCGGGTTCGACTCCCGGTATGGGAA---  
>tdbD00004886 *Gallus\_gallus*\_9031\_Glu\_TTC  
-TCCCACATGGTCTAGC--GGTT-AGGATTCCTGGTTTTACCCAGGCG-----G-CCCGGGTTCGACTCCCGGTGTGGGAA---  
>tdbD00004887 *Gallus\_gallus*\_9031\_Glu\_TTC  
-TCCCATATGGTCTAGT--GGTT-AGGATTCGGTTTTACCCAGGCG-----G-CCCGGGTTCGACTCCCGGTATGGGAA---  
>tdbD0000666 *Homo\_sapiens*\_9606\_Glu\_TTC  
-TCCCTGGTGGTCTAGT--GGCT-AGGATTCGGCGCTTTCACCGCCGCG-----C-CCCGGGTTCGATTCCCGGCCAGGAAT---  
>tdbD0000667 *Homo\_sapiens*\_9606\_Glu\_TTC  
-TCCCTGGTGGTCTAGT--GGCT-AGGATTCGGCGCTTTCACCGCCGCG-----G-CCCGGGTTCGATTCCCGGTCAGGAAT---  
>tdbD00004690 *Homo\_sapiens*\_9606\_Glu\_CTC  
-CCCCTGGTGGTCTATC--GGTT-AGGATTCAGACCTCTCACCCTGCT-----A-CCCATGCTCGATTCTGGTTCAGGGA---  
>tdbD00004695 *Homo\_sapiens*\_9606\_Glu\_TTC  
-ACCCTG-TGGTCTAGT--GGCT-AAGACTTGTGCTTTCATTGCTGCA-----T-CCTAGGTTCAATTCAGTCAGGGA---  
>tdbD00004696 *Homo\_sapiens*\_9606\_Glu\_TTC  
-TCCCTGGTGGTCTAGT--GGCT-AGGATTCGGCGCTTTCACCGCCTGC-----AGCTCGAGTTCGATTCTGGTTCAGGGA---  
>tdbD00004697 *Homo\_sapiens*\_9606\_Glu\_TTC  
-GCGTTGGTGGTGTAGT--GGTG-AGCACAGCTGCCTTCAAGCAGTTA-----A-CGCGGGTTCGATTCCCGGTAACGA---  
>tdbD00004698 *Homo\_sapiens*\_9606\_Glu\_TTC  
-TCCCTGGTGGTCTAGT--GGCT-AGGATTCGGCGCTTTCACCGCTGCG-----G-CCCGGGTTCGATTCCCGGTCAGGGA---  
>tdbD00004699 *Homo\_sapiens*\_9606\_Glu\_TTC  
-TCCCTGGTGGTCTAGT--GGCT-AGGATTCGGCGCTTTCACCGCCGCG-----G-CCCGGGTTCGATTCCCGGTCAGGGAA---  
>tdbD00004700 *Homo\_sapiens*\_9606\_Glu\_TTC  
-TCCCTGGTGGTCTAGT--GGCT-AGGATTCGGCGCTTTCACCGCCGCG-----G-CCCGGGTTCGATTCCCGGCCAGGGAA---  
>tdbD00004701 *Homo\_sapiens*\_9606\_Glu\_TTC  
-TCCCACATGGTCTAGC--GGTT-AGGATTCCTGGTTTTACCCAGGCG-----G-CCCGGGTTCGACTCCCGGTGTGGGA---  
>tdbD00004702 *Homo\_sapiens*\_9606\_Glu\_TTC  
-TCCCATATGGTCTAGC--GGTT-AGGATTCCTGGTTTTACCCAGGTG-----G-CCCGGGTTCGACTCCCGGTATGGGA---  
>tdbD0000656 *Mus\_musculus*\_10090\_Glu\_CTC  
-TCCCTGGTGGTCTAGT--GGTT-AGGATTCGGCGCTCTCACCGCCGCG-----G-CCCGGGTTCGATTCTCGGTTCAGGGAA---  
>tdbD00004907 *Pan\_troglodytes*\_9598\_Glu\_TTC  
--ACCCTGTGGTCTAGT--GGCT-AAGACTTGTGCTTTCATTGCTGCA-----T-CCTAGGTTCAATTCAGTCAGGGAA---  
>tdbD00004909 *Pan\_troglodytes*\_9598\_Glu\_TTC  
-TCCCTGGTGGTCTAGT--GGCT-AGGATTCGGCGCTTTCACCGCCGCA-----G-CTCGGGTTCGATTCTCGGTGAGGGAA---  
>tdbD00004910 *Pan\_troglodytes*\_9598\_Glu\_TTC  
-TCCCTGGTGGTTTTAGT--GGCT-AGGGTTCGGGGCTTTCACCACTGCG-----A-CCCGGGTTCGATTCCCGGTCAGGGAA---  
>tdbD00004911 *Pan\_troglodytes*\_9598\_Glu\_TTC  
-TCCCTGGTGGTCTAGT--GGCT-AGGATTCGGCGCTTTCACCATCGCG-----G-CCCGGGTTCGATTCCCGGTCGGGGGA---  
>tdbD00004912 *Pan\_troglodytes*\_9598\_Glu\_TTC  
-TCCCTGGTGGTCTAGT--GGCT-AGGATTTGGCGCTTTCACCGCCGCG-----G-CCCGGGTTCGATTCCCGGTCAGGGAA---  
>tdbD00004875 *Plasmodium\_falciparum*\_3D7\_36329\_Glu\_CTC  
-TCCCACGTGGTCTAGT--GGCT-AGGATATTCGGCTCTCACCAGAAAG-----G-CCCGGGTTCGATTCCCGGTCAGGGAA---  
>tdbD00004876 *Plasmodium\_falciparum*\_3D7\_36329\_Glu\_TTC  
-TCCCATGTAGTCTAGGC--GGTT-AGGATATTCGGCTTTCACCCGAACG-----A-CCCGGGTTCGAGTCCCGGTCAGGGAA---  
>tdbD0000657 *Rattus\_norvegicus*\_10116\_Glu\_CTC  
-TCCTTGGTGGTCTAGT--GGTT-AGGATTCGGCGCTCTCACCGCCGCG-----G-CCCGGGTTCGATTCCCGGTCAGGGAA---  
>tdbD0000659 *Rattus\_norvegicus*\_10116\_Glu\_CTC  
-TCGCTGGTGGTCTAGT--GGTT-AGGATTCGGCGCTCTCACCGCCGCG-----G-CCCGGGTTCGATTCCCGGTCAGGGAA---  
>tdbD0000660 *Rattus\_norvegicus*\_10116\_Glu\_CTC  
-GGTCCATGGTGTAA--GGTG-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCGATTCCCGGTCAGGGAA---  
>tdbD0000661 *Rattus\_norvegicus*\_10116\_Glu\_CTC  
-GGTCCATGGTGTAA--GGTT-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCGATTCCCGGTCAGGGAA---  
>tdbD0000662 *Rattus\_norvegicus*\_10116\_Glu\_CTC  
-GGTCCATGGTGTAA--GGTT-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCGATTCCCGGTCAGGGAA---  
>tdbD0000663 *Rattus\_norvegicus*\_10116\_Glu\_TTG  
-GGTCCATGGTGTAA--GGTT-AGCACTCTGGACTTTGAATCCAGCG-----A-TCCGAGTTCGATTCCCGGTCAGGGAA---  
>tdbD0000664 *Rattus\_norvegicus*\_10116\_Glu\_TTG  
-GGTCCATGGTGTAA--GGTT-AGCACTCTGGACTTTGAATCCAGCA-----A-TCTGAGTTCGATTCCCGGTCAGGGAA---  
>tdbD0000665 *Rattus\_norvegicus*\_10116\_Glu\_TTG  
-GGTCTCATGGTGTAA--GGTT-AGCACTCTGGACTTTGAATCCAGCG-----A-TCCGAGTTCGAGTCTCGGTGAGGCCT---  
>tdbD0000645 *Saccharomyces\_cerevisiae*\_4932\_Glu\_CTC  
-TCCGATGTAGTGTAA--GGCT-ATCACATCAGTCTCACCCTGGAG-----A-CCCGGGTTCGACTCCCGGTCAGGGAA---  
>tdbD0000646 *Saccharomyces\_cerevisiae*\_4932\_Glu\_TTC

-TCCGATATAGTGTAAC--GGCT-ATCACATCAGCCTTACCCGTTGGAG-----A-CCGGGTTTCGACTCCCCGTAGCGGAG---  
>tdbD0000648 Schizosaccharomyces\_pombe 4896 Glu CTC  
-TCCGTCATGGTCCAGT--GGCT-AGGATTCATCGCTCTCACCATGCG-----G-CGGGGTTTCGATTCCCCGTAGCGGAG---  
>tdbD0000647 Schizosaccharomyces\_pombe 4896 Glu TTC  
-TCCGTTGGTCCAAC--GGCT-AGGATTCGTCGCTTACCCGACGCG-----G-TCGGGTTTCGACTCCCCGCAACGGAG---  
>tdbD00004888 Takifugu\_rubripes 31033 Glu CTC  
-TCCCTGGTGGTCTAGT--GGTC-AGGATTCGGCGCTCTCACTGCCGTG-----G-CCTGGGTTTCGATTCCCAGTCAGGGAA---  
>tdbD00004889 Takifugu\_rubripes 31033 Glu CTC  
-TCCCTGGTGGTCTAGT--GGTC-AGGATTCGACGCTCTCACCCTCGCG-----G-CCCGGTTTCGATTCCCAGTCAGGGAA---  
>tdbD00004890 Takifugu\_rubripes 31033 Glu CTC  
-TCCCTGGTGGTCTAGT--GGTC-AGGATTCGGCGCTCTCACCGCCGCG-----G-CCCGGTTTCGATTCCCAGTCAGGGAA---  
>tdbD00004892 Takifugu\_rubripes 31033 Glu CTC  
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>tdbD00004894 Takifugu\_rubripes 31033 Glu TTC  
-TCCCATATGCTCTAGT--GGTC-AGGATTCCTGGCTTTCACCAGGTG-----G-CATAGGTTCAATTCCTCAATATGGGAG---  
>tdbD00004895 Takifugu\_rubripes 31033 Glu TTC  
-TCCCATATGCTCTAAC--GGTG-AGGATTCCTGGTTCACCAGGTG-----G-CCCGGTTCAACTCCCAGTCAGGGAA---  
>tdbD00004896 Takifugu\_rubripes 31033 Glu TTC  
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>tdbD00004897 Takifugu\_rubripes 31033 Glu TTC  
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>tdbD00004898 Takifugu\_rubripes 31033 Glu TTC  
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>tdbD00004899 Takifugu\_rubripes 31033 Glu TTC  
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>tdbD00004900 Takifugu\_rubripes 31033 Glu TTC  
-TCCCTGGTGGTCTAGT--GGTC-AGGATTCAGCGCTTTCACCCTCGCG-----G-CCTGGGTTTCGATTCCCAGTCAGGGAA---  
>tdbD00008606 Arabidopsis\_thaliana 3702 Gln CTG  
-GGTTCATAGTCTAGC--GGTT-AGGACATTGGACTCTGAATCCAGTA-----A-CCCGAGTTCAATTCCTCGGTAGAACCT---  
>tdbD00008607 Arabidopsis\_thaliana 3702 Gln CTG  
-GGTTCATAGTCTAGT--GGTC-AGGACATTGGACTCTGAATCCAGTA-----A-CCCGAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00008608 Arabidopsis\_thaliana 3702 Gln CTG  
-GGTCCATAGTCTAGT--GGTC-AGGACATTGGACTCTGAATCCAGTA-----A-CCCGAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00008609 Arabidopsis\_thaliana 3702 Gln CTG  
-GGTCCATAGTCTAGT--GGTC-AGGACATTGGACTCTGAATCCAGTA-----A-CCCGAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00008610 Arabidopsis\_thaliana 3702 Gln CTG  
-GGTTCATAGTCTAGC--GGTT-AGGACACTAGACTCTGAATCTAGTA-----A-CCCGAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00008611 Arabidopsis\_thaliana 3702 Gln TTG  
-TGGAGTATAGCCAAGT--GGT--AAGGCACCGGTTTTGGTACCGCA-----TGCAAAGGTTTCGAATCCTTTTACTCCAG---  
>tdbD00008612 Arabidopsis\_thaliana 3702 Gln TTG  
-GGTTCATAGTGTAGT--GGTT-AGCACTCAGGACTTTGAATCCTCGC-----A-CCTGGGTTTCGACTCCCAGTCAGGGAA---  
>tdbD00008613 Arabidopsis\_thaliana 3702 Gln TTG  
-GGTTCATAGTGTAGT--GGTT-AGCACTCAGGACTTTGAATCCTCGC-----A-CCTGGGTTTCGACTCCCAGTCAGGGAA---  
>tdbD00002398 Caenorhabditis\_elegans 6239 Gln CTG  
-GGTTCATAGTGTAGC--GGTT-AGCACTCAGGACTCTGAATCCTCGC-----A-CCCGAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00002397 Caenorhabditis\_elegans 6239 Gln TTG  
-GGTTCATAGTGTAGC--GGTT-AGCACTCAGGACTTTGAATCCTCGC-----A-CCCGAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00008614 Caenorhabditis\_elegans 6239 Gln CTG  
-GGTTCATAGTGTAGC--GGTT-AGCACTCAGTACTCTGAATCCTCGC-----A-CCCGAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00008616 Caenorhabditis\_elegans 6239 Gln CTG  
-GGTTCATAGTGTAGT--GGTT-AGCACTCAGGACTCTGAATCCTCGC-----A-CCCGAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00008617 Caenorhabditis\_elegans 6239 Gln TTG  
-GGTTCATAGTGTAGC--GGTT-AGCACTCAGGACTTTGAATCCTCGC-----A-TCCAAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00008619 Caenorhabditis\_elegans 6239 Gln TTG  
-GGTTCATAGTGTAGC--GGTT-AGCACTCAGTACTCTGAATCCTCGC-----A-CCCGAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00008751 Candida\_glabrata\_CBS\_138 284593 Gln CTG  
-GGTCTATAGTGTAGT--GGTT-ATCACTTTCGGTCTGTATCCGAACA-----A-CCCGGTTTCGAATCCGGGTAGGACCT---  
>tdbD00008750 Candida\_glabrata\_CBS\_138 284593 Gln TTG  
-GGTCTATAGTGTAGT--GGTT-ATCACTTTCGGTCTGTATCCGAACA-----A-CCCGGTTTCGAATCCGGGTAGGACCT---  
>tdbD00002390 Crithidia\_fasciculata 5656 Gln CTG  
-GCTCTATAGTGTAGC--GGTT-ATCACCTCGGACTCTGAATCCGATA-----A-CCCTGGTTTCGAGTCCAGGTAGGAGTGA---  
>tdbD00002385 Dictyostelium\_discoideum 44689 Gln TTG  
-GGTTTTATAGTGAATT--GGTT-AGCACCCAGGACTTTGAATCCTGTA-----A-TCTGAGTTTCGAGTCTCAGTAGAACCA---  
>tdbD00008625 Drosophila\_melanogaster 7227 Gln CTG  
-GGTTCATAGTGTAAAT--GGTT-AGCACTTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAGTCTCGGTAGAACCT---  
>tdbD00008626 Drosophila\_melanogaster 7227 Gln CTG  
-GGTTCATAGTGTAAAT--GGTT-AGCACTCAGGACTCTGAATCCTCGC-----A-TCCGAGTTCAAGTCTCGGTAGAACCT---  
>tdbD00008627 Drosophila\_melanogaster 7227 Gln CTG  
-GGTTCATAGTGTAAAT--GGTT-AGCACTCAGGACTCTGAATCCTCGC-----A-TCCGAGTTCAAGTCTCGGTAGAACCT---  
>tdbD00008629 Drosophila\_melanogaster 7227 Gln TTG  
-GGTTCATAGTGTAAAT--GGTT-AGCACTCAGGACTTTGAATCCAGCG-----A-TCCGAGTTCAAGTCTCGGTAGAACCT---  
>tdbD00008630 Drosophila\_melanogaster 7227 Gln TTG  
-GGTTCATAGTGTAAAT--GGTT-AGCACTCAGGACTTTGAATCCAGCG-----A-TCCGAGTTCAAGTCTCGGTAGAACCT---  
>tdbD00008656 Encephalitozoon\_cuniculi\_GB-M1 284813 Gln CTG  
-GGTTCGCTGGTGAAT--GGTT-ATCACTTCAGACTCTGAATCTGACA-----A-TCTGAGTTTCGAATCCTCGGCGGACCA---

>tdbD00008657 *Encephalitozoon\_cuniculi*\_GB-M1\_284813\_Gln\_TTG  
-GGTCCATAGTGTAAT--GGTT-AGCACCTGGACTTTGAATCCAGTA-----A-TCTGAGTTCAATCTCGGTGGAACCA---  
>tdbD00008774 *Gallus\_gallus*\_9031\_Gln\_CTG  
-GGTCCCGTGGTGTAATA--GGTG-AGCACTCTGGACTCTGAATCCAGCA-----A-TCTGAGTTCAAATCTCAGTGGGACCT---  
>tdbD00008775 *Gallus\_gallus*\_9031\_Gln\_CTG  
-GGTCCCATGGTGTAATA--GGTG-AGCACTCTGGACTCTGAATCCAGCG-----A-TCTGAGTTCAAATCTCAGTGGGACCT---  
>tdbD00008777 *Gallus\_gallus*\_9031\_Gln\_TTG  
-GGTTCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTAGAACCT---  
>tdbD00002406 *Homo\_sapiens*\_9606\_Gln\_GTT  
-GTCTCTGTGGCGCAATC--GGTT-AGCGCGTTCGGCTGTAAACCGAAAG-----ATTGGTGGTTCGAGCCCACCCAGGGACG---  
>tdbD00008589 *Homo\_sapiens*\_9606\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTG-ACCACCTTGGACTCTGAATACAGTG-----A-TCAGAGTTCAAGTCTCACTGGAACC---  
>tdbD00008590 *Homo\_sapiens*\_9606\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTG-AGCACTCTGGACTCTGAATACAGTG-----A-TCAGAGTTCAAGTCTCACTGGGACC---  
>tdbD00008591 *Homo\_sapiens*\_9606\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTA-AGCACTCTGGACTCTGAATCCAGCC-----A-TCTGAGTTCAAGTCTCTGTGGAACC---  
>tdbD00008592 *Homo\_sapiens*\_9606\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTG-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGGACC---  
>tdbD00008593 *Homo\_sapiens*\_9606\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGGACC---  
>tdbD00008594 *Homo\_sapiens*\_9606\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTA-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAGTCTCACTGGGACC---  
>tdbD00008595 *Homo\_sapiens*\_9606\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTG-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAGTCTCACTGGGACC---  
>tdbD00008596 *Homo\_sapiens*\_9606\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAGTCTCACTGGGACC---  
>tdbD00008598 *Homo\_sapiens*\_9606\_Gln\_TTG  
-TAGGATATGGTTAATA--GGT--AGCATGGAGAATTTGGAGTCTCAG-----G-GATAGTTCAATCTCTATAGTTCCA---  
>tdbD00008599 *Homo\_sapiens*\_9606\_Gln\_TTG  
-TAGGACTTGGTGTAAT--GGGT-AGCACAGAGAATTTGGATTCTCAG-----G-GGTGGTTCAATCTCTTCGTCCTA---  
>tdbD00008601 *Homo\_sapiens*\_9606\_Gln\_TTG  
-TAGGACATGGTGTAATA--GGT--AGAATGGAGAATTTGAATCTCAG-----G-GGTAGTTCAATCTCTATAGTTCTA---  
>tdbD00008602 *Homo\_sapiens*\_9606\_Gln\_TTG  
-GGTCCCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCA-----A-TCCGAGTTCAATCTTGGTGGGACC---  
>tdbD00008603 *Homo\_sapiens*\_9606\_Gln\_TTG  
-GGCCCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGGACCT---  
>tdbD00008604 *Homo\_sapiens*\_9606\_Gln\_TTG  
-GGTCCCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCA-----A-TCCGAGTTCAATCTCGGTGGGACCT---  
>tdbD00002391 *Leishmania\_mexicana*\_5665\_Gln\_CTG  
-GCTCTATAGTGTAGC--GGTT-ATCACCTCGGACTCTGAATCCGATA-----A-CCCTGGTTCGAGTCCAGGTAGGAGTG---  
>tdbD00002384 *Leishmania\_tarentolae*\_5689\_Gln\_TTG  
-GGTCTATAGTGTAGT--GGTT-ATCACTTCGGACTTTGAATCCGAAA-----A-CCCAGTTCAATCTCTGGTAGGACCA---  
>tdbD00002396 *Nicotiana\_rustica*\_4093\_Gln\_CTG  
-GGTCCATGGTCTAGT--GGTC-AGGACATTGGACTCTGAATCCAGTA-----A-CCCAGTTCAAATCTCGGTGGAACCT---  
>tdbD00008788 *Pan\_troglodytes*\_9598\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTG-AGCACTTTGGACTCTGAATACAGTG-----A-TCAGAGTTCAAGTCTCACTGGGACCT---  
>tdbD00008789 *Pan\_troglodytes*\_9598\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTG-AGCACTTTGGACTCTGAATACAGTG-----A-TCAGAGTTCAAGTCTCACTGGGACCT---  
>tdbD00008790 *Pan\_troglodytes*\_9598\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTG-AGCACTCTGGACTCTGAATCCAGCT-----A-TCCGAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00008791 *Pan\_troglodytes*\_9598\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTG-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00008792 *Pan\_troglodytes*\_9598\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTCTGAATCCAGTA-----A-TCCGAGTTCAAATCTCGGTGGAACCT---  
>tdbD00008795 *Pan\_troglodytes*\_9598\_Gln\_TTG  
-TAGGATATGGTTAATA--GGT--AGCATGGAGAATTTGGAGTCTCAG-----G-GATAGTTCAATCTCTATAGTTCCAG---  
>tdbD00008796 *Pan\_troglodytes*\_9598\_Gln\_TTG  
-TAGGACTTGGTGTAAT--GGGT-AGCACAGAGAATTTGGATTCTCAG-----G-GGTGGTTCAATCTCTTCGTCCTAG---  
>tdbD00008769 *Plasmodium\_falciparum*\_3D7\_36329\_Gln\_CTG  
-GGTTCGTAGTGTAGT--GGTT-AGCACTGCAGACTCTGACTCTGCAA-----A-CCTGGTTCAATCCCAGCAGAACCT---  
>tdbD00008770 *Plasmodium\_falciparum*\_3D7\_36329\_Gln\_TTG  
-GGTTTCGTAGTGTAGT--GGTT-AGCACTGAGGACTTTGAATCCCTCA-----A-CCCGGTTCAAGTCCCAGGAGACCT---  
>tdbD00002401 *Rattus\_norvegicus*\_10116\_Gln\_CTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTCTGAATCCAGCG-----A-TCTGAGTTCAAATCTCGGTGGGACCT---  
>tdbD00002387 *Saccharomyces\_cerevisiae*\_4932\_Gln\_CTG  
-GGTCTATAGTGTAGT--GGTT-ATCACTTTCGGTTCTGATCCGAACA-----A-CCCAGTTCAATCCCAGGTTGGGACC---  
>tdbD00002386 *Saccharomyces\_cerevisiae*\_4932\_Gln\_TTG  
-GGTCTATAGTGTAGT--GGTT-ATCACTTTCGGTTTGTATCCGGACA-----A-CCCGGTTCAATCCCAGGTTAGGACCT---  
>tdbD00002388 *Saccharomyces\_cerevisiae*\_4932\_Gln\_TTG  
-GGTCTATAGTGTAGT--GGTT-ATCACTTTCGGTTTGTATCCGGACA-----A-CCCGGTTCAATCCCAGGTTAGGACCT---  
>tdbD00008622 *Saccharomyces\_cerevisiae*\_4932\_Gln\_TTG  
-GGTTTTATAGTGTAGT--GGTT-ATCACTTTCGGTTTGTATCCGGACA-----A-CCCGGTTCAATCCCAGGTTAAGACC---  
>tdbD00008624 *Saccharomyces\_cerevisiae*\_4932\_Gln\_TTG  
-GGTTTTATAGTGTAGT--GGTT-ATCACTTTCGGTTTGTATCCGAACA-----A-CCCGGTTCAATCCCAGGTTAAGACC---  
>tdbD00002389 *Schizosaccharomyces\_pombe*\_4896\_Gln\_TTG

-GGTTGTATGGTGTAAT--GGTT-AGCACGTGAGATTTTGATTCTCGAG-----A-CCTGGGTTTCGATTCCCAGTACGACCT---  
>tdbD00008631 Schizosaccharomyces\_pombe 4896 Gln CTG  
-GGTTGTATGGTGTAAT--GGTT-AGCACGTGAGATTTTGATTCTCGAG-----A-CCTGGGTTTCGATTCCCAGTACGACCT---  
>tdbD00008632 Schizosaccharomyces\_pombe 4896 Gln TTG  
-GGTTGTATGGTGTAAT--GGTT-AGCACGTGAGATTTTGATTCTCGAG-----A-TCTGGGTTTCGACTCCCAGTACGACC---  
>tdbD00008779 Takifugu\_rubripes 31033 Gln CTG  
-GGTTCTGTGGTGTAAT--GGTC-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGAGGACCT---  
>tdbD00008780 Takifugu\_rubripes 31033 Gln CTG  
-GGTTCTATGGTGTAAT--GGTT-AGCACTCTGGACTCTGAATCCAGCG-----A-TCTGAGTTCAAATCTCAGTAGAACCT---  
>tdbD00008781 Takifugu\_rubripes 31033 Gln CTG  
-GGTTCCATGGTGTAAT--GGTC-AGCACTCTGGACTCTGAATCCAGCG-----A-TCTGAGTTCGAATCTCAGTGGAACCT---  
>tdbD00008783 Takifugu\_rubripes 31033 Gln TTG  
-GGTCTCATGGTGTAAT--GGTT-AGCACTTTGGACTTTGAATCCAGTG-----A-TCCGAGTTCAAATCTGGGTGGGACCT---  
>tdbD00008784 Takifugu\_rubripes 31033 Gln TTG  
-GGTTCCATGGTGTAAT--GGTC-AGCACTTTGGACTTTGAATCCAGCG-----A-TCCGAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00008785 Takifugu\_rubripes 31033 Gln TTG  
-GGTTCCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGACTCCAGTG-----A-TCTGAGTTCAAGTCTCAGTGGAACCT---  
>tdbD00002383 Tetrahymena\_thermophila 5911 Gln TTA  
-GGTTCCATAGTATAGT--GGTT-AGTACTGGGGACTTTAAATCCCTTG-----A-CCTGGGTTTCGAATCCCAGTGGGACCT---  
>tdbD00002394 Toxoplasma\_gondii 5811 Gln TTG  
-TAAAAAGTAGCCAAGT--GGT--AAGGCAACGGATTTTGATTCCGAGA-----TACATAGGTTTCGAATCCTTTCTTTTAA---  
>tdbD00009100 Arabidopsis\_thaliana 3702 Arg ACG  
-GACTCCATGGCCCAAT--GGAT-AAGGCGCTGGTCTACGAAACCAGAG-----ACTCTGGGTTTCGATCCCCAGTGGAGTC---  
>tdbD00009101 Arabidopsis\_thaliana 3702 Arg ACG  
-GACTTCATGGCCCAAT--GGAT-AAGGCGCTGGTCTACGAAACCAGAG-----ATTCTGGGTTTCGATCCCCAGTGAAGTC---  
>tdbD00009102 Arabidopsis\_thaliana 3702 Arg ACG  
-GACTCTGTGGCCCAAT--GGAT-AAGGCGCTGGTCTACGAAACCAGAG-----ATTCTGGGTTTCGATCCCCAGCAGAGTC---  
>tdbD00009103 Arabidopsis\_thaliana 3702 Arg ACG  
-GGTTCCATGGCCCAAT--GGAT-AAGGCGCTGGTCTACGAAACCAGAG-----ATTCTGGGTTTCGATCCCCAGTGGAAATC---  
>tdbD00009104 Arabidopsis\_thaliana 3702 Arg ACG  
-GACTCCATGGCCCAAT--GGAT-AAGGCGCTGGTCTACGAAACCAGAG-----ATTCTGGGTTTCGATCCCCAGTGGAGTC---  
>tdbD00009105 Arabidopsis\_thaliana 3702 Arg ACG  
-GACTCCGTGGCCCAAT--GGAT-AAGGCGCTGGTCTACGAAACCAGAG-----ATTCTGGGTTTCGATCCCCAGCGGAGTC---  
>tdbD00009106 Arabidopsis\_thaliana 3702 Arg CCG  
-GACCGCTGGCCTAAT--GGAT-AAGGCGCTCGCCTCCGGAGCGGGAG-----ATTGTGGGTTTCGAGTCCCACCGTGGTC---  
>tdbD00009107 Arabidopsis\_thaliana 3702 Arg CCG  
-GTTTGCCTGGCCTAAT--GGAT-AAGGCGCTCGCCTCCGAAGCGGGAG-----ATTGTGGGTTTCGAATCCCATCGCGAAC---  
>tdbD00009108 Arabidopsis\_thaliana 3702 Arg CCG  
-GATCCCATAGCGGAGT--GGAT-ATCGCGTTAGACTCCGAATCTAAAG-----GTCGTGGGTTTCGATTCCCAGTGGGATC---  
>tdbD00009110 Arabidopsis\_thaliana 3702 Arg CCT  
-GCGCCTGTAGCTCAGT--GGAT-AGAGCGTCTGTTTCTTAAGCAGAAA-----GTCGAAGGTTTCGACCCCTTCTGGCGC---  
>tdbD00009111 Arabidopsis\_thaliana 3702 Arg CCT  
-GCGTCTGTAGCTCAGT--GGAT-AGAGCGTCTGTTTCTTAAGCAGAAAG-----GTCGTAGGTTTCGACCCCTACCTGACGC---  
>tdbD00009112 Arabidopsis\_thaliana 3702 Arg CCT  
-GCGCCTGTAGCTCAGT--GGAT-AGAGCGTCTGTTTCTTAAGCAGAAAG-----GTCGTAGGTTTCGACCCCTACCTGGCGC---  
>tdbD00009113 Arabidopsis\_thaliana 3702 Arg TCG  
-GACCGCATAGCGCAGT--GGATTAGCGCGTCTGACTTCGGATCAGAAG-----GTCGTGGGTTTCGACTCCCAGTGGGTC---  
>tdbD00009114 Arabidopsis\_thaliana 3702 Arg TCG  
-GACCGCATAGCGCAGT--GGATTAGCGCGTCTGACTTCGGATCAAAAG-----GTCGTGGGTTTCGACTCCCAGTGGGTC---  
>tdbD00009115 Arabidopsis\_thaliana 3702 Arg TCT  
-GCACCCGTGGCCTAAT--GGAT-AAGGCGTTGACTTCTAATCAAGCG-----ATTGTGGGTTTCGAGTCCCACCGGGTGT---  
>tdbD00009116 Arabidopsis\_thaliana 3702 Arg TCT  
-GCGCTCGTGGCCCAAT--GGAT-AAGGCGTCTGACTTCTAATCAGACG-----ATTGTGGGTTTCGATCCCCACCGAGCGT---  
>tdbD00009117 Arabidopsis\_thaliana 3702 Arg TCT  
-GCACCCATGGCCTAAT--GGAT-AAGGCGTCTGACTTCTAATCAAGCG-----ATTGTGGGTTTCGAGTCCCAGTGGGTC---  
>tdbD00009118 Arabidopsis\_thaliana 3702 Arg TCT  
-GCACCCGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCTAATCAAGCG-----ATTGTGGGTTTCGAGTCCCACCGGGTGT---  
>tdbD00009119 Arabidopsis\_thaliana 3702 Arg TCT  
-GCGCCGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCTAATCAAGCG-----ATTGTGGGTTTCGAGTCCCACCGGGCGT---  
>tdbD00009120 Arabidopsis\_thaliana 3702 Arg TCT  
-GCACCCATGGCCTAAT--GGAT-AAGGCGTCTGACTTCTAATCAAGCG-----ATTGTGGGTTTCGAATCCCAGTGGGTC---  
>tdbD00002591 Caenorhabditis\_elegans 6239 Arg ACG  
-GGCCGCTGGCGCAAT--GGAT-AACGCGTCTGCCACGGAGCAGAAG-----ATTGCAGGTTTCGAATCCTGCGGTGGTCG---  
>tdbD00002594 Caenorhabditis\_elegans 6239 Arg TCG  
-GGCCGCTGGCCTAAT--GGAT-AAGGCACAGACTTCGAATCTGGGG-----ATTGCAGGTTTCGAGTCTGCGGTGGTCG---  
>tdbD00002593 Caenorhabditis\_elegans 6239 Arg TCT  
-GGCCTGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCTAATCAGAAG-----ATTGCAGGTTTCGACCCCTGCTGGGTCA---  
>tdbD00009121 Caenorhabditis\_elegans 6239 Arg ACG  
---GGCCGTGGCGCAAT--GGAT-AACGCGTCTGCCACGGAGCAGAAG-----ATTGTAGGTTTCGAATCCTGCGGTGGTC---  
>tdbD00009123 Caenorhabditis\_elegans 6239 Arg ACG  
-GGCCGCTGGCGCAAT--GGAT-AACGCGTCTGCCACGGAGCAGAAG-----ATTGTAGGTTTCGAATCCTGCGGTGGTCG---  
>tdbD00009124 Caenorhabditis\_elegans 6239 Arg ACG  
-GGCCGCTGGCGCAAT--GGAT-AACGCGTCTGCCACGGAGCAGAAG-----ATTGTAGGTTTCGAATCCTGCGGTGGTCG---  
>tdbD00009126 Caenorhabditis\_elegans 6239 Arg CCG  
-GCCCGCTGGCCTAAT--GGAT-AAGGCACCGACTCCGGAACCGGGA-----A-TGGGGGTTTCGAGTCCCCCGCGAGC---

>tdbD00009127 *Caenorhabditis elegans* 6239 Arg CCG  
-GCTCGCGTGGCCTAAT--GGAT-AAGGCACCGACTCCGGAACCGGA-----A-TGGGGTTCAAGTCCCTCCGCGAGC----

>tdbD00009128 *Caenorhabditis elegans* 6239 Arg CCT  
-GCCAGCGTGGCCAGTGTGGTCAAAGGCGTGAGACTCCTGTCTCTTTCGG----GCAA----CCGATCGCAGGTTTCAATCCTGCCCGTGGC----

>tdbD00009129 *Caenorhabditis elegans* 6239 Arg CCT  
-GGCCGTGTGGCCTAAT--GGAT-AAGGCGTGGTCTCCTAACCAGAA-----ACTGCAGGTTTCAGTCTGCCTCGGTC----

>tdbD00009131 *Caenorhabditis elegans* 6239 Arg TCG  
-GGCCGTGTGGCCTAAT--GGAT-AAGGCATCAGACTTCGAATCTATGG-----GG-----ATTGCAGGTTTCAGTCCCTGCCGTGGTC----

>tdbD00009133 *Caenorhabditis elegans* 6239 Arg TCG  
-GGCCGTGTGGCCTAAT--GGAT-AAGGCATCAGACTTCGAATCTGGGG-----ATTGCAGGTTTCAGTCCCTGCCGTGGTC----

>tdbD00009135 *Caenorhabditis elegans* 6239 Arg TCG  
-GGCCGTGTGGCCTAAT--GGAT-AAGGCACCGACTTCGAATCTGGGG-----ATTGCAGGTTTCAGTCCCTGCCGTGGTCG----

>tdbD00009137 *Caenorhabditis elegans* 6239 Arg TCT  
-GGCCTTGTGGCCTAAT--GGAT-AAGGCGTGTGACTTCTAATCAGAAG-----ATTGCAGGTTTCAGCCCTGCCTGGGTCA----

>tdbD00009138 *Caenorhabditis elegans* 6239 Arg TCT  
-GGCCTTGTGGCCTAAT--GGAT-AAGGCGTGTGACTTCTAATCAGAAG-----ATTGCAGGTTTCAGTCCCTGCCTGGGTCA----

>tdbD00009456 *Candida glabrata* CBS\_138 284593 Arg ACG  
-TTCCCTGTGGCCCAAT--GGAT-AAGGCGTGGCTACGAACCGAAG-----ATTCCAGGTTTCAGTCTGGCGGGGAAG----

>tdbD00009459 *Candida glabrata* CBS\_138 284593 Arg CCG  
-GCCCTTTTAGTGCAAT--GGAT-AGCATACATTTTCCGGTGGATGTG-----A-TCCGGTTTCAGTCCCGGAGGGGCT----

>tdbD00009458 *Candida glabrata* CBS\_138 284593 Arg CCT  
-GTCCCGTGGCCTAAT--GGT--AAGCCTGTCCCTCCTAAGCAGAAG-----ACTGCGGTTTCAGTCCCGTACGGATCG----

>tdbD00009457 *Candida glabrata* CBS\_138 284593 Arg TCT  
-GCTCGGTGGCGTAAT--GGC--AAGCCTGTGACTTCTAATCAGAAG-----ATTATGGTTTCAGCCCCATCGTGAGTG----

>tdbD00002582 *Dictyostelium discoideum* 44689 Arg ACG  
-GGACTATAGTTTGT--GGAT-ATAACACCGGCTACGAACCGGTAG-----GTCTCAGGTTTCAGCCCTGATGGTCTCG----

>tdbD00002583 *Dictyostelium discoideum* 44689 Arg TCT  
-GCCCGTTTAGCAAAGTT--GGA--ATTGCGGACGCTTCTAAGCTGCAG-----GTCGTGGGATTCAGACCCACAATGGGTG----

>tdbD00002595 *Drosophila melanogaster* 7227 Arg ACG  
-GGTCCGTGGCCTAAT--GGAT-AAGCCTGTGACTACGGATCAGAAG-----ATTCCAGGTTTCAGTCTGGCAGGATCG----

>tdbD00002596 *Drosophila melanogaster* 7227 Arg TCG  
-GACCGTGTGGCCTAAT--GGAT-AAGGCGTGGACTTCGGATCCGAAG-----ATTGCAGGTTTCGAATCCTGTACAGGTCG----

>tdbD00002597 *Drosophila melanogaster* 7227 Arg TCG  
-GACCGTGTGGCCTAAT--GGAT-AAGGCGTGGACTTCGGATCCGAAG-----ATTGCAGGTTTCAGTCTGTACAGGTCG----

>tdbD00009145 *Drosophila melanogaster* 7227 Arg CCT  
-GCCCCAGTGGCCTAAT--GGAT-AAGGCATCGCCTCCTAAGCCGGGG-----ATTGTGGTTTCAGTCCCATCTGGGGT----

>tdbD00009146 *Drosophila melanogaster* 7227 Arg TCG  
-GACCGTGTGGCCTAAT--GGAT-AAGGCGTGGACTTCGAATCCGAAG-----ATTGCAGGTTTCAGTCTGTACAGGTCG----

>tdbD00009147 *Drosophila melanogaster* 7227 Arg TCG  
-GACCGTGTGGCCTAAT--GGAT-AAGGCGTGGACTTCGAATCCGAAG-----ATTGCAGGTTTCAGTCTGTACAGGTCG----

>tdbD00009150 *Drosophila melanogaster* 7227 Arg TCT  
-GGCCGTGTAGCCTAAT--GGAT-AAGGCGTGGATTCTGTATCCGAAA-----ATTGCGGTTTCAGTCCCCTCATGGTC----

>tdbD00009151 *Drosophila melanogaster* 7227 Arg TCT  
-GACCTTTAGCGCATT--GGAT-AGCGGTTGGACTTCTAATCCAAAG-----GTGGCGGTTTCAGTCCCAGAGGGTT----

>tdbD00009152 *Drosophila melanogaster* 7227 Arg TCT  
-GTCCTTTGGCGCAGA--GGAT-AGCGGTTGGACTTCTAATCCAAAG-----GTCGCGGTTTCAGTCCCAGAGGGAT----

>tdbD00009216 *Encephalitozoon uniculi* GB-M1 284813 Arg ACG  
-GGCCTCATAGCTCAAT--GGAT-AGAGTGTGGCCTACGGAGCCGAAG-----GCTGAGGTTTCAGTCCCTCTGGGGTCG----

>tdbD00009219 *Encephalitozoon uniculi* GB-M1 284813 Arg CCT  
-GTTCTGTAGCTCAGT--GGAT-AGAGCGGCTCTCCTAAGCTGAG-----GTCGTGGTTTCAGTCCCACCTGGAACG----

>tdbD00009217 *Encephalitozoon uniculi* GB-M1 284813 Arg TCG  
-GGTCTTTAGTATAAT--GGT--AGAACAATTGGCTTCGGACCAATA-----G-TCCGGTTTCGAATCCCAGGACTCG----

>tdbD00009218 *Encephalitozoon uniculi* GB-M1 284813 Arg TCT  
-GCCCTGATAGCGTAA--GGAT-AAGCCTGTGCTTCTAAGCAGAAG-----ACTGCGGTTTCAGTCCCCTCAGGGTG----

>tdbD00009511 *Gallus gallus* 9031 Arg ACG  
-GGCCAGTGGCGCAAT--GGAT-AAGCCTGTGACTACGGATCAGAAG-----ATTGTAGTTTCAGTCTGCCTGGCTCG----

>tdbD00009512 *Gallus gallus* 9031 Arg ACG  
-GGCCAGTGGCGCAAT--GGAT-AAGCCTGTGACTACGGATCAGAAG-----ATTCTAGTTTCAGTCTGCCTGGCTCG----

>tdbD00009513 *Gallus gallus* 9031 Arg ACG  
-GGCCAGTGGCGCAAT--GGAT-AAGCCTGTGACTACGGATCAGGAG-----ATTGCAGTTTCACTCCTGCCTGGCTCG----

>tdbD00009514 *Gallus gallus* 9031 Arg CCG  
-GGCCAGTGGCCTAAT--GGAT-AAGGCATCAGCTCCGGAGCTGGGG-----ATTGTGGTTTCAGTCCCCTCAGGGTCG----

>tdbD00009515 *Gallus gallus* 9031 Arg CCT  
-GCCCCAGTGGCCTAAT--GGAT-AAGGCATGGCCTCCTAAGCCAGGG-----ACTGTGGTTTCAGTCCCCTCAGGGTG----

>tdbD00009516 *Gallus gallus* 9031 Arg CCT  
-GCCCCAGTGGCCTAAT--GGAT-AAGGCATGGCCTCCTAAGCCAGGG-----ATTGTGGTTTCAGTCCCCTCAGGGTG----

>tdbD00009517 *Gallus gallus* 9031 Arg CCT  
-GCCCCAGTGGCCTAAT--GGAT-AAGGCATGGCCTCCTAAGCCAGGG-----ATTGTGGTTTCAGTCCCCTCAGGGTG----

>tdbD00009518 *Gallus gallus* 9031 Arg TCG  
-GACCAGTGGCCTAAT--GGAT-AAGGCGTGTGACTTCGGATCAGAAG-----ATTGAGGTTTCAGTCCCCTCAGGGTG----

>tdbD00009519 *Gallus gallus* 9031 Arg TCG  
-GACCAGTGGCCTAAT--GGAT-AAGGCGTGTGACTTCGGATCAGAAG-----ATTGAGGTTTCAGTCCCCTCAGGGTG----

>tdbD00009521 *Gallus gallus* 9031 Arg TCT  
-GCCCCAGTGGCCTAAT--GGAT-AAGGCATGGCCTCCTAAGCCAGGG-----ACTGTGGTTTCAGTCCCACCTGGGGTG----

>tdbD00009522 *Gallus gallus* 9031 Arg TCT



-GGCTCCGTGGCGCAAT--GGAT-AGCGCATTGGACTTCTAATTCAAAAG-----GTTCCGGGTTTCGAGTCCCAGGCGAGTCG---  
>tdbD00009523 Gallus\_gallus 9031 Arg TCT  
-GGCTCTGTGGCGCAAT--GGAT-AGCGCATTGGACTTCTAATTCAAAAG-----GTTGTGGGTTTCGAGTCCCACCAGAGTCG---  
>tdbD00002599 Homo\_sapiens 9606 Arg ACG  
-GGCCAGTGGCGCAAT--GGAT-AACGCGTCTGACTACGGATCAGAAG-----ATTCCAGGTTTCGACTCCTGGCTGGCTCG---  
>tdbD00002600 Homo\_sapiens 9606 Arg TCG  
GGACCAGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCGGATCAGAAG-----ATTGAGGTTTCGAATCCCTTCGTGGTT---  
>tdbD00009084 Homo\_sapiens 9606 Arg CCG  
-GGCCGCTGGCCTAAT--GGAT-AAGGCGTCTGATTCGGATCAGAAG-----ATTGAGGTTTCGAGTCCCTTCGTGGTC---  
>tdbD00009086 Homo\_sapiens 9606 Arg CCT  
-GCCCCAGTGGCCTAAT--GGAT-AAGGCGTGGCCTCCTAAGCCAGGG-----ATTGTGGGTTTCGAGTCCCACCTGGGGT---  
>tdbD00009087 Homo\_sapiens 9606 Arg CCT  
-GCCCCGCTGGCCTAAT--GGAT-AAGGCATTGGCCTCCTAAGCCAGGG-----ATTGTGGGTTTCGAGTCCCACCCGGGGT---  
>tdbD00009091 Homo\_sapiens 9606 Arg TCG  
-GACCAGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCGGATCAGAAG-----ATTGAGGTTTCGAATCCCTTCGTGGTT---  
>tdbD00009093 Homo\_sapiens 9606 Arg TCG  
-GACCAGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCGGATCAGAAG-----ATTGAGGTTTCGAATCCCTCCGTGGTT---  
>tdbD00009094 Homo\_sapiens 9606 Arg TCG  
-GGCCGCTGGCCTAAT--GGAT-AAGGCGTCTGACTTCGGATCAGAAG-----ATTGCAGGTTTCGAGTCCCTGCCGCGGTC---  
>tdbD00009095 Homo\_sapiens 9606 Arg TCT  
-GTCTCTGTGGCGCAAT--GGACGAGCGCGTGGACTTCTAATCCAGAG-----GTTCCGGGTTTCGAGTCCCAGGCGAGAT---  
>tdbD00009096 Homo\_sapiens 9606 Arg TCT  
-GGTCCGTGGCGCAAT--GGAT-AGCGCATTGGACTTCTAATTCAAAAG-----GTTCCGGGTTTCGAGTCCCAGGCGAGTC---  
>tdbD00009097 Homo\_sapiens 9606 Arg TCT  
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>tdbD00009098 Homo\_sapiens 9606 Arg TCT  
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>tdbD00002580 Leishmania\_tarentolae 5689 Arg ACG  
-GTCCGTGTGGCTCAAT--GGA--AGAGCATCTGACTACGGATCAGAGG-----GTTGCAGGTTTCGAATCCCTGTACAGGATG---  
>tdbD00002581 Leishmania\_tarentolae 5689 Arg TCG  
-GGCCTCTTGGCGCAAT--GGA--AGCGCATCAGACTTCGGATCTGAGG-----G-TTGCAGTTTCGATCCTGCAGGGGGTCG---  
>tdbD00002584 Neurospora\_crassa 5141 Arg ACG  
-GGTCCGCTGGCTCAAT--GGC--AGAGCGTCTGACTACGAATCAGGAG-----GTTCCAGGTTTCGACCCCTGGGTGGATCG---  
>tdbD00009555 Pan\_troglodytes 9598 Arg CCG  
-GACCCAGTGGCCTAAT--GGAT-AAGGCATCAGCCTCCGGAGCTGGGG-----ATTGTGGGTTTCGAGTCCCATCTGGGTTCG---  
>tdbD00009556 Pan\_troglodytes 9598 Arg CCG  
-GGCCGCTGGCCTAAT--GGAT-AAGGCGTCTGATTCGGATCAGAAG-----ATTGAGGTTTCGAGTCCCTTCGTGGTTCG---  
>tdbD00009557 Pan\_troglodytes 9598 Arg CCT  
-GCCCCGCTGGCCTAAT--GGAT-AAGACATTGGCCTCCTAAGCCAGGG-----ATTGTGGGTTTCGAGTCCCACCCGGGGTA---  
>tdbD00009558 Pan\_troglodytes 9598 Arg CCT  
-GCCCCAGTGGCCTAAT--GGAT-AAGGCATTGGCCTCCTAAGCCAGGG-----ATTGTGGGTTTCGAGTCCCATCTGGGGTG---  
>tdbD00009559 Pan\_troglodytes 9598 Arg CCT  
-GCCCCAGTGGCCTAAT--GGAT-AAGGCGTGGCCTCCTAAGCCAGGG-----ATTGTGGGTTTCGAGTCCCACCTGGGGTG---  
>tdbD00009560 Pan\_troglodytes 9598 Arg CCT  
-GCCCCAGTGGCCTAAT--GGAT-AAGGCGTGGCCTCCTAAGCCAGGG-----ATTGTGGGTTTCGAGTCCCACCTGGGGTA---  
>tdbD00009561 Pan\_troglodytes 9598 Arg CCG  
-GCCGTGATCGTATAGT--GGTT-AGTACTCTGCGTTGCGGCTGCAGCA-----A-CCTCGGTTTCGAATCCGAGTCACGGCA---  
>tdbD00009562 Pan\_troglodytes 9598 Arg TCG  
-GACCAGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCGGATCAGAAG-----ATTGAGGTTTCGAATCCCTTCGTGGTTG---  
>tdbD00009563 Pan\_troglodytes 9598 Arg TCG  
-GACCAGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCGGATCAGAAG-----ATTGAGGTTTCGAATCCCTTCGTGGTTA---  
>tdbD00009565 Pan\_troglodytes 9598 Arg TCG  
-GGCCGCTGGCCTAAT--GGAT-AAGGCGTCTGACTTCGGATCAGAAG-----ATTGCAGGTTTCGAGTCCCTGCCACGGTCG---  
>tdbD00009566 Pan\_troglodytes 9598 Arg TCG  
-GACCAGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCGGATCAGAAG-----ATTGAGGTTTCGAATCCCTCCGTGGTTA---  
>tdbD00009567 Pan\_troglodytes 9598 Arg TCG  
-GGCCGCTGGCCTAAT--GGAT-AAGGCGTCTGACTTCGGATCAGAAG-----ATTGCAGGTTTCGAGTCCCTGCCGCGGTCG---  
>tdbD00009568 Pan\_troglodytes 9598 Arg TCT  
-GTCTCTGTGGCGCAAT--GGACGAGCGCGCTGGACTTCTAATCCAGAG-----GTTCCGGGTTTCGAGTCCCAGGCGAGATG---  
>tdbD00009570 Pan\_troglodytes 9598 Arg TCT  
-GGCTCTGTGGCGCAAT--GGAT-AGCGCATTGGACTTCTAATTCAAAAG-----GTTGCGGGTTTCGAGTCCCAGGCGAGTCG---  
>tdbD00009571 Pan\_troglodytes 9598 Arg TCT  
-GGCTCTGTGGCGCAAT--GGAT-AGCGCATTGGACTTCTAATTCAAAAG-----GTTGTGGGTTTCGAATCCCACCAGAGTCG---  
>tdbD00002575 Plasmodium\_falciparum 5833 Arg ACG  
-AAACTTGTAAATTTAAT--GGAT-AAAATATATAAAATACGAATATAAAA-----A-TAAAAGTTCAATTCTTTTCAAGTTTA---  
>tdbD00002576 Plasmodium\_falciparum 5833 Arg TCT  
-AAATCTATAATTTAAT--GGAT-AAAATAAAAACCTTCTAAGTTTTAT-----A-TGTAAGTTCAAATCTTACTAGATTTA---  
>tdbD00009499 Plasmodium\_falciparum\_3D7\_36329 Arg CCT  
-GCACCAAGTGGCGTAAT--GGAT-AGCGCAATGCCTTCCTAAGGCAAAG-----GTTATGGGTTTCGAGTCCCATCTGGTGTA---  
>tdbD00009500 Plasmodium\_falciparum\_3D7\_36329 Arg TCG  
-GACGCGTAGCCTAAT--GGAT-AAGGCGTCTGCTTCGGAAACCGAAG-----ATTGCGGGTTTCGAGTCCCCTCGTCGTTA---  
>tdbD00009501 Plasmodium\_falciparum\_3D7\_36329 Arg TCT  
-GCCTCTGTGGCGCAAT--GGAT-AGCGCGTGGACTTCTAATCCAAAAG-----GCTGCGGGTTTCGAATCCCAGGCGGGTA---  
>tdbD00002585 Saccharomyces\_cerevisiae 4932 Arg ACG  
-TTCTCTGTGGCCCAAT--GGTC-ACGGCGTCTGGCTACGAACAGAAAG-----ATTCCAGGTTTCAGTCCCTGGCGGGGAAG---

>tdbD00002587 *Saccharomyces cerevisiae* 4932 Arg CCT  
-GTTCCGTGGCGTAAT--GGT--AAGCGCTCTCCCTCCTAAGGAGAAG-----ACTGCGGGTTCGAGTCCCGTACGGAACG---  
>tdbD00009139 *Saccharomyces cerevisiae* 4932 Arg ACG  
-TTCCCTCGTGGCCCAAT--GGTC-ACGGCGTCTGGCTACGAACCAGAG-----ATTCCAGGTTTCGAGTCTGGCGGGGAAG---  
>tdbD00009141 *Saccharomyces cerevisiae* 4932 Arg CCG  
-GCTCCTGTAGTCAAT--GGTT-AAGCATGCATCTTCCGGTGGCTGTG-----A-TCCGGGTTTCGAGTCCCGGGAGGAGC---  
>tdbD00002588 *Schizosaccharomyces pombe* 4896 Arg ACG  
-GGTCTCGTGGCCCAAT--GGTT-AAGGCGCTTGACTACGAATCAAGAG-----ATTCCAGGTTTCGACTCTGGCGGGATCG---  
>tdbD00002589 *Schizosaccharomyces pombe* 4896 Arg ACG  
-GGTCTCGTGGCCCAAT--GGTT-AAGGCGCTTGACTACGAATCAAGAG-----ATTCCAGGTTTCGACTCTGGCGGGATCG---  
>tdbD00009155 *Schizosaccharomyces pombe* 4896 Arg CCT  
-TTACCGTGGCGCAAT--GGT--AGGCGATCTCATTCTAACCAGAGAAG-----GTTGCGGGTTCGAGTCCCGTCTGTAA---  
>tdbD00009156 *Schizosaccharomyces pombe* 4896 Arg TCG  
-GGGTGTGAGCCTAAT--GGTT-AAGGCGTGGTTCGGGACCAAG-----ACTGCAGGTTTCGAGTCTGTACACTC---  
>tdbD00009157 *Schizosaccharomyces pombe* 4896 Arg TCT  
-GCTCCGTGGCCTAAT--GGCT-AGGCGATTTGACTTCTAATCAAGGG-----ATTGTGGGTTTCGAGTCCCGCCGGGAGC---  
>tdbD00009158 *Schizosaccharomyces pombe* 4896 Arg TCT  
-GCTCCGTGGCCTAAT--GGCT-AGGCGATTTGACTTCTAATCAAGGG-----ATTGTGGGTTTCGAGTCCCGCCGGGAGC---  
>tdbD00009525 *Takifugu rubripes* 31033 Arg ACG  
-GGCCAGTGGCGCAAT--GGAT-AAGCGCTGACTACGGATCAGAAG-----ATTCTAGGTTTCGACTCTGGCTGGTTCGG---  
>tdbD00009528 *Takifugu rubripes* 31033 Arg CCG  
-AACCAGTGGCCTAAT--GGAT-AAGGCATCAGCCTCCGGAGCTGGGG-----ATTGTGGGTTCAAGTCCCACCTGGGTG---  
>tdbD00009530 *Takifugu rubripes* 31033 Arg CCG  
-GGCCAGTGGCCTAAT--GGAT-AAGGTATCAGCCTCCGGAGCTGGGG-----ATTGTGGGTTCAAGTCCCACCTGGGTG---  
>tdbD00009531 *Takifugu rubripes* 31033 Arg CCT  
-GCCCTAGTGGCCTAAT--GGAC-AAGGCATGGCCTCCTAAGCCAGGG-----ATTGTGGGTTCAATCCCCTCTGGGGTG---  
>tdbD00009532 *Takifugu rubripes* 31033 Arg CCT  
-GGCCAGTGGCCTAAT--GGAT-AAGGCATGGCCTCCTAAGCCAGGG-----ATTGTGGGTTCAAGTCCCCTCTGGGGTG---  
>tdbD00009533 *Takifugu rubripes* 31033 Arg CCT  
-GGCCAGTGGCCTAAT--GGAC-AAGGCATGGCCTCCTAAGCCAGGG-----ATTGTGGGTTCAAGTCCCCTCTGGGGTG---  
>tdbD00009535 *Takifugu rubripes* 31033 Arg CCT  
-GGCCAGTGGCCTAAT--GGAT-AAGGCATGGCCTCCTAAGCCAGAG-----ATTGTGGGTTCAAGTCCCCTCTGGGGTG---  
>tdbD00009538 *Takifugu rubripes* 31033 Arg TCG  
-GACCATGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCGGATCAGAAG-----ATTGAGGTTTCGAGTCCCTTCATGGTTG---  
>tdbD00009539 *Takifugu rubripes* 31033 Arg TCG  
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-GGTCTGTGGCGCAAT--GGAG-AGCGATTGGACTTCTAATCCAAAG-----TTTGTGGGTTTCGAGTCCCACCGAGTCT---  
>tdbD00002590 *Toxoplasma gondii* 5811 Arg ACG  
-GAGTCAATAGCTCAGTT-GGA--AGAGTATGTGGCTACGGACTACAAT-----GACGGGGTTTCAATCCCTCTTACTCT---  
>tdbD00002577 *Trypanosoma brucei* 5691 Arg CCT  
-GCCCCGTAGCCCAAT--GGAT-AAGGCGTTCGCTTCTAAGCGAAAG-----ATTGCGGGTTCGAGTCCCGCCGGAGGTA---  
>tdbD00002578 *Trypanosoma brucei* 5691 Arg TCT  
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>tdbD00002907 Bos\_taurus 9913 Ser TGA  
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>tdbD00002901 Caenorhabditis\_elegans 6239 Ser GCT  
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>tdbD00002903 Caenorhabditis\_elegans 6239 Ser TGA  
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>tdbD00009871 Caenorhabditis\_elegans 6239 Ser AGA  
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>tdbD00009874 Caenorhabditis\_elegans 6239 Ser CGA  
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>tdbD00010173 Candida\_glabrata CBS\_138 284593 Ser AGA  
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>tdbd00010176 Candida\_glabrata\_CBS\_138\_284593\_Ser\_CGA  
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>tdbd00010174 Candida\_glabrata\_CBS\_138\_284593\_Ser\_GCT  
-GTCCAGTGGCCGAGT--GGTT-AAGGCGATGCCCTGCTATGGCATTGGGT-----TTT-----ACCTGCGCAGGTTTCAAATCCTGTCTGTGACG---  
>tdbd00010175 Candida\_glabrata\_CBS\_138\_284593\_Ser\_TGA  
-GGCACTATGGCCGAGT--GGTT-AAGGCGACAGACTTGAATCTGTGGG----TCT-----GCCCGCGCTGGTTCAAATCCTGTCTGGTGTGCG---  
>tdbd00002667 Cyanophora\_paradoxa\_2762\_Ser\_GGA  
-GGAGAGATGGCCGAGT--GGTTGAAGGCGCAGCACTGGAAATGCTGTTTAAAGGT--TTT--CCCTTAA-CGAGGTTTCAAATCCCTCTCTCTCCG---  
>tdbd00002873 Dictyostelium\_discoideum\_44689\_Ser\_AGA  
-GACATCGTAGCAAAGT--GGTTAATGCGTCTGACTAGAAATCAGATCCCT-----TCG-----GGGG-CGAGGTTTCAAACCTGCCGATGTGCG---  
>tdbd00002872 Dictyostelium\_discoideum\_44689\_Ser\_GCT  
-GACACCTTAGCAAAGT--GGTT-AATGCGGCGCCCTGCTAAGGCGTCTCT-----TTCG-----GAGGCGCAGGTTTCAAACCTGCCGATGTGCG---  
>tdbd00002871 Dictyostelium\_discoideum\_44689\_Ser\_TGA  
-GACATCGTAGCAAAGT--GGTTAATGCGTCTGACTAGAAATCAAATCTCT-----CTAG-----GAGGCGCAGGTTTCAAACCTGCCGATGTGCG---  
>tdbd00002904 Drosophila\_melanogaster\_7227\_Ser\_AGA  
-GCAGTCGTGGCCGAGC--GGTT-AAGGCGTCTGACTAGAAATCAGATTCCT-----TCT-----GGGAGCGTAGGTTTCAAATCCTACCGACTGCG---  
>tdbd00002905 Drosophila\_melanogaster\_7227\_Ser\_CGA  
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>tdbd00009891 Drosophila\_melanogaster\_7227\_Ser\_AGA  
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>tdbd00009893 Drosophila\_melanogaster\_7227\_Ser\_AGA  
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>tdbd00009895 Drosophila\_melanogaster\_7227\_Ser\_GCT  
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>tdbd00009896 Drosophila\_melanogaster\_7227\_Ser\_GCT  
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>tdbd00009897 Drosophila\_melanogaster\_7227\_Ser\_TGA  
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>tdbd00009898 Drosophila\_melanogaster\_7227\_Ser\_TGA  
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>tdbd00009956 Encephalitozoon\_cuniculi\_GB-M1\_284813\_Ser\_CGA  
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>tdbd00009958 Encephalitozoon\_cuniculi\_GB-M1\_284813\_Ser\_GCT  
-GACCTCGTAGCAAAGT--GGTT-AACGCGTAGATTGCTAATCTATTTCCT-----TCT-----GGGAGCGCAGGTTTCAAATCCTGCCGAGGTCG---  
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>tdbd00010232 Gallus\_gallus\_9031\_Ser\_AGA  
-GGGAATTAGTCAAAT--GGT--AGAGCGCTCGCTTAGAGTGCAGAG-----GTAGCGGGATCGATGCCCGCATTCTCTCT---  
>tdbd00010233 Gallus\_gallus\_9031\_Ser\_AGA  
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-GCCTCCGTAGCATAGT--GGT--ATTGCGTTCGCTTCGTAAGCGAAAG-----GCCCGAGTTTCGATCCTCGCCGGGGGC-----  
>tdbD00010501 Arabidopsis\_thaliana 3702 Thr TGT  
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>tdbD00010734 Candida\_glabrata\_CBS\_138\_284593 Thr CGT  
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>tdbD00010732 Candida\_glabrata\_CBS\_138\_284593 Thr TGT  
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>tdbD00003077 Dictyostelium\_discoideum 44689 Thr AGT  
-GGTCCTTAGCATAGT--GGT--ATTGCGTTTCCCTAGTAAGGAAGAG-----GTCATGAGTTCGATCCTCATAGGAGCCT----  
>tdbD00003078 Dictyostelium\_discoideum 44689 Thr CGT  
-GCCATAGTAGTCTAGT--GGT--AAGACATTTCTCTCGTAAAGAAGGA-----T-CCCGTGTTCGATTACCGGCTTTGGCA----  
>tdbD00003090 Drosophila\_melanogaster 7227 Thr AGT  
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>tdbD00010512 Drosophila\_melanogaster 7227 Thr CGT  
-GCCTCTTTAGCTCAGT--GGT--AGAGCGTTGGTCTCGTAAACCAAAG-----GCCGTGAGTTCAACCTCACAGGAGGC----  
>tdbD00010520 Drosophila\_melanogaster 7227 Thr TGT  
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>tdbD00010521 Drosophila\_melanogaster 7227 Thr TGT  
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>tdbD00010563 Encephalitozoon\_cuniculi\_GB-M1\_284813 Thr AGT  
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>tdbD00010562 Encephalitozoon\_cuniculi\_GB-M1\_284813 Thr CGT  
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>tdbD00010777 Gallus\_gallus 9031 Thr AGT  
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>tdbD00010476 Homo\_sapiens 9606 Thr AGT  
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>tdbD00010482 Homo\_sapiens 9606 Thr CGT  
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>tdbD00010487 Homo\_sapiens 9606 Thr TGT  
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>tdbD00010809 Pan\_troglodytes 9598 Thr AGT  
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>tdbD00010812 Pan\_troglodytes 9598 Thr AGT  
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>tdbD00010820 Pan\_troglodytes 9598 Thr CGT  
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>tdbD00010826 Pan\_troglodytes 9598 Thr TGT  
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>tdbD00003086 Phaseolus\_vulgaris 3885 Thr TGT  
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>tdbD00003074 Plasmodium\_falci parum 5833 Thr TGT  
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>tdbD00010767 Plasmodium\_falci parum 3D7 36329 Thr AGT  
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>tdbD00010768 Plasmodium\_falci parum 3D7 36329 Thr CGT  
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-GCCTCCTTAGCTTAGT--GGT--AGAGCGTTGCACCTGTA ATGCAAAAG-----GTCGTTAGTTCAAATCTGACAGGTGGCA---  
>tdbD00003082 Schizosaccharomyces\_pombe 4896 Thr CGT  
-GCTCTGTAGCTCAGT--GGT--AGAGCGCCTGTCTCGTA AAC CAGGAG-----GTCCAGTGTTCGAGTCACTGCCGAGCA---  
>tdbD00010522 Schizosaccharomyces\_pombe 4896 Thr AGT  
-GCTCTGTAGCTCAGT--GGT--AGAGCGCCTGTCTCGTA AAC CAGGAG-----GCCCAGTGTTCGAGTCACTGCTGGAGC---  
>tdbD00010523 Schizosaccharomyces\_pombe 4896 Thr AGT  
-GCTCTGTAGCTCAGT--GGT--AGAGCGCCTGTCTCGTA AAC CAGGAG-----GCCCAGTGTTCGAGTCACTGCTGGAGC---  
>tdbD00010525 Schizosaccharomyces\_pombe 4896 Thr TGT  
-GCCTCTATGGCTTAGT--GGT--ACAGCATCGCACTGTA ATGCGGAAG-----ATCCTTGGTTTCGATTCCGAGTGGAGGC---  
>tdbD00010526 Schizosaccharomyces\_pombe 4896 Thr TGT  
-GCCCTATGGCTTAGT--GGT--ACAGCATCGCACTGTA ATGCGGAAG-----ATCCTTGGTTTCGATTCCGAGTGGGGC---  
>tdbD00010786 Takifugu\_rubripes 31033 Thr AGT  
-GGCGCGTGGCTTAGTT--GGTC-AAAGCGCCTGTCTAGTA AAC CAGGA-----C--GGGTTTCAATCCCAGCGGTGCC---  
>tdbD00010788 Takifugu\_rubripes 31033 Thr AGT  
-GGTGTGTGGCTTAGCT--GGTC-AAAGCGCCTGTCTAGTA AAC CAGGAG-----ATCCTGGGTTTCAATCCCAGCAGTGCCT---  
>tdbD00010790 Takifugu\_rubripes 31033 Thr AGT  
-GACACTGTGGCTTAGTT--GGTT-ATAGCACCTGTCTAGTA AAC CAGGAG-----AGCCTGGGTTTCAATCCCAGCAGTGCCT---  
>tdbD00010791 Takifugu\_rubripes 31033 Thr AGT  
-GGTGTGTGGCTTAGCT--GGTT-AAAGTGCCTGTCTAGTA AAC CAGGAG-----ATCCTGGGTTTCAATCCCAGCAGTGCCT---  
>tdbD00010792 Takifugu\_rubripes 31033 Thr AGT  
-GGCACTGTAGCTTAGCT--GGTC-AAAGTGCCTGTCTAGTA AAC CAGGAG-----AGCCTGGGTTTCAATCCCAGCAGTGCCT---  
>tdbD00010793 Takifugu\_rubripes 31033 Thr AGT  
-GGCGCTGTGGCTTAGTT--GGTT-AAAGCGCCTGTCTAGTA AAC CAGGAG-----ATCCTGGGTTTCAATCCCAGCAGTGCCT---  
>tdbD00010795 Takifugu\_rubripes 31033 Thr CGT  
-GGCGCTGTGGCTTAGCT--GGTC-AAAGCGCCTGTCTCGTA AAC CAGGCG-----AGCCTGGGTTTCAATCCCAGCAGTGTCT---  
>tdbD00010796 Takifugu\_rubripes 31033 Thr CGT  
-GGCGCTGTAGCTTAGCT--GGTC-AAAGTGCCTGTCTCGTA AAC CAGGAG-----AGCCTGGGTTTCAATCCCAGCAGTGCCT---  
>tdbD00010797 Takifugu\_rubripes 31033 Thr CGT  
-GGTGTGGTGGCCAAGT--GGT--AAGGCGTTGGTCTCGTA AAC CAAAG-----ATCATGGGTTTCAATCCCATCCATACCT---  
>tdbD00010798 Takifugu\_rubripes 31033 Thr CGT  
-GGCTCCATAGCTCAGG--GGTT-AGAGCACTGGTCTCGTA ATCCAGGG-----GTCATGAGTTCAAATCTCATGGGGCCT---  
>tdbD00010799 Takifugu\_rubripes 31033 Thr CGT  
-GGCGCTGTGGCTTAGCT--GGTT-ATAGCACCTGTCTCGTA AAC CAGGAG-----ATCCTGGGTTTCAATCCCAGCAGTGCCT---  
>tdbD00010802 Takifugu\_rubripes 31033 Thr TGT



-GGCACTGTAGCTTAGTT--GGTC--AAAGTACCTGTCTTGTAACACAGGAG-----AGCCTGGGTTTCGAATCCCAGCAGTGCCT---  
>tdbD00010803 Takifugu rubripes 31033 Thr TGT  
-GGCTCTATAGCTCAGT--GGTT--AGAGCACTGGTCTTGTAACACAGGG-----GTCATGAGTTCGATCCTCATTAGGGCCT---  
>tdbD00010805 Takifugu rubripes 31033 Thr TGT  
-GGCTCTATAGCTCAGT--GGTT--AGAGCACTGGTCTTGTAACACAGGG-----GTCGTGAGTTCGATCCTCACTAGGGCCT---  
>tdbD00010806 Takifugu rubripes 31033 Thr TGT  
-GGCCTCATAGCTCAGT--GGTT--AGAGCACTGGTCTTGTAACACAGGG-----GTCGCGAGTTCGAATTCGCTGGGGCCT---  
>tdbD00003075 Trypanosoma brucei 5691 Thr CGT  
-GGCCGCTTAGCACAT---GGC--AGTGCACCACTCTCGTAAAGTGGGG-----GTCGCGAGTTCGATTCTCGCAGTGGCCT---  
>tdbD00008219 Arabidopsis thaliana 3702 Pro AGG  
-GGGCATTTGGTCTAGT--GGT--ATGATTCTTGCTTAGGGTGCAGAG-----GCCCCGAGCTCAATTCGGAACACCC---  
>tdbD00008220 Arabidopsis thaliana 3702 Pro AGG  
-TGGCATTTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGAGTTCGAATTCGGAATGCCCC---  
>tdbD00008221 Arabidopsis thaliana 3702 Pro AGG  
-GGGCATTTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGAGTTCGAATTCGGAATGCCCC---  
>tdbD00008222 Arabidopsis thaliana 3702 Pro AGG  
-GGGCATTTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGAGTTCGAATTCGGAATGCCCC---  
>tdbD00008223 Arabidopsis thaliana 3702 Pro CGG  
-GGCGTTTTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGAGTTCGAATTCGGAACGCCCC---  
>tdbD00008224 Arabidopsis thaliana 3702 Pro CGG  
-GGGCATTTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGAGTTCGAATTCGGAATGCCCC---  
>tdbD00008225 Arabidopsis thaliana 3702 Pro CGG  
-GGGTGTTTTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGAGTTCGATTCTCGGAACACCC---  
>tdbD00008226 Arabidopsis thaliana 3702 Pro CGG  
-GGGTGTTTTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGAGTTCGATTCTCGGAACACCC---  
>tdbD00008227 Arabidopsis thaliana 3702 Pro TGG  
-CGAGGTGTAGCGCAGTCTGGTC--AGCGCATCTGTTTTGGGTACAGAGG-----GCCATAGTTCGAATCCTGTCACTTGA---  
>tdbD00008228 Arabidopsis thaliana 3702 Pro TGG  
-CAGCATTTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGAGTTCGATTCTCGGAATGCC---  
>tdbD00008229 Arabidopsis thaliana 3702 Pro TGG  
-GGGCATTTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGAGTTCGATTCTCGCAATGCCCC---  
>tdbD00008230 Arabidopsis thaliana 3702 Pro TGG  
-GGGCATTTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGAGTTCGATTCTCGGAATGCCCC---  
>tdbD00008231 Arabidopsis thaliana 3702 Pro TGG  
-GGCGTTTTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGAGTTCGATTCTCGGAACGCCCC---  
>tdbD00002246 Caenorhabditis elegans 6239 Pro AGG  
-GGCTGAGTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGATCGATCCCCGGCTCAGCCC---  
>tdbD00002245 Caenorhabditis elegans 6239 Pro TGG  
-GGCCGAATGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGTTCAATCCCCGGTTCGGCCC---  
>tdbD00008232 Caenorhabditis elegans 6239 Pro AGG  
-GGTCCGATGGCCTAGA--GGT--AAGGCGCTTGCTTAGGGTGCAGAG-----ATCCCGGTTTCGATCCCCGGTTCGACC---  
>tdbD00008233 Caenorhabditis elegans 6239 Pro AGG  
-GGCCGATGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGATCGATCCCCGGTTCGGCC---  
>tdbD00008235 Caenorhabditis elegans 6239 Pro AGG  
-GGCCGATGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGATCGATCCCCGGTTCGGCC---  
>tdbD00008236 Caenorhabditis elegans 6239 Pro CGG  
-GGCCGATGGTCTAGA--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGTTTCGATTCCCGTTCGGCC---  
>tdbD00008238 Caenorhabditis elegans 6239 Pro TGG  
-GGCCGAATGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGTTCAATCCCCAGTTCGGCCC---  
>tdbD00008239 Caenorhabditis elegans 6239 Pro TGG  
-GGCCGAATGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGTTCAATCCCCGGTTCGGCCC---  
>tdbD00008241 Caenorhabditis elegans 6239 Pro TGG  
-GGCCGAATGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGTTCAATCCCCGGTTCGGCCC---  
>tdbD00008242 Caenorhabditis elegans 6239 Pro TGG  
-GGCCGAATGGTCTATT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGTTCAATCCCCGGTTCGGCCC---  
>tdbD00008243 Caenorhabditis elegans 6239 Pro TGG  
-GGCCGAATGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGTTCAATCCCCGGTTCGGCCC---  
>tdbD00008244 Caenorhabditis elegans 6239 Pro TGG  
-GGCCGAATGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGTTCAATCCCCGGTTCGGCCC---  
>tdbD00008246 Caenorhabditis elegans 6239 Pro TGG  
-GGCGTGTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GCCCTGGGTTCAATCCCAGCTCGCCCC---  
>tdbD00008426 Candida glabrata CBS\_138 284593 Pro AGG  
-GGCGTGTGGTCTAGA--GGT--ATGATTCCGCTTAGGGTGCAGAG-----GTCCCGGTTTCGAGTCCCAGCTCGCCCC---  
>tdbD00008425 Candida glabrata CBS\_138 284593 Pro TGG  
-GGCGTGTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GCCCTGGGTTCAATCCCAGCTCGCCCC---  
>tdbD00002247 Drosophila melanogaster 7227 Pro TGG  
-GGCTCAATGGTCTAGG--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGTTCAATCCCAGTTCGAGCCC---  
>tdbD00008255 Drosophila melanogaster 7227 Pro AGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCCGCTTAGGGTGCAGAG-----GTCCCGGTTCAATCCCAGGACGAGCC---  
>tdbD00008256 Drosophila melanogaster 7227 Pro CGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGTTCAATCCCAGGACGAGCC---  
>tdbD00008257 Drosophila melanogaster 7227 Pro CGG  
-GGCTCGTTGGTCTAGA--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGTTCAATCCCAGGACGAGCC---  
>tdbD00008258 Drosophila melanogaster 7227 Pro CGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGTTCAATCCCAGGACGAGCC---

>tdbD00008295 Encephalitozoon\_cuniculi\_GB-M1 284813 Pro AGG  
-GGTGGTATGGTCTAGC--GGT--ATGACGCTTGCTTAGGGTGCAAGAG-----GCCTTGGGTTTCAATCCCAATACCGCCC---  
>tdbD00008297 Encephalitozoon\_cuniculi\_GB-M1 284813 Pro CGG  
-GGCGTCATGGTCCAAT--GGT--ACGATAGCTGCTTCGGGTGCGAGAG-----A-CCCAGATTTCGATTCTCGGTGACGCCC---  
>tdbD00008296 Encephalitozoon\_cuniculi\_GB-M1 284813 Pro TGG  
-GGCTCGGTGGTCTAAG--GGT--ATGATCTCCGCTTTGGGTGCGGAGG-----GCTCCAGGTTCAATCCTGGCCGAGCCC---  
>tdbD00002248 Gallus\_gallus\_9031 Pro AGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTAGGGTGCGAGAG-----GTCCCGGGTTCAATCCCGGACGAGCCC---  
>tdbD00008454 Gallus\_gallus\_9031 Pro CGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTCGGGTGCGAGAG-----GTCCCGGGTTCAACTCCCGGACGAGCCC---  
>tdbD00008457 Gallus\_gallus\_9031 Pro TGG  
-GGCTGTTGGTCTAGG--GGT--ATGATTCTCGCTTTGGGTGCGAGAG-----GTCCCGGGTTCAATCCCGGACAAGCCC---  
>tdbD00008458 Gallus\_gallus\_9031 Pro TGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTTGGGTGCGAGAG-----GTCCCGGGTTCAATCCCGGACGAGCCC---  
>tdbD00008212 Homo\_sapiens\_9606 Pro AGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTAGGATGCGAGAG-----GTCCCGGGTTCAATCCCGGACGAGCCC---  
>tdbD00008213 Homo\_sapiens\_9606 Pro AGG  
-GGCTCGTTGGTCTAGG--GGT--GTGGTCTCGCTTCGGGCGGAGACCC-----AAGA-----GGT-CCCGGGTTCAATCCCGGACGAGCC---  
>tdbD00008214 Homo\_sapiens\_9606 Pro CGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTCGGGTGTGAGAG-----GTCCCGGGTTCAATCCCGGACGAGCCC---  
>tdbD00008217 Homo\_sapiens\_9606 Pro TGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTTGGGTCCGAGAG-----GTCCCGGGTTCAATCCCGGACGAGCCC---  
>tdbD00008218 Homo\_sapiens\_9606 Pro TGG  
-GGCTCGTTGGTCTAGT--GGT--ATGATTCTCGCTTTGGGTGCGAGAG-----GTCCCGGGTTCAATCCCGGACGAGCCC---  
>tdbD00008469 Pan\_troglodytes\_9598 Pro AGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTAGGGTGCGAGAG-----GTCCCGGGTTCAATCCCGGACGAGCCC---  
>tdbD00008470 Pan\_troglodytes\_9598 Pro AGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTAGGGTGCGAGAG-----GTCCCGGGTTCAATCCTGGACGAGCCC---  
>tdbD00008471 Pan\_troglodytes\_9598 Pro AGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTAGGGTGCGAGAG-----GTCCCGGGTTCAATCAGGACGAGCCC---  
>tdbD00008476 Pan\_troglodytes\_9598 Pro CGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTCGGGTGCGAGAG-----GTCCCGGGTTCAATCCCGGACGAGCCC---  
>tdbD00008477 Pan\_troglodytes\_9598 Pro TGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTTGGGTGAGAGAG-----GTCCCGGGTTCAATCCCGGACGAGCCC---  
>tdbD00002239 Plasmodium\_falciparum\_5833 Pro TGG  
-CAGAAATATAGTGTAAT--GGT--AACATATCTATTTTGGGAATAGAG-----AATATAGGTTCAATCCTATTTTCTGA---  
>tdbD00008447 Plasmodium\_falciparum\_3D7\_36329 Pro AGG  
-GGCTACTTAGTCTAGT--GGT--ATGATTCTCTCTTAGGGTGGGAGAG-----GTCCCGGGTTTCGATTCCCGGAGTAGCCC---  
>tdbD00008448 Plasmodium\_falciparum\_3D7\_36329 Pro CGG  
-GGCTACTTGATCTAGT--GGT--ATGATTCTGCTTCGGGTGCAAGAC-----GTCCCGGGTTTCGATTCCCGGAGTAGCCC---  
>tdbD00008449 Plasmodium\_falciparum\_3D7\_36329 Pro TGG  
-GGCTACTTAGTCTAGT--GGT--ATGATTCTCGCTTTGGGTGCGAGAG-----GTCCCGGGTTCAATTCGAGTAGCCC---  
>tdbD00002253 Rattus\_norvegicus\_10116 Pro AGG  
-GGCTCGTTGGTCTAGG--GGT--ATGATTCTCGCTTAGGGTGCGAGAG-----GTCCCTGGGTTCAATCCCGGACGAGCCC---  
>tdbD00002241 Saccharomyces\_cerevisiae\_4932 Pro TGG  
-GGCGGTGGTCTAGT--GGT--ATGATTCTCGCTTTGGGCGCGAGAG-----GCCCTGGGTTCAATTCGAGCTCGCCCC---  
>tdbD00008247 Saccharomyces\_cerevisiae\_4932 Pro AGG  
-GGCGGTGGTCTAGA--GGT--ATGATTCTCGCTTAGGGTGCGGGAG-----GTCCCGGGTTTCGAGTCCCGGCTCGCCC---  
>tdbD00008254 Saccharomyces\_cerevisiae\_4932 Pro TGG  
-GGCGGTGGTCTAGT--GGA--ATGATTCTCGCTTTGGGTGCGAGAG-----GCCCTGGGTTCAATTCGAGCTCGCCCC---  
>tdbD00002242 Schizosaccharomyces\_pombe\_4896 Pro AGG  
-GGCCGTTTGGTCTAGT--GGT--ATGATACCATCTTAGGGTGATGGTG-----GTCGTGGGTTTCGATTCCCAACAGCCC---  
>tdbD00008261 Schizosaccharomyces\_pombe\_4896 Pro CGG  
-GGCCTAATAGTGTAGT--GGTT--AACATACCTCTTTCGGGTAGAGGTG-----ATCCCTGGTTCGAATCCTGGTTAGGCC---  
>tdbD00008262 Schizosaccharomyces\_pombe\_4896 Pro TGG  
-GGTTTCGTTGGTGTAGT--GGT--AGCATACTCTGTTTGGGTGCAAGTG-----GTCACGGGTTCAATCCCGTCAAAC---  
>tdbD00008263 Schizosaccharomyces\_pombe\_4896 Pro TGG  
-GGTTCGTTGGTGTAGT--GGT--AGCATACTCTGTTTGGGTGCAAGTG-----GTCAGGGGTTTCGATCCCCCTCGAAGCC---  
>tdbD00008461 Takifugu\_rubripes\_31033 Pro CGG  
-GGCTCATTGGTTCGAGG--GGA--AGGATCCTCGCCTCGGGTGCGAGTG-----GTCCCGGGTTCAATCCCGGACGAGCCC---  
>tdbD00008463 Takifugu\_rubripes\_31033 Pro CGG  
-GGCTCGTTGGTCTAGT--GGG--ATGATTCTCGCTTCGGGTGCGAGAG-----GTCCCGGGTTTCGACTCCCGGACGAGCCC---  
>tdbD00000956 Arabidopsis\_thaliana\_3702 Gly TCC  
-CGCTCTGTAGTCCAAC--GGTT--AGGATAATTGCCTTCCAAGCAATAG-----A-CCCGGGTTTCGACTCCCGGACGAGCCA---  
>tdbD00000962 Caenorhabditis\_elegans\_6239 Gly TCC  
-CGCTTCGTTGGTGTAA--GGTC--AGCATGGATGCCTTCCAAGCATTCG-----A-CGGGGGTTTCGATTCCCCCGAACGCA---  
>tdbD00005342 Caenorhabditis\_elegans\_6239 Gly TCC  
-CGCTTCGTTGGTGTAA--GGTC--AGCATGGATGCCTTCCAAGCATTCG-----A-CGGGGGTTTCGATTCCCCCGAACGCA---  
>tdbD00005344 Caenorhabditis\_elegans\_6239 Gly TCC  
-CGCTTCGTTGGTGTAA--GGTC--GGCATGGATGCCTTCCAAGCATTCG-----A-CGGGGGTTTCGATTCCCCCGAACGCA---  
>tdbD00005567 Candida\_glabrata\_CBS\_138\_284593 Gly CCC  
-CGCTAAGTAGTATAGT--GGTT--AGAATCTATCCTTCCAAGGATGGG-----A-CCCGGGTTTCGATTCCCGGCTTTCGCA---  
>tdbD00005565 Candida\_glabrata\_CBS\_138\_284593 Gly GCC  
-CGCAGTGGTGTAGT--GGT--AAAATCCAACGTTGCCATCGTTGGG-----C-CCCGGGTTTCGATTCCCGGCTTTCGCA---  
>tdbD00005398 Encephalitozoon\_cuniculi\_GB-M1 284813 Gly TCC

-GCGTTGGTGGTCTAGT--GGAT-AGGATAACAGCCTTCCAAGCTGTTG-----G-CCCGGGTTCGATTCCCGGACATCGCA---  
>tdbD00005605 Gallus\_gallus 9031 Gly CCC  
-GCGCCGCTGGTGTAGT--GGT--ATCATGCAAGATTCCCATTCTTGCG-----A-CCCGGGTTCGATTCCCGGGCGGCGCA---  
>tdbD00005610 Gallus\_gallus 9031 Gly TCC  
-GCGTTGGTGGTATAGT--GGTG-AGCATAGCTGCCTTCCAAGCAGTTG-----A-CCCGGGTTCGATTCTCGGCCAACGCA---  
>tdbD00005612 Gallus\_gallus 9031 Gly TCC  
-GCGTTGGTGGTATAGT--GGTG-AGCATAGCTGCCTTCCAAGCAGTTG-----A-ACCGGGTTCGATTCCCGGCCAACGCA---  
>tdbD00005614 Gallus\_gallus 9031 Gly TCC  
-GCGTTGGTGGTATAGT--GGTG-AGCATAGCTGCCTTCCAAGCAGTTG-----A-CCCGGGTTCGATTCCCGGCCAACGCA---  
>tdbD00005615 Gallus\_gallus 9031 Gly TCC  
-GCGTTGGTGGTATAGT--GGTT-AGCATAGCTGCCTTCCAAGCAGTTG-----A-CCCGGGTTCGATTCCCGGCCAACGCA---  
>tdbD00005643 Pan\_troglodytes 9598 Gly TCC  
-GCGTTGGTGGTATAGT--GGTG-AGCATAGCTGCCTTCCAAGCAGTTG-----A-CCCGGGTTCGATTCCCGGCCAACGCA---  
>tdbD00005644 Pan\_troglodytes 9598 Gly TCC  
-GCGTTGGTGGTATAGT--GGTG-AGCATAGCTGCCTTCCAAGCAGTTG-----A-CCCGGGTTCGATTCCCGGCCAACGCA---  
>tdbD00005599 Plasmodium\_falci-parum\_3D7\_36329 Gly TCC  
-GCGTCAATAGTCTAAC--GGCC-ATGATACCTGCCTTCCAAGCAGTTG-----A-CCCGGGTTCGACTCCCGGTTGACGCA---  
>tdbD00000969 Rattus\_norvegicus 10116 Gly TCC  
-GCGTTGGTGGTATAGT--GGTG-AACATAGCTGCCTTCCAAGCAGTTG-----A-CCCGGGTTCGATTCCCGGCCAACGCA---  
>tdbD00000952 Saccharomyces\_cerevisiae 4932 Gly GCC  
-GCGCAAGTGGTTTGTAGT--GGT--AAAATCCAACGTTGCCATCGTTGGG-----C-CCCGGGTTCGATTCCCGGCGTTGCGCA---  
>tdbD00005619 Takifugu\_rubripes 31033 Gly CCC  
-GCGCCGCTGGTGTAGT--GGT--ATCATGCAAGATTCCCATTCTTGTTG-----A-CCCGGGTTCGATTCCCGGGCGGCGCA---  
>tdbD00005626 Takifugu\_rubripes 31033 Gly TCC  
-GCGTTGGTGGTATAGT--GGTT-AGCATAGCTGCCTTCCAAGCAGTTG-----A-CCCGGGTTCGATTCCCGGCCAACGCA---  
>tdbD00005627 Takifugu\_rubripes 31033 Gly TCC  
-GCGATGGTGGTATAGT--GGTG-AGCATAGCTGCCTTCCAAGCAGTTG-----A-CCCGGGTTCGATTCCCGGCCATCGCA---  
>tdbD00005806 Candida\_glabrata\_CBS\_138\_284593 His GTG  
-GCCATTTTATAGTATAGT--GGTT-AGTACACATCGTTGTGGCCGATGAA-----A-CCCTGGTTCGATTCTAGGAAATGGCA---  
>tdbD00005807 Candida\_glabrata\_CBS\_138\_284593 His GTG  
-GCCATCTTATAGTATAGT--GGTT-AGTACACATCGTTGTGGCCGATGAA-----A-CCCTGGTTCGATTCTAGGAGATGGCA---  
>tdbD00001111 Dictyostelium\_discoideum 44689 His GTG  
-GCCGTGATAGTATAGT--GGT--AGTACATCAGATTGTGGCTCTGATG-----A-CCCTGGTTCGATTCCAGGTCGCGGCA---  
>tdbD00001115 Drosophila\_melanogaster 7227 His GTG  
-GCCGTGATCGTCTAGT--GGTT-AGGACCCACGTTGTGGCCGTTGTTA-----A-CCCAGGTTCGAATCCTGGTCACGGCA---  
>tdbD00005745 Encephalitozoon\_cuniculi\_GB-M1\_284813 His GTG  
-GCTGAATTAGCTTAGT--GGT--AGAGCATGGCGTTGTGGCCGCCAAG-----A-TGCGAGTTCGATTCTCGCATTCAGCA---  
>tdbD00005826 Gallus\_gallus 9031 His GTG  
-GCTGTGATTGTATAGT--GGTC-AGTACTCTGCGTTGTGGCCGCAGCA-----A-CCTCGGTTTCGAATCCGAGTCACAGCA---  
>tdbD00005827 Gallus\_gallus 9031 His GTG  
-GCCGTGATCGTATAGT--GGTC-AGTACTCTGCGTTGTGGCCGCAGCA-----A-CCTCGGTTTCGAATCCGAGTCACAGCA---  
>tdbD00005828 Gallus\_gallus 9031 His GTG  
-GCCGTGATCGTATAGT--GGTT-AGTACTCTGCGTTGTGGCCGCAGCA-----A-CCTCGGTTTCGAATCCGAGTCACAGCA---  
>tdbD00005829 Gallus\_gallus 9031 His GTG  
-GCCGTGATCGTATAGT--GGTT-AGTACTCTGCGTTGTGGCCGCAGCA-----A-CCTCGGTTTCGAATCCGAGTCACAGCA---  
>tdbD00001116 Mus\_musculus 10090 His GTG  
-GCCGTGATCGTATAGG--GGTT-AGTACTCTGCGTTGTGGCCGCAGCA-----A-CCTCGGTTTCGAATCCGAGTCACAGCA---  
>tdbD00005838 Pan\_troglodytes 9598 His GTG  
-GCTATGATCGTACAGT--GGTT-ACTACTCTGCGTTGTGGCCACAGCA-----A-CCTCGGTTTCGAATCCGAGTCATGGCA---  
>tdbD00005840 Pan\_troglodytes 9598 His GTG  
-GCCATGATGGTATAGT--GGTT-AGTACTCTGCGTTGTGGCCGCAGCA-----A-CCTCGGTTTCGAATCCGAGTCACAGCA---  
>tdbD00005821 Plasmodium\_falci-parum\_3D7\_36329 His GTG  
-GTCCAAATCGTCTAGT--GGTT-AGGACTCCACGCTGTGGACGTGGCA-----A-CGTAGGTTTCGAATCCTGCTTTGGACA---  
>tdbD00001113 Schizosaccharomyces\_pombe 4896 His GTG  
-GCTCACATGGTCCAGT--GGTT-AAGACTCATCGTTGTGGCCGATGCG-----A-CCCAGGTTTCGATTCTCGGTTGTTGGCA---  
>tdbD00005830 Takifugu\_rubripes 31033 His GTG  
-GCCGTGATCGTATAGT--GGTC-AGTACTCTGCGTTGTGGCCGCAGCA-----A-CCCAGGTTTCGAATCCGGGTCACAGCA---  
>tdbD00005831 Takifugu\_rubripes 31033 His GTG  
-GCCGTGATCGTATAGT--GGTC-AGTACTCTGCGTTGTGGCCGCAGCA-----A-CCCAGGTTTCGAATCCGGGTCACAGCA---  
>tdbD00005832 Takifugu\_rubripes 31033 His GTG  
-GCCGTGATCGTATAGT--GGTT-AGTACTCTGCGTTGTGGCCGCAGCA-----A-CCCAGGTTTCGAATCCGGGTCACAGCA---  
>tdbD00005833 Takifugu\_rubripes 31033 His GTG  
-GCCGTGATCGTATAGT--GGTC-AGTACTCTGCGTTGTGGCCGCAGCA-----A-CCCAGGTTTCGAATCCGGGTCACAGCA---  
>tdbD00005834 Takifugu\_rubripes 31033 His GTG  
-GCCGTGATCGTATAGT--GGTT-AGTACTCTGTTGTGTGGCCGCAGCA-----A-CCCAGGTTTCGAATCCGGGTCACAGCA---  
>tdbD00005835 Takifugu\_rubripes 31033 His GTG  
-GCCGTGATCGTATAGT--GGTC-AGTACTCTGCGTTGTGGCCGCAGCA-----A-CCCAGGTTTCGAATCCGGGTCACAGCA---  
>tdbD00005836 Takifugu\_rubripes 31033 His GTG  
-GCCGTGATCGTATAGT--GGTT-AGTACTCTGCGTTGTGGCCGCAGCA-----A-CCCAGGTTTCGAATCCGGGTCACAGCA---  
>tdbD00005837 Takifugu\_rubripes 31033 His GTG  
-GCCGTGATCGTATAGT--GGTT-AGTACTCTGCGTTGTGGCCGCAGCA-----A-CCCAGGTTTCGAATCCGGGTCACAGCA---  
>tdbD00000504 Arabidopsis\_thaliana 3702 Asp GTC  
-GTCGTTGTAGTATAGT--GGTA-AGTATTTCCCGCCTGTACCCCGGTTG-----A-CCCGGGTTCGATCCCGGCCAACGGCG---  
>tdbD00000505 Arabidopsis\_thaliana 3702 Asp GTC  
-GTCGTTGTAGTATAGT--GGTA-AGTATTTCCCGCCTGTACCCCGGTTG-----A-CCCGGGTTCGATCCCGGCCAACGGCG---

>tdbD00004461 Arabidopsis\_thaliana 3702 Asp GTC  
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>tdbD00000507 Caenorhabditis\_elegans 6239 Asp GTC  
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>tdbD00000499 Candida\_albicans 5476 Asp GTC  
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>tdbD00004560 Candida\_glabrata CBS\_138 284593 Asp GTC  
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>tdbD00000508 Drosophila\_melanogaster 7227 Asp GTC  
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>tdbD00004489 Encephalitozoon\_cuniculi\_GB-M1 284813 Asp GTC  
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>tdbD00000509 Gallus\_gallus 9031 Asp GTC  
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>tdbD00004579 Gallus\_gallus 9031 Asp GTC  
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>tdbD00004456 Homo\_sapiens 9606 Asp GTC  
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>tdbD00004593 Pan\_troglodytes 9598 Asp GTC  
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>tdbD00004597 Pan\_troglodytes 9598 Asp GTC  
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>tdbD00004575 Plasmodium\_falciiparum\_3D7 36329 Asp GTC  
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>tdbD00000502 Saccharomyces\_cerevisiae 4932 Asp GTC  
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>tdbD00001469 Bombyx\_mori 7091 Lys CTT  
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>tdbD00001467 Caenorhabditis\_elegans 6239 Lys CTT  
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>tdbD00006361 Candida\_glabrata CBS\_138 284593 Lys CTT  
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>tdbD00001462 Dictyostelium\_discoideum 44689 Lys CTT  
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>tdbD00006218 Drosophila\_melanogaster 7227 Lys TTT  
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>tdbD00006220 Drosophila\_melanogaster 7227 Lys TTT  
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>tdbD00001474 Gallus\_gallus 9031 Lys CTT  
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>tdbD00006389 Gallus\_gallus 9031 Lys CTT  
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>tdbD00006390 Gallus\_gallus 9031 Lys TTT  
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>tdbD00006182 Homo\_sapiens 9606 Lys CTT  
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>tdbD00006195 Homo\_sapiens 9606 Lys TTT  
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>tdbD00001460 Leishmania\_tarentolae 5689 Lys TTT  
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>tdbD00001472 Loligo\_bleekeri 6617 Lys CTT  
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>tdbD00001475 Mus\_musculus 10090 Lys TTT  
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>tdbD00006412 Pan\_troglodytes 9598 Lys CTT  
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-ACCCTGGTGTACAGG--GGCT-AATATGTTGGGCTTTTACCCTTCA-----G-CCCAGGTTTCGATTCTGTTAGGAA---  
>tdbD00006422 Pan\_troglodytes 9598 Lys TTT  
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>tdbD00006423 Pan\_troglodytes 9598 Lys TTT  
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>tdbD00001456 Plasmodium\_falciparum 5833 Lys TTT  
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>tdbD00006382 Plasmodium\_falciparum\_3D7 36329 Lys CTT  
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>tdbD00006383 Plasmodium\_falciparum\_3D7 36329 Lys TTT  
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>tdbD00006213 Saccharomyces\_cerevisiae 4932 Lys CTT  
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>tdbD00001466 Schizosaccharomyces\_pombe 4896 Lys CTT  
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>tdbD00006395 Takifugu\_rubripes 31033 Lys CTT  
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>tdbD00006400 Takifugu\_rubripes 31033 Lys TTT  
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>tdbD00006402 Takifugu\_rubripes 31033 Lys TTT  
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>tdbD00006406 Takifugu\_rubripes 31033 Lys TTT  
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>tdbD00001457 Trypanosoma\_brucei 5691 Lys CTT  
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>tdbD00001473 Xenopus\_laevis 8355 Lys TTT  
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>tdbD00007899 Arabidopsis\_thaliana 3702 Asn GTT  
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>tdbD00008057 Pan\_troglodytes 9598 Asn GTT  
-GTCTCTGTGGCGCAATT-GGTT-AGCGCGTTCGGCTGTTAACTGAAAG-----GTTGGTGGTTCGAGCCCACCCAGGGACG---  
>tdbD00008058 Pan\_troglodytes 9598 Asn GTT  
-GTCTCTGTGGCGCAATT-GGTT-AGCGCGTTCGGCTGTTAACCGAAAAG-----GTTGGTGGTTCGAGCCCACCCAGGGACG---  
>tdbD00002079 Petunia\_sp. 4104 Asn GTT  
-TCCTCAGTAGCTCAGT--GGT--AGAGCGTTCGGCTGTTAACCGATTG-----GTCGTAGGTTTCGAATCCTACTTGGGGAG---  
>tdbD00002071 Plasmodium\_falci-parum 5833 Asn GTT  
-TTCTTAATAGCTTAGT--GGTT-AAAGCATTCGGCTGTTAACCGAAAAT-----A-CACTAGTTCGAATCCTACTTAAAGAAG---  
>tdbD00008028 Plasmodium\_falci-parum 3D7\_36329 Asn GTT  
-GGTCCGTAGCTCAGT--GGTT-AGAGCGTTCGGCTGTTAACCGCAAAG-----GTCGTGGTTCGATCCCAGCCGGTACCG---  
>tdbD00002076 Saccharomyces\_cerevisiae 4932 Asn GTT  
-GACTCCATGGCCAAGTT-GGTT-AAGGCGTTCGACTGTTAATCGCAAAG-----ATCGTGAGTTCGAACCTCACTGGGGTTCG---  
>tdbD00002077 Schizosaccharomyces\_pombe 4896 Asn GTT  
-GGTCGGGTAGCATAGT--GGTT-ATTGCGCAGACTGTTAATCGTGAG-----GTCGAGGGTTCGAGTCCCTCCCTGACCG---  
>tdbD00007913 Schizosaccharomyces\_pombe 4896 Asn GTT  
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>tdbD00008042 Takifugu\_rubripes 31033 Asn GTT  
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>tdbD00008043 Takifugu\_rubripes 31033 Asn GTT  
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>tdbD00008046 Takifugu\_rubripes 31033 Asn GTT  
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>tdbD00008047 Takifugu\_rubripes 31033 Asn GTT  
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>tdbD00008048 Takifugu\_rubripes 31033 Asn GTT  
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>tdbD00008049 Takifugu\_rubripes 31033 Asn GTT  
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>tdbD00008051 Takifugu\_rubripes 31033 Asn GTT  
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>tdbD00008052 Takifugu\_rubripes 31033 Asn GTT  
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>tdbD00002074 Tetrahymena\_pyriformis 5908 Asn GTT  
-GCTCGATTAGCTCAGCT-GGTT-AGAGCATGCGGCTGTTAACCGCAAAG-----GTCGTAGGTTTCGATCCCTACATCGAGCG---  
>tdbD00002072 Trypanosoma\_brucei 5691 Asn GTT  
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>tdbD00002073 Trypanosoma\_brucei 5691 Asn GTT  
-TCCTCCCTGGCGCAGTC-GGC--AGCGCGTTAGGCTGTTAACTACAG-----G-TGTTGGTTCGAATCCAACGGGAGGAG---  
>tdbD00000792 Arabidopsis\_thaliana 3702 Phe GAA  
-CGGGGATAGCTCAGTT-GGG--AGAGCGTTCAGACTGAAGATCTGAAG-----GTCGCGTGTTCGATCCACGCTCACC GCA---  
>tdbD00004998 Arabidopsis\_thaliana 3702 Phe GAA  
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>tdbD00005094 Candida\_glabrata\_CBS\_138\_284593 Phe GAA  
-CGGGTTTTAGCTCAGTT-GGG--AGAGCGTTCAGACTGAAGATCTGAAG-----GTCCTGTGTTCGATCCACAGAAATCGCA---  
>tdbD00000793 Drosophila\_melanogaster 7227 Phe GAA  
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>tdbD00000796 Gallus\_gallus 9031 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTTCAGACTGAAGATCTAAAG-----GTCCCTGGTTCGATCCCGGGTTTCGGCA---

>tdbD00005116 Gallus\_gallus 9031 Phe GAA  
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>tdbD00005117 Gallus\_gallus 9031 Phe GAA  
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>tdbD00005118 Gallus\_gallus 9031 Phe GAA  
-GCCGAAATAGCTCAGCT-GGG--AGAGCGTTAGACTGAAGATCTAAAG-----GTCCCTGGTTCAATCCCGGGTTTCGGCA---  
>tdbD00004995 Homo\_sapiens 9606 Phe GAA  
-GCCGAGATAGCTCAGTT-GGG--AGAGCGTTAGACTGAAGATCTAAAG-----GTCCCTGGTTCAATCCCGGGTTTCGGCA---  
>tdbD00004996 Homo\_sapiens 9606 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTTAGACTGAAGATCTAAAG-----GTCCCTGGTTCAATCCCGGGTTTCGGCA---  
>tdbD00000784 Neurospora\_crassa 5141 Phe GAA  
-GCGGGTTTAGCTCAGTT-GGG--AGAGCGTCAGACTGAAGATCTGAAG-----GTCGTGTGTTTCGATCCACACAAACCAGCA---  
>tdbD00005130 Pan\_troglodytes 9598 Phe GAA  
-GCCGAAATAGCTCAATT-GGG--AGAGTGTAGACTGAAGATCTTCTG-----CAG-----GTCTCTGGTTCAATTCCGGGTTTCGACA---  
>tdbD00005131 Pan\_troglodytes 9598 Phe GAA  
-GTCGAAATAGCTCAGTT-GGG--AGAGCATTAGACTGAAGATCTAAAG-----GTCCCTGGTTTCGATCCCGGGTTTCAGCA---  
>tdbD00005132 Pan\_troglodytes 9598 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTTAGACTGAAGATCTAAAG-----GTCCCTGGTTCAATCCCGGGTTTCGGCA---  
>tdbD00005133 Pan\_troglodytes 9598 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTTAGACTGAAGATCTAAAG-----GTCCCTGGTTTCGATCCCGGGTTTCGGCA---  
>tdbD00005111 Plasmodium\_falciparum\_3D7\_36329 Phe GAA  
-GCCGTGATAGCTCAGTT-GGG--AGAGCGTCAGACTGAAGATCTGAAG-----GTCCCTGGTTTCGATCCCTGGTCACGGCA---  
>tdbD00000795 Podocoryne\_carnea 6096 Phe GAA  
-GCCGTGATAGCTCAGTT-GGG--AGAGCGTCAGACTGAAGATCTGAAG-----GTCCCTGGTTCAATCCCGGGTTCGGCA---  
>tdbD00000797 Rattus\_norvegicus 10116 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTTAGACTGAAGATCTAAAG-----GCCCTGGTTTCGATCCCGGGTTTCGGCA---  
>tdbD00000785 Saccharomyces\_cerevisiae 4932 Phe GAA  
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>tdbD00000786 Saccharomyces\_cerevisiae 4932 Phe GAA  
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>tdbD00000787 Saccharomyces\_cerevisiae 4932 Phe GAA  
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>tdbD00000788 Saccharomyces\_cerevisiae 4932 Phe GAA  
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>tdbD00005005 Saccharomyces\_cerevisiae 4932 Phe GAA  
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>tdbD00000789 Schizosaccharomyces\_pombe 4896 Phe GAA  
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>tdbD00000790 Schizosaccharomyces\_pombe 4896 Phe GAA  
-GTCGCGATGGTGTAGTT-GGG--AGCATGACAGACTGAAGATCTGTG-----GTCATCGGTTTCGATCCCGGTTTCGTGACA---  
>tdbD00005122 Takifugu\_rubripes 31033 Phe GAA  
-GCCGAAATAGCTCAGCT-GGG--AGAGCGTTAGACTGAAGTCTAAAG-----GACCCTCGTTCAACCTGGGTTTCGGCA---  
>tdbD00005123 Takifugu\_rubripes 31033 Phe GAA  
-GCCGAAATAGCTCAGTTGGG--AGAGCGTTAGACTGAAGTCTAAAG-----GTCCCTGGTTTCGATCCCGGGTTTCGGCA---  
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>tdbD00005125 Takifugu\_rubripes 31033 Phe GAA  
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>tdbD00005127 Takifugu\_rubripes 31033 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTCAGACTGAAGATCTGAAG-----GTCCCTGGTTTCGATCCCGGGTTTCGGCA---  
>tdbD00000222 Arabidopsis\_thaliana 3702 Ala TGC  
-GGGGATGTAGCTCATAT-GGT--AGAGCGCTCGCTTTCGCATGCGAGAG-----GCACAGGGTTTCGATCCCTGCATCTCCA---  
>tdbD00003864 Arabidopsis\_thaliana 3702 Ala AGC  
-GGGGATGTAGCTCAGAT-GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GCACGGGGATCGATAACCCCGCATCTCC---  
>tdbD00003865 Arabidopsis\_thaliana 3702 Ala AGC  
-GGGGATGTAGCTCAAAT-GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTACGGGGATCGATAACCCCGCATCTCC---  
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-GGGGATGTAGCTCAGAT-GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTACGGGGATCGATAACCCCGCATCTCCA---  
>tdbD00003867 Arabidopsis\_thaliana 3702 Ala CGC  
-GGGGGTGTAGCTCATAT-GGT--AGAGCGCTCGTTTCGCATGCGAGAG-----GCACGGGGTTTCGATCCCCGCACCTCC---  
>tdbD00003868 Arabidopsis\_thaliana 3702 Ala CGC  
-GGGGATGTAGCTCATAT-GGT--AGAGCGCTCGCTTTCGCATGCGAGAG-----GCACGGGGTTTCGATCCCCGCATCTCC---  
>tdbD00003869 Arabidopsis\_thaliana 3702 Ala CGC  
-GGGGGTGTAGCTCATAT-GGT--AGAGCGCTCGCTTTCGCATGCGAGAG-----GCACGGGGTTTCGATCCCCGCACCTCC---  
>tdbD00003871 Arabidopsis\_thaliana 3702 Ala TGC  
-GGGGATGTAGCTCAAAT-GGT--AGAGCGCTCGCTTTCGCATGCGAGAG-----GCACGGGGTTTCGATCCCCCGCATCTCC---  
>tdbD00000228 Bombyx\_mori 7091 Ala AGC  
-GGGGCGTAGCTCAGAT-GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTACGGGGATCGATAACCCGGCGCTCCA---  
>tdbD00000229 Bombyx\_mori 7091 Ala AGC  
-GGGGCGTAGCTCAGAT-GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTACGGGGATCGATAACCCGGCGCTCCA---  
>tdbD00000223 Brassica\_napus 3708 Ala TGC  
-GGGGATGTAGCTCATAT-GGT--AGAGCACTCGATTTGCATGCGAGAG-----GCACAGGGTTTCGATCCCTGCATCTCCA---  
>tdbD00000227 Caenorhabditis\_elegans 6239 Ala AGC  
-GGGGGTATAGCTCAGT--GGT--AGAGCGCTCCCTTAGCATGGGAGAG-----GGCTGGGGTTCAATTCCCCATACCTCCA---  
>tdbD00000225 Caenorhabditis\_elegans 6239 Ala TGC



-GGGGGTATAGCTCAGG--GGT--AGAGCGCTCGCTTTGCATGCGAGAA-----GTCTGGGGTTTCGATTCCCCATACCTCCA---  
>tdbD00003876 *Caenorhabditis\_elegans* 6239 Ala AGC  
-CGGGGTATAGCTCAGT--GGT--AGAGCGCTCCCTTAGCATGGGAGAG-----GGCTGGGGTTCAATTCCCCATACCTCCA---  
>tdbD00003878 *Caenorhabditis\_elegans* 6239 Ala CGC  
-GGGGGTATAGCTCAGG--GGT--AGAGCGCTCGCTTCGCATGTGAGAA-----GTCTGGGGTTCAATTCCCCATACCTCC---  
>tdbD00003879 *Caenorhabditis\_elegans* 6239 Ala CGC  
-GGGGGTATAGCTCAGG--GGT--AGAGCGCTCGCTTCGCATGCGAGAA-----GTCTGGGGTTCAATTCCCCATACCTCCA---  
>tdbD00003880 *Caenorhabditis\_elegans* 6239 Ala CGC  
-GGGGGCATAGCTCAGA--GGT--AGAGCGCCCGCTTCGCATGCGGGAA-----GTCCGGGGTTCAATCCCCCGTGCCTCC---  
>tdbD00003881 *Caenorhabditis\_elegans* 6239 Ala CGC  
-GGGGGCATAGCTCAGG--GGT--AGAGCGCTCGCTTCGCATGCGAGAA-----GTCCGGGGTTCAATTCCCCGTGCCTCC---  
>tdbD00003882 *Caenorhabditis\_elegans* 6239 Ala TGC  
-GGGCACATGGCGCAGTT--GGT--AGCGCGCTTCTCTTGAAGGAAGAG-----T-CATCGGTTTCGATTCTGGTTGCGTCC---  
>tdbD00003884 *Caenorhabditis\_elegans* 6239 Ala TGC  
-GGGCACATGGCGCAGTT--GGT--AGCGCGCTTCCCTTGAAGGAAGAG-----GTCATCGGTTTCGATTCCGGTTGCGTCCA---  
>tdbD00000217 *Candida\_albicans* 5476 Ala AGC  
-GGGCGTGTGGCGTAGTT--GGT--AGCGCGTTCCTTAGCATGGGAAAG-----GTCATGAGTTTCGACTCTTATCTCGTCCA---  
>tdbD00004056 *Candida\_glabrata* CBS\_138 284593 Ala AGC  
-GGGCGTGTGGCGTAGTT--GGT--AGCGCGTTCCTTAGCATGGGAGAG-----GTCTTGGGTTTCGATTCCCAACTCGTCCA---  
>tdbD00000097 *Cyanophora\_paradoxa* 2762 Ala TGC  
-GGGGGTATAGCTCAGTT--GGT--AGAGCGCTGCCTTTGAAGGCAGAT-----GTCAGCGGTTTCGAGTCCGCTTACCTCCA---  
>tdbD00000230 *Drosophila\_melanogaster* 7227 Ala AGC  
-GGGGATGTAGCTCAGAT--GGT--AGAGCGCTCGCTTAGCATGTGAGAG-----GTACGGGGATCGATGCCCGCATCTCCA---  
>tdbD00003888 *Drosophila\_melanogaster* 7227 Ala AGC  
-GGGGATGTAGCTCAGAT--GGT--AGAGCGCTCGCTTAGCATGTGAGAG-----GTACGGGGATCGATGCCCGCATCTCCA---  
>tdbD00003889 *Drosophila\_melanogaster* 7227 Ala CGC  
-GGGGACGTAGCTCAGT--GGT--AGAGCGCTCGCTTCGCATGTGAGAA-----GTCCCGGGTTCAAACCCCGCGTCTCC---  
>tdbD00003890 *Drosophila\_melanogaster* 7227 Ala TGC  
-GGGGATGTAGCTCAGT--GGT--AGAGCGCTCGCTTTGCATGTGAGAG-----GCCCCGGGTTCAATCCCCGGCATCTCC---  
>tdbD00003891 *Drosophila\_melanogaster* 7227 Ala TGC  
-GGGGATGTAGCTCAGT--GGT--AGAGCGCTCGCTTTGCATGTGAGAG-----GCCCCGGGTTTCGATCCCCGGCATCTCC---  
>tdbD00003929 *Encephalitozoon\_cuniculi* GB-M1 284813 Ala AGC  
-GGGGAGTTAGCTCAGC--GGT--AGAGCGCTTGCTTAGCATGTAAGAG-----GTCATGGGTTCAAATCCCATATTCTCCA---  
>tdbD00003930 *Encephalitozoon\_cuniculi* GB-M1 284813 Ala CGC  
-GGGGGATTATCTTAGT--GGT--AGAGTGTGCTTCGCATGCAAGTG-----G-CCCGGGTTTCGATTCTCGATCTCTCCA---  
>tdbD00003928 *Encephalitozoon\_cuniculi* GB-M1 284813 Ala TGC  
-GGGGTGTGCTTAGT--GGT--ATGATACCTGCTTTGCACCGAGTTG-----G-CCCGGGTTTCGATTCTCGCAACTCCA---  
>tdbD00000232 *Gallus\_gallus* 9031 Ala TGC  
-GGGGATGTAGCTCAGT--GGT--AGTGCATGCTTTGCATGTATGAG-----GCCCCGGGTTCAAATCCCCGGCATCTCCA---  
>tdbD00000233 *Gallus\_gallus* 9031 Ala TGC  
-GGGGATGTAGCTCAGC--GGT--AGAGCGCATGCTTTGCATGTATGAG-----GTCCCGGGTTCAAATCCCCGGCATCTCCA---  
>tdbD00004087 *Gallus\_gallus* 9031 Ala AGC  
-GGGGAATTAGCTCAAGT--GGT--AGAGCGCTTGCTTAGCATGTGAGAG-----GCAGCGGGATCGATGCCCGCATCTCTCCA---  
>tdbD00004088 *Gallus\_gallus* 9031 Ala AGC  
-GGGGAATTAGCTCAAGT--GGT--AGAGCGCTCGCTTAGCATGTGAGAG-----GCAGTGGGATCGATGCCCGCATCTCTCCA---  
>tdbD00004089 *Gallus\_gallus* 9031 Ala AGC  
-GGGGAATTAGCTCAAAT--GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTAGCGGGATCAATGCCCGCATCTCTCCA---  
>tdbD00004090 *Gallus\_gallus* 9031 Ala AGC  
-GGGGAATTAGCTCAAAT--GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTAGCGGGATCGATGCCCGCATCTCTCCA---  
>tdbD00004091 *Gallus\_gallus* 9031 Ala AGC  
-GGGGGATTAGCTCAAAT--GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTAGCGGGATCGATGCCCGCATCTCTCCA---  
>tdbD00004092 *Gallus\_gallus* 9031 Ala CGC  
-GGGGATGTAGCTCAGT--GGT--AGAGCGCATGCTTCGCATGTGTGAG-----GTCCAGGTTCAAATCCCTGGCATCTCTCCA---  
>tdbD00004093 *Gallus\_gallus* 9031 Ala CGC  
-GGGGATGTAGCTCAGC--GGG--AGAGCGCTTGCTTCGCATGTAAGAG-----GTCCTGGGTTCAAATCCCCAGCATCTCTCCA---  
>tdbD00004094 *Gallus\_gallus* 9031 Ala CGC  
-GGGGATGTAGCTCAGT--GGT--AGAGCGCGCGCTTCGCATGTGTGAG-----GTCCCGGGTTCAAATCCCCGGCATCTCTCCA---  
>tdbD00004097 *Gallus\_gallus* 9031 Ala TGC  
-GGGGATGTAGCTCAGC--GGT--AGAGCGCCTGCTTTGCATGCGAGGAG-----GCCCTGGGTTCAAACCCAGCATCTCTCCA---  
>tdbD00004098 *Gallus\_gallus* 9031 Ala TGC  
-GGGGATGTAGCTCAGT--GGT--AGAGCGCATGCTTTGCATGTATGAG-----GCCCCGGGTTCAAATCCCCGGCATCTCTCCA---  
>tdbD00000241 *Homo\_sapiens* 9606 Ala TGC  
-GGGGGTAGCTCAGT--GGT--AGAGCGCATGCTTTGCATGTATGAG-----G-CCTCGGTTTCGATCCCCGACACTCCA---  
>tdbD00003830 *Homo\_sapiens* 9606 Ala AGC  
-GGGGGATTAGCTCAAGC--GGT--AGGGTGCCTGCTTAGCATGCAAGAG-----GTAGCAGGATCGACGCTGCATTCTCC---  
>tdbD00003833 *Homo\_sapiens* 9606 Ala AGC  
-GGGGGATTAGCTCAAAT--GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTAGCGGGATCGATGCCCG-ATCCTCC---  
>tdbD00003834 *Homo\_sapiens* 9606 Ala AGC  
-GGGGAATTGCTCAAGC--GGT--AGAGCGCTTGCTTAGCATGCAAGAG-----GTAGCAGGATCGACGCTGCATTCTCC---  
>tdbD00003835 *Homo\_sapiens* 9606 Ala AGC  
-GGGGAATTAGCGCAAGT--GGT--AGAGTGTGCTTAGCATGCAAGAG-----GTAGTGGGATCGATGCCACATTCTCC---  
>tdbD00003836 *Homo\_sapiens* 9606 Ala AGC  
-GGGGAATTAGCCCAAGT--GGT--AGAGCGCTTGCTTAGCATGCAAGAG-----GTAGTGGGATCGATGCCACATTCTCC---  
>tdbD00003837 *Homo\_sapiens* 9606 Ala AGC  
-GGGGAATTAGCTCAAGT--GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTAGTGGGATCGATGCCCGCATCTCTCC---

>tdbD00003838 Homo\_sapiens 9606 Ala AGC  
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>tdbD00003839 Homo\_sapiens 9606 Ala AGC  
-GGGAATTAGCTCAAGC-GGT--AGAGCGCTTGCTTAGCATGCAAGAG-----GTAGTGGGATCGATGCCACATTCTCC----  
>tdbD00003840 Homo\_sapiens 9606 Ala AGC  
-GGGAATTAGCTCAAGT-GGT--AGAGCGCTTGCTTAGCATGCAAGAG-----GTAGTGGGATCGATGCCACATTCTCC----  
>tdbD00003841 Homo\_sapiens 9606 Ala AGC  
-GGGAATTAGCTCAAAAT-GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTAGCGGGATCGATGCCCGCATTCTCC----  
>tdbD00003842 Homo\_sapiens 9606 Ala AGC  
-GGGAATTAGCTCAAGT-GGT--AGAGCGCTTGCTTAGCACGCAAGAG-----GTAGTGGGATCGATGCCACATTCTCC----  
>tdbD00003844 Homo\_sapiens 9606 Ala AGC  
-GGGGTGTAGCTCAGT--GGT--AGAGCGTATGCTTAGCATTCATGAG-----GCTCTGGGTTTCGATCCCCAGCACTTCC----  
>tdbD00003845 Homo\_sapiens 9606 Ala AGC  
-GGGGTGTAGCTCAGT--GGT--AGAGCGCTTGCTTAGCATGCACGAG-----GCCCGGGTTCAATCCTTGGCACCTCC----  
>tdbD00003846 Homo\_sapiens 9606 Ala AGC  
-GGGGTATAGCTCAGC--GGT--AGAGCGCTTGCTTAGCATGCACGAG-----GTCTTGGGTTCAATCCCCAATACCTCC----  
>tdbD00003847 Homo\_sapiens 9606 Ala AGC  
-GGGGTGTAGCTCAGT--GGT--AGAGCGCTTGCTTAGCATGCACGAG-----GCCCTGGGTTCAATCCCCAGCACCTCC----  
>tdbD00003848 Homo\_sapiens 9606 Ala AGC  
-GGGGTGTAGCTCAGT--GGT--AGAGCGCATGCTTAGCATGCATGAG-----GTCCCGGGTTTCGATCCCCAGCATCTCC----  
>tdbD00003849 Homo\_sapiens 9606 Ala AGC  
-GGGGTGTAGCTCAGT--GGT--AGAGCGCTTGCTTAGCATGTACGAG-----GTCCCGGGTTCAATCCCCGGCACCTCC----  
>tdbD00003850 Homo\_sapiens 9606 Ala AGC  
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>tdbD00003851 Homo\_sapiens 9606 Ala AGC  
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>tdbD00003853 Homo\_sapiens 9606 Ala CGC  
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>tdbD00003854 Homo\_sapiens 9606 Ala CGC  
-GGGATGTAGCTCAGT--GGT--AGAGCGCTTGCTTGCATGTGTAG-----GTCCCGGGTTCAATCCCCGGCATCTCC----  
>tdbD00003855 Homo\_sapiens 9606 Ala CGC  
-GGGATGTAGCTCAGT--GGT--AGAGCGCATGCTTGCATGTATGAG-----GCCCGGGTTTCGATCCCCGGCATCTCCA---  
>tdbD00003856 Homo\_sapiens 9606 Ala CGC  
-GGGATGTAGCTCAGT--GGT--AGAGCGCATGCTTGCATGTATGAG-----GTCCCGGGTTTCGATCCCCGGCATCTCCA---  
>tdbD00003857 Homo\_sapiens 9606 Ala TGC  
-GGGATGTAGTTTACAT--GGTT-AAAACATAAGTTTTGCAAACCTTAAG-----T-ACAGGGTTCAATTCCTGCTTCTCC----  
>tdbD00003859 Homo\_sapiens 9606 Ala TGC  
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>tdbD00003860 Homo\_sapiens 9606 Ala TGC  
-GGGGTGTAGCTCAGT--GGT--AGAGCGCATGCTTGCATGTATGAG-----GCCTGGGTTTCGATCCCCGACACCTCC----  
>tdbD00003861 Homo\_sapiens 9606 Ala TGC  
-GGGATGTAGCTCAGT--GGT--AGAGCGCATGCTTGCATGTATGAG-----GCCCGGGTTTCGATCCCCGGCATCTCCA---  
>tdbD00003862 Homo\_sapiens 9606 Ala TGC  
-GGGATGTAGCTCAGT--GGT--AGAGCGCATGCTTGCATGTATGAG-----GTCCCGGGTTTCGATCCCCGGCATCTCCA---  
>tdbD00003863 Homo\_sapiens 9606 Ala TGC  
-GGGGTGTAGCTCAGT--GGT--AGAGCGCATGCTTGCATGTATGAG-----GTCCCGGGTTTCGATCCCCGGCACCTCCA---  
>tdbD00000238 Nephila clavipes 6915 Ala AGC  
-GGGGCGTAGCTCAGAT--GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTACGGGGATCGATAACCCCGCCTTCCA---  
>tdbD00000240 Nephila clavipes 6915 Ala AGC  
-GGGGCGTAGCTCAGAT--GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTACGGGGATCGATAACCCCGCCTTCCA---  
>tdbD00000236 Oryctolagus cuniculus 9986 Ala AGC  
-GGGGTGTAGCTCAGT--GGTT-AGAGCGCTGCTTAGCATGCACGAG-----GCCCGGGTTCAATCCCCGGCACCTCCACCA  
>tdbD00004113 Pan troglodytes 9598 Ala AGC  
-GGGGATTAGCTCAAGC--GGT--AGAGCGCTGCTTAGCATGCAAGAG-----GTGGCAGGATCGACGCTGCATTCTCCA---  
>tdbD00004114 Pan troglodytes 9598 Ala AGC  
-AGGAATTAGCTCAGGC--GGT--AGAGCGCTCGCTCAGCATGCGAGAG-----GTAGCGGGATCGACGCCCGCATTCTCCG---  
>tdbD00004115 Pan troglodytes 9598 Ala AGC  
-GGGAATTAGCTCAAGT--GGT--AGAGCGCTTGCTTAGCATGCAAGA-----G-----GTAGTGGGATCGATGCCACATTCTCCA---  
>tdbD00004116 Pan troglodytes 9598 Ala AGC  
-GTGGATTAGCTCAAGC--GGT--AGAGCGCTTGCTTAGCATGCAAGAG-----GTAGCAGGATCGACGCTGCATTCTCCA---  
>tdbD00004118 Pan troglodytes 9598 Ala AGC  
-GGGAATTAGCTCAAGC--GGT--AGAGCGCTTGCTTAGCATGCAAGAG-----GCAGTGGGATCGACGCCACATTCTCCA---  
>tdbD00004119 Pan troglodytes 9598 Ala AGC  
-GGGGTATAGCTCAGC--GGT--AGAGCTCGTCTTAGCATGCACAAG-----GTCCTGGGTTCAATCCTCAGCACCTCCT---  
>tdbD00004120 Pan troglodytes 9598 Ala AGC  
-GGGAATTAGCTCAAGT--GGT--AGAGCGCTTGCTTAGCATGCAAGAG-----GTAGTGGGATCAATGCCACATTCTCCA---  
>tdbD00004121 Pan troglodytes 9598 Ala AGC  
-GGGAATTAGCTCAAGT--GGT--AGAGCGCTTGCTTAGCATGCAAGAG-----GTAGTGGGATCGATGCCACATTCTCCA---  
>tdbD00004123 Pan troglodytes 9598 Ala AGC  
-GGGAATTAGCTCAGGC--GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTAGCGGGATCGACGCCCGCATTCTCCA---  
>tdbD00004125 Pan troglodytes 9598 Ala AGC  
-GGGAATTAGCTCAGGC--GGT--AGAGCGCTCGCTCAGCATGCGAGAG-----GTAGCGGGATCGATAACCCGATTCTCCA---  
>tdbD00004126 Pan troglodytes 9598 Ala AGC  
-GGGGTGTAGCTCAGT--GGT--AGAGCGCTGCTTAGCATGCACGAG-----GCCCTGGGTTCAATCCCCGGCACCTCCA---  
>tdbD00004127 Pan troglodytes 9598 Ala AGC

-GGGGAATTAGCTCAAGT--GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTAGTGGGATCGATACCCACATTCTCCA---  
>tdbD00004128 Pan\_troglodytes 9598 Ala AGC  
-GGGGGTAGCTCAGT--GGT--AGAGCGTATGCTTAGCATGCATGAG-----GCCCTGGGTTTCGATCCCCAGCACCTCCA---  
>tdbD00004129 Pan\_troglodytes 9598 Ala AGC  
-GGGGGTAGCTCAGT--GGT--AGAGCGGTGCTTAGCATGCACGAG-----GCCCTGGGTTCAATCCCCAGCACCTCCA---  
>tdbD00004130 Pan\_troglodytes 9598 Ala AGC  
-GGGGATGATAGCTCAGT--GGT--AGAGCGCATGCTTAGCATGCATGAG-----GTCCCGGGTTTCGATCCCCAGCATCTCCA---  
>tdbD00004131 Pan\_troglodytes 9598 Ala AGC  
-GGGGGTATAGCTCAGT--GGT--AGAGCGCGTGCCTTAGCATGCACGAG-----GCCCTGGGTTTCGATCCCCAGTACCTCCA---  
>tdbD00004132 Pan\_troglodytes 9598 Ala AGC  
-GGGGGTAGCTCAGT--GGT--AGAGCGCGTGCCTTAGCATGCACGAG-----GCCCGGGTTCAATCCCCGGCACCTCCA---  
>tdbD00004133 Pan\_troglodytes 9598 Ala CGC  
-GGGGGTAGCTCAGT--GGT--AGAGCGCGTGCCTTCGCATGTACGAG-----GCCCGGGTTTCGACCCCCGGCTCCTCCA---  
>tdbD00004134 Pan\_troglodytes 9598 Ala CGC  
-GGGGGTAGCTCAGT--GGT--AGAGCGCGTGCCTTCGCATGTACGAG-----GTCCCTGGTTCAATCCCTGGCACCTCCA---  
>tdbD00004139 Pan\_troglodytes 9598 Ala TGC  
-GGGGATGATAGCTCAGT--GGT--AGAGCGCATGCTTTCGCATGTATGAG-----GCCCTGGGTTTCGATCCCCGGCATCTCCA---  
>tdbD00004142 Pan\_troglodytes 9598 Ala AGC  
-GGGGGTAGCTCAGT--GGT--AGAGCACATGCTTTCGCATGTATGAG-----GCCCGGGTTTCGATCCCCGGCACCTCCA---  
>tdbD00000215 Plasmodium\_falciparum 5833 Ala TGC  
-GGGAATATAGTTTAAAT--GGT--AAAATCTTATTTTGCATAATAAAG-----A-TAGTAGTTCAATTCTACTTATTTCCA---  
>tdbD00004081 Plasmodium\_falciparum\_3D7 36329 Ala AGC  
-GGGCGACTAGCTCAAGT--GGT--AGAGCGCTCGCTTAGCATGCGAGAG-----GTACGGGGATCGATACCCGGTCGTCCA---  
>tdbD00004082 Plasmodium\_falciparum\_3D7 36329 Ala CGC  
-GGGCTAGTAGTGTAGT--GGT--ATCACGTTCGCTTCGCATGCGAAAAG-----TTCCCGGGTTTCGATTCCTGGCTGGTCCA---  
>tdbD00004083 Plasmodium\_falciparum\_3D7 36329 Ala TGC  
-GGGCAGGTGGTGTAGT--GGT--ATCACGCTTGATTTGCATTCGAAGAG-----GTCCGGGGTTCAATTCCTGGCTGTCCA---  
>tdbD00000098 Pylaiella\_littoralis 2885 Ala TGC  
-GGGGTATAGCTCAGTT--GGT--AGAGCGTTGCTTTTCGCATAGCAGAG-----GTCAGCAGTTTCGAGTCTGCTTATCTCCA---  
>tdbD00000219 Saccharomyces\_cerevisiae 4932 Ala AGC  
-GGGCGTGTGGCGTAGTC--GGT--AGCGCGCTCCCTTAGCATGGGAGAG-----GTCTCCGGTTTCGATTCCTGGACTCGTCCA---  
>tdbD00003893 Schizosaccharomyces\_pombe 4896 Ala CGC  
-GGGGATGATGTTTAGG--GGT--ATAACGTTTCATTCGCATTTGAAAAG-----GTCCCGGGTTTCGATTCCTGGCATCTCC---  
>tdbD00003894 Schizosaccharomyces\_pombe 4896 Ala TGC  
-GGGCATGTGATGCAGT--GGT--AGCATGCTCGCTTTCGCATGCGAGTC-----GTCCTGGGTTCAATCCCCAGCGTGTCC---  
>tdbD00000224 Solanum\_tuberosum 4113 Ala TGC  
-GGGGATGATAGCTCATAT--GGT--AGAGCGCTCGCTTTCGCATGCGAGAG-----GTACAGGGTTTCGATCCCCTGCATCTCCA---  
>tdbD00004101 Takifugu\_rubripes 31033 Ala AGC  
-GGGGAATTAGCTCAAAA--GGT--AGAGCGCTCGCTTAGCATGTGAGAG-----GTAGTGGGATCGATGCCACATTCTCCA---  
>tdbD00004105 Takifugu\_rubripes 31033 Ala CGC  
-GGGGATGATAGCTCAGT--GGT--AGAGCGTGTGCTTCGCATGTATGAG-----GTCCTGGGTTCAATCCCCAGCATCTCCA---  
>tdbD00004106 Takifugu\_rubripes 31033 Ala CGC  
-GGGGATGATAGCTCAGT--GGT--AGAGTGTGTGCTTCGCATGCATGAG-----GTCCTGGGTTCAATCCCCAGCATCTCCA---  
>tdbD00004107 Takifugu\_rubripes 31033 Ala CGC  
-GGGGATGATAGCTCAGT--GGT--AGAGCGGTGCTTCGCATGTATGAG-----GTCCCGGGTTCAATCCCCGGCATCTCCA---  
>tdbD00004108 Takifugu\_rubripes 31033 Ala TGC  
-GGGGAATTAGCTCAAAA--GGT--AGAGCGCTCGCTTTCGCATGTGAGAG-----GTAGTGGGATCGATGCCACATTCTCCA---  
>tdbD00004109 Takifugu\_rubripes 31033 Ala TGC  
-GGGGAATTAGCTCAAGT--GGT--AGAGCGCTCGCTTTCGCATGTGAGAG-----GTAGTGGGATCGATGCCACATTCTCCA---  
>tdbD00004111 Takifugu\_rubripes 31033 Ala TGC  
-GGGGATGATAGCTCAGT--GGT--AGAGCGCTTGCCTTTCGCATGTAAGCG-----GTCCTGGGTTCAATCCCCAGCATCTCCA---  
>tdbD00000221 Toxoplasma\_gondii 5811 Ala TGC  
-AGGGATATAGCTCAGGA--GGT--AGAGCACTTTTTTGCAAAAAAGAA-----ATTTACGGTTCAAGTCCGTTTATCTCCA---  
>tdbD00000231 Xenopus\_laevis 8355 Ala TGC  
-GGGGGTAGCTCAGT--GGT--AGAGCGCATGCTTTCGCATGTATGAG-----GTCTTGGGTTCAATCCCCAGCATCTCCA---

Eukaryota - siblings

>tdbD00011009 Caenorhabditis\_elegans 6239 Val AAC  
-GGTCTCGTGGTGTAGT--GGTT-ATCACATCTGTCTAACACACAGAAAG-----GTCGGTGGTTCGAGCCCGCCGAGATCA---  
>tdbD00011022 Drosophila\_melanogaster 7227 Val AAC  
-GTTTCCGTGGTGTAGT--GGTT-ATCACATCCGCCTAACACGCGGAAG-----GCCCCGGTTCATCCCGGGCGGAAACA---  
>tdbD00011024 Drosophila\_melanogaster 7227 Val CAC  
-GTTTTCGTAGTGTAGT--GGTT-ATCACGTGTGCTTCACACGCACAAG-----GTCCCGGTTTCGAAACCCGGGCGGAAACA---  
>tdbD00003259 Homo\_sapiens 9606 Val AAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCACGTTCGCCTAACACGCGAAAG-----GTCCCGGTTTCGAAACCCGGGCGGAAACA---  
>tdbD00010989 Homo\_sapiens 9606 Val AAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCACGTTCGCCTAACACGCGAAAG-----GTCCCTGGATCAAACCAGGCGGAAACA---  
>tdbD00010990 Homo\_sapiens 9606 Val AAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCACGTTCGCCTAACACGCGAAAG-----GTCCCGGTTTCGAAACCCGGGCGGAAACA---  
>tdbD00010991 Homo\_sapiens 9606 Val AAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCACGTTCGCCTAACACGCGAAAG-----GTCCCGGTTTCGAAACCCGGGCGGAAACA---  
>tdbD00011000 Homo\_sapiens 9606 Val CAC  
-GTTTCCGTAGTGTAGC--GGTT-ATCACATTCGCCTAACACGCGAAAG-----GTCCCGGTTTCGATCCCGGGCGGAAACA---  
>tdbD00011001 Homo\_sapiens 9606 Val CAC  
-GTTTTCGTAGTGTAGT--GGTT-ATCACGTTCGCCTAACACGCGAAAG-----GTCCCGGTTTCGAAACCCGGGCGGAAACA---  
>tdbD00011002 Homo\_sapiens 9606 Val CAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCACGTTCGCCTAACACGCGAAAG-----GTCCCGGTTTCGAAACCCGGGCGGAAACA---  
>tdbD00003249 Leptomonas\_collosoma 5686 Val TAC  
-GCGTGGGTGATCTAGT--GGTT-ATGATGTCTGCTTTACACGCAGAAC-----GTCGGGGTTCGAAACCCCGCCCGCGTA---  
>tdbD00011268 Pan\_troglodytes 9598 Val AAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCACGTTCGCCTAACACGCGAAAG-----GTCCCGGTTTCGAAACCCGGGCGGAAACA---  
>tdbD00011277 Pan\_troglodytes 9598 Val CAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCACGTTCGCCTAACACGCGAAAG-----GTCCCGGTTTCGAAACCCGGGCGGAAACA---  
>tdbD00011284 Pan\_troglodytes 9598 Val TAC  
-GGTCCATAGTGTAGT--GGTT-ATCACGTCTGCTTTACACGCAGAAG-----GTCCTGGGTTTCGAGCCCCAGTGAACCA---  
>tdbD00003245 Saccharomyces\_cerevisiae 4932 Val AAC  
-GGTTTCGTGGTCTAGTC--GGTT-ATGGCATCTGCTTAACACGCAGAAC-----GTCCCGAGTTCGATCCTGGGCGAAATCA---  
>tdbD00011018 Saccharomyces\_cerevisiae 4932 Val AAC  
-GGTTTCGTGGTCTAGTC--GGTT-ATGGCATCTGCTTAACACGCAGAAC-----GTCCCGAGTTCGATCCTGGGCGAAATCA---  
>tdbD00011020 Saccharomyces\_cerevisiae 4932 Val TAC  
-GGTCCAATGGTCCAGT--GGTTCAAGACGTCGCCTTTACACGGCGAAG-----ATCCCGAGTTCGAAACCTCGGTTGGATCA---  
>tdbD00011026 Schizosaccharomyces\_pombe 4896 Val AAC  
-GTCGTGTGGTTTATAGT--GGTT-ATAATTTCTGCTTAACACGCAGACG-----GTCCCAAGTTCGAGTCTTGGCACGATCA---  
>tdbD00011027 Schizosaccharomyces\_pombe 4896 Val AAC  
-GTCGTGTGGTTTATAGT--GGTT-ATAATTTCTGCTTAACACGCAGACG-----GTCCCAAGTTCGAGTCTTGGCACGATCA---  
>tdbD00011255 Takifugu\_rubripes 31033 Val AAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCACGTTCGCCTAACACGCGAAAG-----GTCCCGGTTTCGAAACCCGGGCGGAAACA---  
>tdbD00011258 Takifugu\_rubripes 31033 Val CAC  
-GTTTCCGTAGTGTAGT--GGTT-ATCACGTTCGCCTAACACGCGAAAG-----GTCCCGGTTTCGAAACCCGGGCGGAAACA---  
>tdbD00011263 Takifugu\_rubripes 31033 Val TAC  
-GGTCCATAGTGTAGC--GGTT-ATCACGTCTGCTTTACACGCAGAAG-----GTCCTGGGTTTCGAGCCCCAGTGAACCA---  
>tdbD00005933 Caenorhabditis\_elegans 6239 Ile TAT  
-GCCCCATTGGCGCAGTC--GGTT-AGCGCGTGGTACTTATAATGCCAAG-----GTCGCCAGTTCGAGCCTGGCATGGGGCA---  
>tdbD00005937 Drosophila\_melanogaster 7227 Ile AAT  
-GGCCATTAGCTCAGTT--GGTT-AGAGCGTGTGCTAATAACGCGAAG-----GTCGGGGTTCGATCCCCTCATGGGCCA---  
>tdbD00005939 Drosophila\_melanogaster 7227 Ile TAT  
-GCTCCAGTGGCGCAATT--GGTT-AGCGCACGGTACTTATAATGCCGGG-----GTTGTGAGTTCGAGCCTCACCTGGAGC---  
>tdbD00005916 Homo\_sapiens 9606 Ile AAT  
-GGCCGGTTAGCTCAGTT--GGTT-AGAGCGTGGTGTGCTAATAACGCCAAG-----GTCGGGGTTCGATCCCCGTACGGGCCA---  
>tdbD00005922 Homo\_sapiens 9606 Ile TAT  
-GCTCCAGTGGCGCAATC--GGTT-AGCGCGCGTACTTATAATGCCGAG-----GTTGTGAGTTCGAGCCTCACCTGGAGC---  
>tdbD00001324 Leptomonas\_collosoma 5686 Ile AAT  
-GCTCTCATAGCTCAGTC--GGTT-AGAGCGTGGGTCTAATAAGCCCAAG-----GTCACAGGTTTCGACCCCTGTTGGGAGCA---  
>tdbD00001325 Leptomonas\_seymouri 5684 Ile AAT  
-GCTCTCATAGCTCAGTC--GGTT-AGAGCGTGGGTCTAATAAGCCCAAG-----GTCACAGGTTTCGACCCCTGTTGGGAGCA---  
>tdbD00001329 Mus\_musculus 10090 Ile AAT  
-GGCCGGTTAGCTCAGTT--GGTT-AGAGCGTGGTGTGCTAATAACGCCAAG-----GTCGGGGTTCGATCCCCGTACGGGCCA---  
>tdbD00006057 Pan\_troglodytes 9598 Ile AAT  
-GGCCGGTTAGCTCAGTT--GGTT-AGAGCGTGGTGTGCTAATAACGCCAAG-----GTCGGGGTTCGATCCCCGTACGGGCCA---  
>tdbD00006058 Pan\_troglodytes 9598 Ile AAT  
-GGTGGTTAGCTCAGTT--GGTT-AGAGCGTGGTGTGCTAATAACGCCAAG-----GTCGGGGTTCGATCCCCGTACTGGGCCA---  
>tdbD00006062 Pan\_troglodytes 9598 Ile TAT  
-GCTCCAGTGGCGCAATC--GGTT-AGCGCGCGTACTTATAATGCCGAG-----GTTGTGAGTTCGAGCCTCACCTGGAGCA---  
>tdbD00001320 Saccharomyces\_cerevisiae 4932 Ile AAT  
-GGTCTTTGGCCAGTT--GGTT-AAGGCACCGTGTGCTAATAACGCGGGG-----ATCAGCGGTTTCGATCCCCTAGAGACCA---  
>tdbD00005934 Saccharomyces\_cerevisiae 4932 Ile AAT  
-GGTCTTTGGCCAGTT--GGTT-AAGGCACCGTGTGCTAATAACGCGGGG-----ATCAGCGGTTTCGATCCCCTAGAGACCA---  
>tdbD00005935 Saccharomyces\_cerevisiae 4932 Ile TAT  
-GTCGTGTAGCTCAGT--GGTT-AGAGCTTCGTGCTTATAACGCGACC-----GTCGTGGGTTCAATCCCCACCTCGAGCA---  
>tdbD00006049 Takifugu\_rubripes 31033 Ile AAT

-GGCCGGTTAGCTCAGTT-GGTT-AGAGCGTGGTGCTAATAACGCCAAG-----GTCGCGGGTTCGATCCCCGTACGGGCCA---  
>tdbD00006052 Takifugu\_rubripes 31033 Ile TAT  
-GCTCCAGTGGCGCAATC-GGTT-AGCGCGGTACTTATAATGCCGAG-----GTTGTGAGTTCGAGCCTCACCTGGAGCA---  
>tdbD00001765 Caenorhabditis\_elegans 6239 Leu AAG  
-GGAGAGATGGCCGAGC--GGTCTAAGGCGCTGGTTTAAGGCACCAGTCCCT----TCG----GGGG-CGTGGGTTTCGAATCCCCTCTCTTCA---  
>tdbD00006780 Caenorhabditis\_elegans 6239 Leu AAG  
-GGAGAGATGGCCGAGC--GGTCTAAGGCGCTGGTTTAAGGCACCAGTCCCT----TCG----GGGG-CGTGGGTTTCGAATCCCCTCTCTTCA---  
>tdbD00006791 Caenorhabditis\_elegans 6239 Leu CAG  
-GCCGTTCTGGCCGAGT--GGTCTAAGGCGCTGCGTTCAGGTTCGAGTCCCT----TCCG----GAGGGCGCAGGTTTCGAATCCTGCGGACGGCA---  
>tdbD00006794 Caenorhabditis\_elegans 6239 Leu TAA  
-AGCACGATGGCCGAGT--GGTT-AAGGCGTGGACTTAAGTTCCAATGGTGG----ATA----ACACCTCGTGGGTTTCGAACCCCTCTGTGCTA---  
>tdbD00006795 Caenorhabditis\_elegans 6239 Leu TAG  
-GGTGAAGATGGCCGAGT--GGTCTAAGGCGCTGGTTTAAAGGCACCAGTCCCT----CCG----GGGG-CGTGGGTTTCGAATCCCCTCTCATCA---  
>tdbD00006800 Drosophila\_melanogaster 7227 Leu CAA  
-GTCAGGATGGCCGAGC--GGTCTAAGGCGCCAGACTCAAGTTCTGGTCCCT----TCT----GAGGGCGTGGGTTTCGAATCCCCTTCTGACA---  
>tdbD00006807 Drosophila\_melanogaster 7227 Leu CAA  
-GTCAGGATGGCCGAGC--GGTCTAAGGCGCCAGACTCAAGTTCTGGTCCCT----TCT----GAGGGCGTGGGTTTCGAATCCCCTTCTGACA---  
>tdbD00006809 Drosophila\_melanogaster 7227 Leu CAG  
-GTCAGGATGGCCGAGC--GGTCTAAGGCGCCAGACTCAAGTTCTGGTCCCT----TCT----GAGGGCGTGGGTTTCGAATCCCCTTCTGACA---  
>tdbD00006810 Drosophila\_melanogaster 7227 Leu CAG  
-GTCAGGATGGCCGAGT--GGTCTAAGGCGCTGCGTTCAGGTTCGAGTCTAC----TCT----GTAGGCGTGGGTTTCGAATCCCCTTCTGACA---  
>tdbD00001777 Homo\_sapiens 9606 Leu AAG  
-GGTAGCGTGGCCGAGC--GGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCT----TCG----GGGG-CGTGGGTTTCGAATCCCACCGCTGCCA---  
>tdbD00006741 Homo\_sapiens 9606 Leu AAG  
-GGTAGCGTGGCCGAGC--GGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCT----TCG----GGGG-CGTGGGTTTCGAATCCCACCGCTGCCA---  
>tdbD00006751 Homo\_sapiens 9606 Leu CAG  
-GTCAGGATGGCCGAGC--GGTCTAAGGCGCTGCGTTCAGGTTCGAGTCTCC----CCT----GGAGGCGTGGGTTTCGAATCCCCTCTGACA---  
>tdbD00001772 Mus\_musculus 10090 Leu CAG  
-GTCAGGATGGCCGAGC--GGTCTAAGGCGCTGCGTTCAGGTTCGAGTCTCC----CCT----GGAGGCGTGGGTTTCGAATCCCCTCTGACA---  
>tdbD00007269 Pan\_troglodytes 9598 Leu AAG  
-GGTAGCGTGGCCGAGC--GGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCT----TCG----GGGG-CGTGGGTTTCGAATCCCACCGCTGCCA---  
>tdbD00007270 Pan\_troglodytes 9598 Leu AAG  
-GGTAGCGTGGCCGAGC--GGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCT----TTCG----GAGGCGTGGGTTTCGAATCCCACCGCTGCCA---  
>tdbD00007277 Pan\_troglodytes 9598 Leu CAG  
-GTCAGGATGGCCGAGC--GGTCTAAGGCGCTGCGTTCAGGTTCGAGTCTCC----CCT----GGAGGCGTGGGTTTCGAATCCCCTTCTGACA---  
>tdbD00007278 Pan\_troglodytes 9598 Leu CAG  
-GTCAGGATGGCCGAGC--GGTCTAAGGCGCTGCGTTCAGGTTCGAGTCTCC----CCT----GGAGGCGTGGGTTTCGAATCCCCTCTGACA---  
>tdbD00007287 Pan\_troglodytes 9598 Leu TAG  
-GGTAGCGTGGCCGAGT--GGTCTAAGGCGCTGGATTAAGGCTCCAGTCTAT----TTCG----ATGGCGTGGGTTTCGAATCCCACCGCTGCCA---  
>tdbD00007289 Pan\_troglodytes 9598 Leu TAG  
-GGTAGCGTGGCCGAGC--GGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCT----TTCG----GAGGCGTGGGTTTCGAATCCCACCGCTGCCA---  
>tdbD00001775 Rattus\_norvegicus 10116 Leu CAG  
-GTCAGGATGGCCGAGC--GGTCTAAGGCGCTGCGTTCAGGTTCGAGTCTCC----CCT----GGAGGCGTGGGTTTCGAATCCCCTCTGACA---  
>tdbD00001756 Saccharomyces\_cerevisiae 4932 Leu TAA  
-GGAGGTTGGCCGAGT--GGTCTAAGGCGCCAGACTTAAGATCTGTTGGAC----GGTT----GTCCGCGCGAGTTTCGAACCTCGCATCCTTCA---  
>tdbD00006796 Saccharomyces\_cerevisiae 4932 Leu CAA  
-GGTTGTTTGGCCGAGC--GGTCTAAGGCGCCTGATTAAGCTCAGGTATC----GTAA----GATGCAAGAGTTTCGAATCTCTTAGCAACCA---  
>tdbD00006797 Saccharomyces\_cerevisiae 4932 Leu CAA  
-GGTTGTTTGGCCGAGC--GGTCTAAGGCGCCTGATTAAGCTCAGGTATC----GTAA----GATGCAAGAGTTTCGAATCTCTTAGCAACCA---  
>tdbD00006798 Saccharomyces\_cerevisiae 4932 Leu CAA  
-GGTTGTTTGGCCGAGC--GGTCTAAGGCGCCTGATTAAGCTCAGGTATC----GTAA----GATGCAAGAGTTTCGAATCTCTTAGCAACCA---  
>tdbD00006799 Saccharomyces\_cerevisiae 4932 Leu CAA  
-GGTTGTTTGGCCGAGC--GGTCTAAGGCGCCTGATTAAGCTCAGGTATC----GTAA----GATGCAAGAGTTTCGAATCTCTTAGCAACCA---  
>tdbD00006800 Saccharomyces\_cerevisiae 4932 Leu CAA  
-GGTTGTTTGGCCGAGC--GGTCTAAGGCGCCTGATTAAGCTCAGGTATC----GTAA----GATGCAAGAGTTTCGAATCTCTTAGCAACCA---  
>tdbD00006802 Saccharomyces\_cerevisiae 4932 Leu TAA  
-GGAGGTTGGCCGAGT--GGTCTAAGGCGCCAGACTTAAGATCTGTTGGAC----GGTT----GTCCGCGCGAGTTTCGAACCTCGCATCCTTCA---  
>tdbD00007262 Takifugu\_rubripes 31033 Leu TAA  
-ACCAGGATGGCCGAGT--GGTT-AAGGCGTGGACTTAAGATCCAATGGAC----GTAT----GTCCGCGTGGGTTTCGAACCCCTCTCTGGTA---  
>tdbD00007265 Takifugu\_rubripes 31033 Leu TAG  
-GGTAGCGTGGCCGAGT--GGTCTAAGGCGCTGGATTAAGGCTCCAGTCTAT----TTCG----ATGGCGTGGGTTTCGAATCCCACCGCTGCCA---  
>tdbD00001771 Xenopus\_laevis 8355 Leu CAG  
-GTCAGGATGGCCGAGC--GGTCTAAGGCGCTGCGTTCAGGTTCGAGTCTCC----CCT----GGAGGCGTGGGTTTCGAATCCCCTTCTGACA---  
>tdbD00007469 Arabidopsis\_thaliana 3702 Met CAT  
-GGGGTGGTGGCGCAGTT-GGCT-AGCGCGTAGGTCTCATAATCTGAG-----GTCGAGAGTTTCGAGCCTCTCTCACCCCA---  
>tdbD00007756 Gallus\_gallus 9031 Met CAT  
-ACCTACTTGACTCAGC--GGTT-AGAGTATCGCTTACATACGCGCAGA-----GTCATTTGGTTCAAATCCAATAGTAGGTA---  
>tdbD00007455 Homo\_sapiens 9606 Met CAT  
-AGCAGAGTGGCGCAGC--GGA--AGCGTGTGGGCCCATAAACCAGAG-----GTCGATGGATCGAAACCATCCTCTGCTA---  
>tdbD00007787 Pan\_troglodytes 9598 Met CAT  
-AGCAGAGTGGCGCAGC--GGA--AGCGTGTGGGCCCATAAACCAGAG-----GTCGATGGATCGAAACCATCCTCTGCTA---  
>tdbD00007473 Saccharomyces\_cerevisiae 4932 Met CAT  
-GCTTCAGTAGCTCAGTA-GGA--AGAGCGTCAAGTCTCATAATCTGAAG-----GTCGAGAGTTTCGAACCTCCCCTGGAGCA---  
>tdbD00007777 Takifugu\_rubripes 31033 Met CAT  
-AGCAGAGTGGCGCAGC--GGA--AGCGTGTGGGCCCATAAACCAGAG-----GTCGATGGATCGAAACCATCCTCTGCTA---

>tdbD00004242 Arabidopsis\_thaliana 3702 Cys GCA  
-GGGTCCATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCACCGGTTTCAACCCGGTTGGGCCCT---  
>tdbD00004226 Homo\_sapiens 9606 Cys GCA  
-GGGGGTATAGCTCAGG--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCCCGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00000375 Nicotiana\_rustica 4093 Cys GCA  
-GGGTCTTAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCACCGGTTTCAACCCGGTAGGGCCCT---  
>tdbD00004364 Pan\_troglodytes 9598 Cys GCA  
-GGGGGTATAGCTCAGG--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCTCTGGTTCAAATCCAGGTGCCCCCT---  
>tdbD00004369 Pan\_troglodytes 9598 Cys GCA  
-GGGGGTATAGCTCAGG--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCCTGGTTCAAATCCAGGTGCCCCCT---  
>tdbD00004370 Pan\_troglodytes 9598 Cys GCA  
-GGGGGTATAGCTCAGG--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCCCGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00004372 Pan\_troglodytes 9598 Cys GCA  
-GGGGGTATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCCTGGTTCAAATCCAGGTGCCCCCT---  
>tdbD00004375 Pan\_troglodytes 9598 Cys GCA  
-GGGGGTATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00004377 Pan\_troglodytes 9598 Cys GCA  
-GGGGGTATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCCCGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00004247 Saccharomyces\_cerevisiae 4932 Cys GCA  
-GCTCGTATGGCGCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCTTAGTTTCAATCCAGGTGCCCCCT---  
>tdbD00004253 Schizosaccharomyces\_pombe 4896 Cys GCA  
-GGGGTATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00004358 Takifugu\_rubripes 31033 Cys GCA  
-GGGGGTATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCCCCGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011653 Arabidopsis\_thaliana 3702 Tyr GTA  
-CCGACCTTAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCATGTTTCAATCCAGGTGCCCCCT---  
>tdbD00011654 Arabidopsis\_thaliana 3702 Tyr GTA  
-CCGACCTTAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCATGTTTCAATCCAGGTGCCCCCT---  
>tdbD00011655 Arabidopsis\_thaliana 3702 Tyr GTA  
-CCGACCTTAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCATGTTTCAATCCAGGTGCCCCCT---  
>tdbD00011667 Caenorhabditis\_elegans 6239 Tyr GTA  
-CCGTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCATGTTTCAATCCAGGTGCCCCCT---  
>tdbD00011669 Caenorhabditis\_elegans 6239 Tyr GTA  
-CCGTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCATGTTTCAATCCAGGTGCCCCCT---  
>tdbD00011672 Caenorhabditis\_elegans 6239 Tyr GTA  
-CCGTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCATGTTTCAATCCAGGTGCCCCCT---  
>tdbD00011673 Caenorhabditis\_elegans 6239 Tyr GTA  
-CCGTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCATGTTTCAATCCAGGTGCCCCCT---  
>tdbD00011681 Drosophila\_melanogaster 7227 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011682 Drosophila\_melanogaster 7227 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011683 Drosophila\_melanogaster 7227 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011684 Drosophila\_melanogaster 7227 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011685 Drosophila\_melanogaster 7227 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011686 Drosophila\_melanogaster 7227 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011687 Drosophila\_melanogaster 7227 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00003670 Homo\_sapiens 9606 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00003671 Homo\_sapiens 9606 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011637 Homo\_sapiens 9606 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011639 Homo\_sapiens 9606 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011640 Homo\_sapiens 9606 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011641 Homo\_sapiens 9606 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00003661 Nicotiana\_rustica 4093 Tyr GTA  
-CCGACCTTAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCATGTTTCAATCCAGGTGCCCCCT---  
>tdbD00011802 Pan\_troglodytes 9598 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011803 Pan\_troglodytes 9598 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011807 Pan\_troglodytes 9598 Tyr GTA  
-CCTTCGATAGCTCAGT--GGT--AGAGCATTGACTGCAGATCAAGAG-----GTCGCTGGTTCAAATCCGGGTGCCCCCT---  
>tdbD00011677 Saccharomyces\_cerevisiae 4932 Tyr GTA  
-CTCTCGGTAGCAAGT--GGTTAAGGCGCAAGACTGTAATCTTGAG-----ATCGGGGTTTCAATCCAGGTGCCCCCT---  
>tdbD00011678 Saccharomyces\_cerevisiae 4932 Tyr GTA

-CTCTCGGTAGCCAAGTT-GGTTTAAGCGCGCAAGACTGTAATCTTGAG-----ATCGGGCGTTTCTGACTCGCCCCGGGAGA---  
>tdbD00011794 Takifugu\_rubripes 31033 Tyr GTA  
-CCTTCGATAGCTCAGTT-GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTCAAATCCGGCTCGAAGGA---  
>tdbD00003663 Triticum\_aestivum 4565 Tyr GTA  
-CCGACCTTAGCTCAGTT-GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCAGTGGTTTCAATCCGGTAGGTCGGA---  
>tdbD00003668 Xenopus\_laevis 8355 Tyr GTA  
-CCTTCGATAGCTCAGCT-GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTCAAATCCGGCTCGAAGGA---  
>tdbD00003669 Xenopus\_laevis 8355 Tyr GTA  
-CCTTCGATAGCTCAGCT-GGT--AGAGCGGAGGACTGTAGATCCTTAG-----GTCGCTGGTTTCAATCCGGCTCGAAGGA---  
>tdbD00011362 Caenorhabditis\_elegans 6239 Trp CCA  
-GACTGCTTGGCGCAAT--GGT--AGCGCGTTCGACTCCAGATCGAAAG-----GTTGGGCGTTTCGATCCGCTCAGTGGTCA---  
>tdbD00011467 Gallus\_gallus 9031 Trp CCA  
-GACCTCGTGGCGCAAC--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GCTGCGTGTTCGAATCACGTCGGGGTCA---  
>tdbD00011352 Homo\_sapiens 9606 Trp CCA  
-GACCTCGTGGCGCAAC--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GCTGCGTGTTCGAATCACGTCGGGGTCA---  
>tdbD00011479 Pan\_troglodytes 9598 Trp CCA  
-GACCTCGTGGCGCAAC--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GCTGCGTGTTCGAATCACGTCGGGGTCA---  
>tdbD00011480 Pan\_troglodytes 9598 Trp CCA  
-GACCTCGTGGCGCAAC--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCGAATCACGTCGGGGTCA---  
>tdbD00011481 Pan\_troglodytes 9598 Trp CCA  
-GACCTCGTGGCGCAAT--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCGAATCACGTCGGGGTCA---  
>tdbD00003403 Saccharomyces\_cerevisiae 4932 Trp CCA  
-GAAGCGGTGGCTCAAT--GGT--AGAGCTTTCGACTCCAAATCGAAGG-----GTTGCAGGTTCAAATCCTGTCCGTTTCA---  
>tdbD00011364 Saccharomyces\_cerevisiae 4932 Trp CCA  
-GAAGCGGTGGCTCAAT--GGT--AGAGCTTTCGACTCCAAATCGAAGG-----GTTGCAGGTTCAAATCCTGTCCGTTTCA---  
>tdbD00011368 Schizosaccharomyces\_pombe 4896 Trp CCA  
-GGCCCTTAAGTCAAGT--GGT--AGAGTGTGAGATTCAAATCTCAA---GTCAGTGTTCGAATCACGTCAGTGGGGTCA---  
>tdbD00011475 Takifugu\_rubripes 31033 Trp CCA  
-GACCTCGTGGCGCAAC--GGT--AGCGCGTCTGACTCCAGATCAGAAG-----GTTGCGTGTTCGAATCACGTCGGGGTCA---  
>tdbD00004704 Arabidopsis\_thaliana 3702 Glu CTC  
-TCCGTTGTAGTCTAGCT-GGTC-AGGATACTCGGCTCTCACCAGAG-----A-CCCGGGTTCGAGTCCCGGCAACGGAG---  
>tdbD00004716 Caenorhabditis\_elegans 6239 Glu CTC  
-TCCGTTGTGGTCTAGT--GGTT-AGGATTTATGGCTCTCACCATAAG-----G-CCGGGGTTCGATTCGCCGCAACGGAA---  
>tdbD00004719 Caenorhabditis\_elegans 6239 Glu TTC  
-TCCCATGTGGTCTAGT--GGTT-AGGATTCGTGGTTTTTACCACCGCG-----G-CCCGGGTTCGATTCGCCGTCAGGGAA---  
>tdbD00004723 Drosophila\_melanogaster 7227 Glu CTC  
-TCCCATATTTGCTAGT--GGTT-AGGATATCCGGCTCTCACCAGGAG-----G-CCCGGGTTCGAATTCGCCGTATGGGAA---  
>tdbD00004725 Drosophila\_melanogaster 7227 Glu TTC  
-TCCCATATGGTCTAGT--GGCT-AGGATATCTGGCTTTCACCAGAG-----G-CCCGGGTTCGATTCGCCGTATGGGAA---  
>tdbD00004883 Gallus\_gallus 9031 Glu TTC  
-GTCCCTTTTCTCCAGT--GGTT-AGGACATCGTCTTTTTCATGTGCAAG-----A-CACGGGTTTCGATTCGCCGTAAGGGATA---  
>tdbD00004694 Homo\_sapiens 9606 Glu CTC  
-TCCCTGGTGGTCTAGT--GGTT-AGGATTCGGCGCTCTCACCAGCG-----G-CCCGGGTTCGATTCGCCGTCAGGGAA---  
>tdbD00004906 Pan\_troglodytes 9598 Glu CTC  
-TCCCTGGTGGTCTAGT--GGTT-AGGATTCGGCGCTCTCACCAGCG-----G-CCCGGGTTCGATTCGCCGTCAGGGAA---  
>tdbD00004914 Pan\_troglodytes 9598 Glu TTC  
-TCCCTGGTGGTCTAGT--GGCT-AGGATTCGGCGCTCTCACCAGCG-----G-CCCGGGTTCGATTCGCCGTCAGGGAA---  
>tdbD00004915 Pan\_troglodytes 9598 Glu TTC  
-TCCCATATGGTCTAGC--GGTT-AGGATTCCTGGTTTTTACCAGGCG-----G-CCCGGGTTCGACTCCCGGTATGGGAA---  
>tdbD00004916 Pan\_troglodytes 9598 Glu TTC  
-TCCCATATGGTCTAGC--GGTT-AGGATTCCTGGTTTTTACCAGGCG-----G-CCCGGGTTCGACTCCCGGTATGGGAA---  
>tdbD0000658 Rattus\_norvegicus 10116 Glu CTC  
-TCCCTGGTGGTCTAGT--GGTT-AGGATTCGGCGCTCTCACCAGCG-----G-CCCGGGTTCGATTCGCCGTCAGGGAA---  
>tdbD0000644 Saccharomyces\_cerevisiae 4932 Glu TTC  
-TCCGATATAGTGTAAC--GGCT-ATCACATCACGCTTTCACCGTGGAG-----A-CCGGGGTTCGACTCCCGGTATCGGAG---  
>tdbD00004720 Saccharomyces\_cerevisiae 4932 Glu CTC  
-TCCGATGATGTGTAAC--GGCT-ATCACATCACGCTTTCACCGTGGAG-----A-CCGGGGTTCGACTCCCGGTATCGGAG---  
>tdbD00004721 Saccharomyces\_cerevisiae 4932 Glu TTC  
-TCCGATATAGTGTAAC--GGCT-ATCACATCACGCTTTCACCGTGGAG-----A-CCGGGGTTCGACTCCCGGTATCGGAG---  
>tdbD00004722 Saccharomyces\_cerevisiae 4932 Glu TTC  
-TCCGATATAGTGTAAC--GGCT-ATCACATCACGCTTTCACCGTGGAG-----A-CCGGGGTTCGACTCCCGGTATCGGAG---  
>tdbD00004726 Schizosaccharomyces\_pombe 4896 Glu CTC  
-TCCGTCATGGTCCAGT--GGCT-AGGATTCATCGCTCTCACCAGTGG-----G-CGGGGGTTTCGATTCGCCCTGACGGAG---  
>tdbD00004727 Schizosaccharomyces\_pombe 4896 Glu TTC  
-TCCGTTGTGGTCCAAC--GGCT-AGGATTCGTGCTTTCACCGACGCG-----G-TCGGGGTTTCGACTCCCGGCAACGGAG---  
>tdbD00004891 Takifugu\_rubripes 31033 Glu CTC  
-TCCCTGGTGGTCTAGT--GGTT-AGGATTCGGCGCTCTCACCAGCG-----G-CCCGGGTTCGATTCGCCGTCAGGGAA---  
>tdbD00004901 Takifugu\_rubripes 31033 Glu TTC  
-TCCCATATGGTCTAGC--GGTT-AGGATTCCTGGTTTTTACCAGGCG-----G-CCCGGGTTCGACTCCCGGTATGGGAA---  
>tdbD00008615 Caenorhabditis\_elegans 6239 Gln CTG  
-GGTTCCATGGTGTAGC--GGTT-AGCACTCAGGACTTCAATCCTGCG-----A-CCCAGGTTCAAATCTCGGTGGGACCT---  
>tdbD00008620 Caenorhabditis\_elegans 6239 Gln TTG  
-GGTTCCATGGTGTAGC--GGTT-AGCACTCAGGACTTGAATCCTGCG-----A-CCCAGGTTCAAATCTCGGTGGGACCT---  
>tdbD00008628 Drosophila\_melanogaster 7227 Gln CTG  
-GGTTCCATGGTGTAAAT--GGTT-AGCACTCTGACTCTGAATCCAGCG-----A-TCCAGGTTCAAATCTCGGTGGGACCT---

>tdbD00008776 Gallus\_gallus 9031 Gln CTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGAACCT---  
>tdbD00008778 Gallus\_gallus 9031 Gln TTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGGACCT---  
>tdbD00002405 Homo\_sapiens 9606 Gln CTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGAACCT---  
>tdbD00002407 Homo\_sapiens 9606 Gln TTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGGACCT---  
>tdbD00008597 Homo\_sapiens 9606 Gln CTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGAACCT---  
>tdbD00008600 Homo\_sapiens 9606 Gln TTG  
-TAGGACTTGGTGTAAT--GGGT-AGCACAGAGAATTTGGATTCTCAG-----G-GGTGGGTTCAATTCCTTTTCGTCCTA----  
>tdbD00008605 Homo\_sapiens 9606 Gln TTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGGACCT---  
>tdbD00002392 Leptomonas\_collosoma 5686 Gln CTG  
-GCTCCTATAGTGTAGC--GGTT-ATCACCTCGGACTCTGAATCCGATA-----A-CCCTGGTTCGAGTCCAGGTAGGAGTG---  
>tdbD00002393 Leptomonas\_seymouri 5684 Gln CTG  
-GCTCCTATAGTGTAGC--GGTT-ATCACCTCGGACTCTGAATCCGATA-----A-CCCTGGTTCGAGTCCAGGTAGGAGTG---  
>tdbD00008793 Pan\_troglodytes 9598 Gln CTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAGTCTCGGTGGAACCT---  
>tdbD00008794 Pan\_troglodytes 9598 Gln CTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGAACCT---  
>tdbD00008799 Pan\_troglodytes 9598 Gln TTG  
-GGCCCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGGACCT---  
>tdbD00008800 Pan\_troglodytes 9598 Gln TTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCA-----A-TCCGAGTTCAATCTCGGTGGGACCT---  
>tdbD00008801 Pan\_troglodytes 9598 Gln TTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGGACCT---  
>tdbD00002400 Rattus\_norvegicus 10116 Gln CTG  
-GGTCCATGGTGTAAT--GGTG-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGGACCT---  
>tdbD00002403 Rattus\_norvegicus 10116 Gln CTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGAACCT---  
>tdbD00002399 Rattus\_norvegicus 10116 Gln TTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCA-----A-TCTGAGTTCAAATCTCGGTGGGACCT---  
>tdbD00002402 Rattus\_norvegicus 10116 Gln TTG  
-GGTCTCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCG-----A-TCCGAGTTTCGAGTCTCGGTGAGGCCT---  
>tdbD00002404 Rattus\_norvegicus 10116 Gln TTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGGACCT---  
>tdbD00008621 Saccharomyces\_cerevisiae 4932 Gln CTG  
-GGTCTATAGTGTAGT--GGTT-ATCACTTTCGGTCTGTATCCGAACA-----A-CCCGAGTTCAATCCGGGTGGGACC---  
>tdbD00008623 Saccharomyces\_cerevisiae 4932 Gln TTG  
-GGTCTATAGTGTAGT--GGTT-ATCACTTTCGGTCTGTATCCGGACA-----A-CCCGGTTCAATCCGGGTAGGACCT---  
>tdbD00008633 Schizosaccharomyces\_pombe 4896 Gln TTG  
-GGTTGTATGGTGTAAT--GGTT-AGCACGTGAGATTTTGATTCTCGAG-----A-CCTGGGTTTCGATCCAGTACGACCT---  
>tdbD00008782 Takifugu\_rubripes 31033 Gln CTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTCTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGAACCT---  
>tdbD00008786 Takifugu\_rubripes 31033 Gln TTG  
-GGTCCATGGTGTAAT--GGTT-AGCACTCTGGACTTTGAATCCAGCG-----A-TCCGAGTTCAAATCTCGGTGGGACCT---  
>tdbD00002381 Trypanosoma\_brucei 5691 Gln TTG  
-GGTCTATAGTGTAGT--GGTT-ATCACTTCGGACTTTGAATCCGAAA-----A-CCCGAGTTCAATCCTGGTAGGACCA---  
>tdbD00009125 Caenorhabditis\_elegans 6239 Arg ACG  
-GGCCGCTGGCGCAAT--GGAT-AACGCGTCTGCCTACGGAGCAGAAG-----ATTGCAGTTTCGAATCCTGCCGTGGTTCG---  
>tdbD00009134 Caenorhabditis\_elegans 6239 Arg TCG  
-GGCCGCTGGCGCAAT--GGAT-AAGGCACCAGACTTCGAATCTGGGG-----ATTGCAGTTTCGAGTCTCGCCGTGGTTCG---  
>tdbD00009136 Caenorhabditis\_elegans 6239 Arg TCT  
-GGCCTGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCTAATCAGAAG-----ATTGCAGTTTCGACCCCTGCCTGGGTCA---  
>tdbD00009144 Drosophila\_melanogaster 7227 Arg ACG  
-GGTCTGTGGCGCAAT--GGAT-AACGCGTCTGACTACGGATCAGAAG-----ATTCCAGTTTCGACTCCTGGCAGGATCG---  
>tdbD00009148 Drosophila\_melanogaster 7227 Arg TCG  
-GACCGTGTGGCCTAAT--GGAT-AAGGCGTCTGGACTTCGGATCCGAAG-----ATTGCAGTTTCGAGTCTGTACGGTTCG---  
>tdbD00009149 Drosophila\_melanogaster 7227 Arg TCG  
-GACCGTGTGGCCTAAT--GGAT-AAGGCGTCTGGACTTCGGATCCGAAG-----ATTGCAGTTTCGAATCCTGTACGGTTCG---  
>tdbD00002598 Drosophila\_simulans 7240 Arg TCG  
-GACCGTGTGGCCCAAT--GGAT-AAGGCGTCTGGACTTCGGATCCGAAG-----ATTGCAGTTTCGAGTCTGTACGGTTCG---  
>tdbD00009082 Homo\_sapiens 9606 Arg ACG  
-GGGCCAGTGGCGCAAT--GGAT-AACGCGTCTGACTACGGATCAGAAG-----ATTCTAGTTTCGACTCCTGGCTGGCTCG---  
>tdbD00009083 Homo\_sapiens 9606 Arg ACG  
-GGGCCAGTGGCGCAAT--GGAT-AACGCGTCTGACTACGGATCAGAAG-----ATTCCAGTTTCGACTCCTGGCTGGCTCG---  
>tdbD00009088 Homo\_sapiens 9606 Arg CCT  
-GCCCCAGTGGCGCAAT--GGAT-AAGGCACTGGCCTCCTAAGCCAGGG-----ATTGTGGGTTTCGAGTCCCACCTGGGGT---  
>tdbD00009092 Homo\_sapiens 9606 Arg TCG  
-GACCACTGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCGGATCAGAAG-----ATTGAGGTTTCGAATCCCTTCGTGGTT---  
>tdbD00009099 Homo\_sapiens 9606 Arg TCT  
-GGTCTGTGGCGCAAT--GGAT-AGCGATTGGACTTCTAATCAAAG-----GTTGTGGGTTTCGAGTCCCACCAGAGTC---  
>tdbD00009552 Pan\_troglodytes 9598 Arg ACG



-GGGCCAGTGGCGCAAT--GGAT-AACGCGTCTGACTACGGATCAGAAG-----ATTCTAGGTTTCGACTCCTGGCTGGCTCG---  
>tdbD00009553 Pan\_troglodytes 9598 Arg ACG  
-GGGCCAGTGGCGCAAT--GGAT-AACGCGTCTGACTACGGATCAGAAG-----ATTCCAGGTTTCGACTCCTGGCTGGCTCG---  
>tdbD00009564 Pan\_troglodytes 9598 Arg TCG  
-GACCGCGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCGGATCAGAAG-----ATTGAGGGTTTCGAGTCCCTTCGTGGTTCG---  
>tdbD00009569 Pan\_troglodytes 9598 Arg TCT  
-GGCTCTGTGGCGCAAT--GGAT-AGCGCATTGGACTTCTAATTCAAAG-----GTTGTGGGTTTCGAGTCCCACCAGAGTCG---  
>tdbD00009572 Pan\_troglodytes 9598 Arg TCT  
-GGTCCGTGGCGCAAT--GGAT-AGCGCATTGGACTTCTAATTCAAAG-----GTTCCGGGTTTCGAGTCCCAGCGGAGTCG---  
>tdbD00002586 Saccharomyces\_cerevisiae 4932 Arg TCT  
-GCTCGCGTGGCGTAAT--GGC--AACGCGTCTGACTTCTAATCAGAAG-----ATTATGGGTTTCGACCCCCATCGTGAGTG---  
>tdbD00009140 Saccharomyces\_cerevisiae 4932 Arg ACG  
-TTCCTCGTGGCCCAAT--GGTC-ACGGCGTCTGGCTACGAACCAGAAG-----ATTCCAGGTTCAAGTCTGGCGGGGAAG---  
>tdbD00009142 Saccharomyces\_cerevisiae 4932 Arg CCT  
-GTTCCGTGGCGTAAT--GGT--AACGCGTCTCCCTCCTAAGGAGAAG-----ACTGCGGGTTTCGAGTCCCGTACGGAACG---  
>tdbD00009143 Saccharomyces\_cerevisiae 4932 Arg TCT  
-GCTCGCGTGGCGTAAT--GGC--AACGCGTCTGACTTCTAATCAGAAG-----ATTATGGGTTTCGACCCCCATCGTGAGTG---  
>tdbD00009153 Schizosaccharomyces\_pombe 4896 Arg ACG  
-GGTCTCGTGGCCCAAT--GGTT-AAGGCGCTTACTACGGATCAAGAG-----ATTCCAGGTTTCGACTCCTGGCGGGATCG---  
>tdbD00009526 Takifugu\_rubripes 31033 Arg ACG  
-GGGCCAGTGGCGCAAT--GGAT-AACGCGTCTGACTACGGATCAGAAG-----ATTCTAGGTTTCGACTCCTGGCTGGCTCG---  
>tdbD00009527 Takifugu\_rubripes 31033 Arg ACG  
-GGGCCAGTGGCGCAAT--GGAT-AACGCGTCTGACTACGGATCAGAAG-----ATTCCAGGTTTCGACTCCTGGCTGGCTCG---  
>tdbD00009529 Takifugu\_rubripes 31033 Arg CCG  
-GACCCAGTGGCCTAAT--GGAT-AAGGCATCAGCCTCCGGAGCTGGGG-----ATTGTGGGTTTCGAGTCCCATCTGGGTCG---  
>tdbD00009534 Takifugu\_rubripes 31033 Arg CCT  
-GCCCCAGTGGCCTAAT--GGAT-AAGGCACTGGCCTCCTAAGCCAGGG-----ATTGTGGGTTTCGAGTCCCATCTGGGGTG---  
>tdbD00009541 Takifugu\_rubripes 31033 Arg TCG  
-GACCGCGTGGCCTAAT--GGAT-AAGGCGTCTGACTTCGGATCAGAAG-----ATTGAGGGTTTCGAGTCCCTTCGTGGTTCG---  
>tdbD00009547 Takifugu\_rubripes 31033 Arg TCT  
-GGCTCTGTGGCGCAAT--GGAT-AGCGCATTGGACTTCTAATTCAAAG-----GTTGTGGGTTTCGAGTCCCACCAGAGTCG---  
>tdbD00002579 Trypanosoma\_brucei 5691 Arg ACG  
-GTCCGTGTGGCTCAAT--GGA--AGAGCATCTGACTACGGATCAGAGG-----GTTGCAGGTTTCGAATCCTGTTCACGGATG---  
>tdbD00009846 Arabidopsis\_thaliana 3702 Ser AGA  
-GTGGAAGTGGCCGAGT--GGTT-ATCGGGCATGACTAGAAATCATGTGGGC----TTT-----GCCCGCGCAGGTTTCGAATCCTGCCGTTACCG---  
>tdbD00009847 Arabidopsis\_thaliana 3702 Ser AGA  
-GTGGACGTGGCCGAGT--GGTT-ATCGGGCATAACTAGAAATCATGTGGGC----TTT-----GCCCGCGCAGGTTTCGAATCCTGCCGTTACCG---  
>tdbD00009848 Arabidopsis\_thaliana 3702 Ser AGA  
-GTGGACGTGGCCGAGT--GGTT-ATCGGGCATGACTAGAAATCATGTGGGT----TTT-----GCCCGCGCAGGTTTCGAATCCTGCCGTTACCG---  
>tdbD00009879 Caenorhabditis\_elegans 6239 Ser GCT  
-GATCAGGTGGCCGAGT--GGTT-AAGGCGATGGACTGCTAATCCATTGGGG----TTT-----CCCCGCGTAGGTTTCGAATCCTCATCTGATCG---  
>tdbD00009883 Caenorhabditis\_elegans 6239 Ser TGA  
-GCTGCGATGTCCGAGT--GGTT-AAGGAGTTGGACTTGAAATCCAAATGGGC----ATT-----GCCCGCGTAGGTTTCGAACCTGCTCGCAGCG---  
>tdbD00009884 Caenorhabditis\_elegans 6239 Ser TGA  
-GCAACGATGTCCGAGT--GGTT-AAGGAGATGGACTTGAAATCCATTGGGG----TTT-----GCCCGCGTAGGTTTCGATTCTGCTCGTTGCG---  
>tdbD00009892 Drosophila\_melanogaster 7227 Ser AGA  
-GCAGTCGTGGCCGAGT--GGTT-AAGGCGTCTGACTAGAAATCAGATTCCC----TCT-----GGGAGCGTAGGTTTCGAATCCTACCGACTGCG---  
>tdbD00009894 Drosophila\_melanogaster 7227 Ser CGA  
-GCAGTCGTGGCCGAGT--GGTT-AAGGCGTCTGACTCGAAATCAGATTCCC----TCT-----GGGAGCGTAGGTTTCGAATCCTACCGCTGCG---  
>tdbD00002906 Drosophila\_simulans 7240 Ser CGA  
-GCAGTCGTGGCCGAGT--GGTT-AAGGCGTCTGACTCGAAATCAGATTCCC----TCT-----GGGAGCGTAGGTTTCGAATCCTACCGCTGCG---  
>tdbD00010245 Gallus\_gallus 9031 Ser TGA  
-GCAGCGATGGCCGAGT--GGTT-AAGGCGTGGACTTGAAATCCAATGGGG----TCT-----CCCCGCGCAGGTTTCGAACCTGCTCGCTGCG---  
>tdbD00002912 Homo\_sapiens 9606 Ser AGA  
-GTAGTCGTGGCCGAGT--GGTT-AAGGCGATGGACTAGAAATCCAATGGGG----TCT-----CCCCGCGCAGGTTTCGAATCCTGCCGACTACG---  
>tdbD00009827 Homo\_sapiens 9606 Ser AGA  
-GTAGTCGTGGCCGAGT--GGTT-AAGGCGATGGACTAGAAATCCAATGGGG----TTT-----CCCCACGCAGGTTTCGAATCCTGCCGACTACG---  
>tdbD00009828 Homo\_sapiens 9606 Ser AGA  
-GTAGTCGTGGCCGAGT--GGTT-AAGGCGATGGACTAGAAATCCAATGGGG----TCT-----CCCCGCGCAGGTTTCGAATCCTGCCGACTACG---  
>tdbD00009829 Homo\_sapiens 9606 Ser AGA  
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>tdbD00010273 Pan\_troglodytes 9598 Ser AGA  
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>tdbD00010283 Pan\_troglodytes 9598 Ser GCT  
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>tdbD00010289 Pan\_troglodytes 9598 Ser TGA  
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>tdbD00002880 Saccharomyces\_cerevisiae 4932 Ser TGA  
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>tdbD00009887 Saccharomyces\_cerevisiae 4932 Ser AGA  
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>tdbD00009888 Saccharomyces\_cerevisiae 4932 Ser CGA  
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>tdbD00009889 Saccharomyces\_cerevisiae 4932 Ser GCT  
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>tdbD00009890 Saccharomyces\_cerevisiae 4932 Ser TGA  
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>tdbD00009899 Schizosaccharomyces\_pombe 4896 Ser AGA  
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>tdbD00009900 Schizosaccharomyces\_pombe 4896 Ser CGA  
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>tdbD00009902 Schizosaccharomyces\_pombe 4896 Ser TGA  
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>tdbD00009903 Schizosaccharomyces\_pombe 4896 Ser TGA  
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>tdbD00010263 Takifugu\_rubripes 31033 Ser GCT  
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>tdbD00002900 Triticum\_aestivum 4565 Ser TGA  
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>tdbD00010505 Caenorhabditis\_elegans 6239 Thr AGT  
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>tdbD00010512 Caenorhabditis\_elegans 6239 Thr TGT  
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>tdbD00010518 Drosophila\_melanogaster 7227 Thr AGT  
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>tdbD00003092 Homo\_sapiens 9606 Thr TGT  
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>tdbD00010479 Homo\_sapiens 9606 Thr AGT  
-GGTCCGTTGGCTTAGCT--GGTT-AAAGCGCTGTCTAGTAAACAGGAG-----ATCCTGGGTTTCAATCCCAGCGGGGCCT---  
>tdbD00010491 Homo\_sapiens 9606 Thr TGT  
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>tdbD00010811 Pan\_troglodytes 9598 Thr AGT  
-GGCGCGTGGCTTAGCT--GGTT-AAAGCGCTGTCTAGTAAACAGGAG-----ATCCTGGGTTTCAATCCCAGCGGTGCCT---  
>tdbD00010813 Pan\_troglodytes 9598 Thr AGT  
-GGTCCGTTGGCTTAGCT--GGTT-AAAGCGCTGTCTAGTAAACAGGAG-----ATCCTGGGTTTCAATCCCAGCGGGGCCT---  
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>tdbD00010822 Pan\_troglodytes 9598 Thr TGT  
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>tdbD00010823 Pan\_troglodytes 9598 Thr TGT  
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>tdbD00010824 Pan\_troglodytes 9598 Thr TGT  
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>tdbD00010825 Pan\_troglodytes 9598 Thr TGT  
-GGTCCATAGCTCAGT--GGTT-AGAGCACTGGTCTGTGTAACCAGGG-----GTCGCGAGTTTCAATCCTGCTGGGGCCT---  
>tdbD00003081 Saccharomyces\_cerevisiae 4932 Thr TGT  
-GCCTCCTTAGCTTAGT--GGT--AGAGCGTTCACCTGTAATGCAAAG-----GTCGCTAGTTTCAATCCTGGCAGGTGGCA---  
>tdbD00010513 Saccharomyces\_cerevisiae 4932 Thr AGT  
-GCTTCTATGGCCAAGTT--GGT--AAGGCGCCACACTAGTAAATGTGGAG-----ATCATCGGTTTCAATCCGATTGGAAGCA---  
>tdbD00010514 Saccharomyces\_cerevisiae 4932 Thr CGT  
-GCCCTTTGGCCAAGT--GGT--AAGGCATCGCACTCGTAATGCGGGG-----ATCGTGGGTTTCAATCCCACAGAGGGCA---  
>tdbD00010516 Saccharomyces\_cerevisiae 4932 Thr TGT  
-GCCTCCTTAGCTTAGT--GGT--AGAGCGTTCACCTGTAATGCAAAG-----GTCGCTAGTTTCAATCCTGGCAGGTGGCA---  
>tdbD00010524 Schizosaccharomyces\_pombe 4896 Thr CGT

-GCTCTTGTAGCTCAGT--GGT--AGAGCGCCTGTCTCGTAAACAGGAG-----GTCCAGTGTTCGAGTCACTGCCGGAGCA---  
>tdbD00010794 Takifugu rubripes 31033 Thr AGT  
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>tdbD00010800 Takifugu rubripes 31033 Thr CGT  
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>tdbD00010804 Takifugu rubripes 31033 Thr TGT  
-GGTCCATAGCTCAGG--GGTT--AGAGCACTGGTCTTGTAAACAGGG-----GTCCGAGTTCAAATCTCGTGGGGCCT---  
>tdbD00010807 Takifugu rubripes 31033 Thr TGT  
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>tdbD00008234 Caenorhabditis\_elegans 6239 Pro AGG  
-GGTCTAGTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGGGATCGATCCCAGGCTCAGCCC---  
>tdbD00008245 Caenorhabditis\_elegans 6239 Pro TGG  
-GGCGAATGGTCTAGT--GGT--ATGATTCTCGCTTTGGGTGCAGAG-----GTCCCGGGTTCATCCCAGGTTCCGGCCC---  
>tdbD00008259 Drosophila\_melanogaster 7227 Pro TGG  
-GGTCAATGGTCTAGG--GGT--ATGATTCTCGCTTTGGGTGCAGAG-----GTCCCGGGTTCAAATCCCAGGTTGAGCCC---  
>tdbD00002249 Gallus\_gallus 9031 Pro CGG  
-GGTCTGGTCTAGG--GGT--ATGATTCTCGCTTCGGGTGCAGAG-----GTCCCGGGTTCAAATCCCAGGACGAGCCC---  
>tdbD00008453 Gallus\_gallus 9031 Pro AGG  
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>tdbD00008455 Gallus\_gallus 9031 Pro CGG  
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>tdbD00008456 Gallus\_gallus 9031 Pro TGG  
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>tdbD00008215 Homo\_sapiens 9606 Pro CGG  
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>tdbD00002251 Mus\_musculus 10090 Pro AGG  
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>tdbD00002250 Mus\_musculus 10090 Pro CGG  
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>tdbD00008473 Pan\_troglodytes 9598 Pro AGG  
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>tdbD00008475 Pan\_troglodytes 9598 Pro CGG  
-GGTCTGGTCTAGG--GGT--ATGATTCTCGCTTCGGGTGCAGAG-----GTCCCGGGTTCAAATCCCAGGACGAGCCC---  
>tdbD00008478 Pan\_troglodytes 9598 Pro TGG  
-GGTCTGGTCTAGG--GGT--ATGATTCTCGCTTTGGGTGCAGAG-----GTCCCGGGTTCAAATCCCAGGACGAGCCC---  
>tdbD00008479 Pan\_troglodytes 9598 Pro TGG  
-GGTCTGGTCTAGG--GGT--ATGATTCTCGGTTTGGGTCCGAGAG-----GTCCCGGGTTCAAATCCCAGGACGAGCCC---  
>tdbD00008480 Pan\_troglodytes 9598 Pro TGG  
-GGTCTGGTCTAGT--GGT--ATGATTCTCGCTTTGGGTGCAGAG-----GTCCCGGGTTCAAATCCCAGGACGAGCCC---  
>tdbD00002244 Phaseolus\_vulgaris 3885 Pro AGG  
-GGCATTTGGTCTAGT--GGT--ATGATTCTCGCTTAGGGTGCAGAG-----GTCCCGAGTTCAATTTCTCGGAATGCCCC---  
>tdbD00002243 Phaseolus\_vulgaris 3885 Pro TGG  
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>tdbD00002252 Rattus\_norvegicus 10116 Pro CGG  
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>tdbD00002240 Saccharomyces\_cerevisiae 4932 Pro TGG  
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>tdbD00008248 Saccharomyces\_cerevisiae 4932 Pro TGG  
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>tdbD00008260 Schizosaccharomyces\_pombe 4896 Pro AGG  
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>tdbD00008460 Takifugu rubripes 31033 Pro AGG  
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>tdbD00008464 Takifugu rubripes 31033 Pro CGG  
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>tdbD00008467 Takifugu rubripes 31033 Pro TGG  
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>tdbD00005331 Arabidopsis\_thaliana 3702 Gly TCC  
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>tdbD00005343 Caenorhabditis\_elegans 6239 Gly TCC  
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>tdbD00000972 Homo\_sapiens 9606 Gly TCC  
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>tdbD00005321 Homo\_sapiens 9606 Gly TCC  
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>tdbD00005322 Homo\_sapiens 9606 Gly TCC  
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>tdbD00000967 Mus\_musculus 10090 Gly TCC  
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>tdbD00005633 Pan\_troglodytes 9598 Gly CCC  
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>tdbD00005645 Pan\_troglodytes 9598 Gly TCC  
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>tdbD00005646 Pan\_troglodytes 9598 Gly TCC  
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>tdbD00000958 Phaseolus\_vulgaris 3885 Gly TCC  
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>tdbD00000968 Rattus\_norvegicus 10116 Gly TCC  
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>tdbD00000951 Saccharomyces\_cerevisiae 4932 Gly GCC  
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>tdbD00005347 Saccharomyces\_cerevisiae 4932 Gly GCC  
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>tdbD00005618 Takifugu\_rubripes 31033 Gly CCC  
-GCGCCGCTGGTGTAGT--GGT--ATCATGCAAGATTCCCATTCTTTCGCG-----A-CCCGGGTTTCGATTCCCGGGCGGCGCA---  
>tdbD00005628 Takifugu\_rubripes 31033 Gly TCC  
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>tdbD00005728 Drosophila\_melanogaster 7227 His GTG  
-GCCGTGATCGTCTAGT--GGTT-AGGACCCACGTTGTGGCCGTGGTA-----A-CCCAGGTTTCGAATCCTGGTTCACGGCA---  
>tdbD00005717 Homo\_sapiens 9606 His GTG  
-GCCGTGATCGTCTAGT--GGTT-AGTACTCTGCGTTGTGGCCGAGCA-----A-CCTCGGTTTCGAATCCGAGTTCACGGCA---  
>tdbD00005839 Pan\_troglodytes 9598 His GTG  
-GCCGTGATCGTCTAGT--GGTT-AGTACTCTGCGTTGTGGCCGAGCA-----A-CCTCGGTTTCGAATCCGAGTTCACGGCA---  
>tdbD00001112 Saccharomyces\_cerevisiae 4932 His GTG  
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>tdbD00005727 Saccharomyces\_cerevisiae 4932 His GTG  
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>tdbD00005729 Schizosaccharomyces\_pombe 4896 His GTG  
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>tdbD00004462 Arabidopsis\_thaliana 3702 Asp GTC  
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>tdbD00004465 Caenorhabditis\_elegans 6239 Asp GTC  
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>tdbD00004470 Drosophila\_melanogaster 7227 Asp GTC  
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>tdbD00004580 Gallus\_gallus 9031 Asp GTC  
-TCCTCGTGTAGTATAGT--GGTG-AGTATCCCCTGCTCAGCGGGAG-----A-CCCGGGTTTCGATTCCCCGACGGGGAG---  
>tdbD00000506 Glycine\_max 3847 Asp GTC  
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>tdbD00004457 Homo\_sapiens 9606 Asp GTC  
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>tdbD00000510 Mus\_musculus 10090 Asp GTC  
-TCCTCGTGTAGTATAGT--GGTG-AGTATCCCCTGCTCAGCGGGAG-----A-CCCGGGTTTCGATTCCCCGACGGGGAG---  
>tdbD00004595 Pan\_troglodytes 9598 Asp GTC  
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>tdbD00004596 Pan\_troglodytes 9598 Asp GTC  
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>tdbD00000511 Rattus\_norvegicus 10116 Asp GTC  
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>tdbD00004467 Saccharomyces\_cerevisiae 4932 Asp GTC  
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>tdbD00004588 Takifugu\_rubripes 31033 Asp GTC  
-TCCTCGTGTAGTATAGT--GGTG-AGTATCCCCTGCTCAGCGGGAG-----A-CCCGGGTTTCGATTCCCCGACGGGGAG---  
>tdbD00006210 Caenorhabditis\_elegans 6239 Lys CTT  
-GCCCGGTTAGCTCAGTC-GGT--AGAGCACCAGACTCTTAATCTGGTT-----GTCGCGGGTTTCGAGCCCCGATTGGGCT---  
>tdbD00001470 Drosophila\_melanogaster 7227 Lys CTT  
-GCCCGGTTAGCTCAGTC-GGT--AGAGCATGAGACTCTTAATCTCAGG-----GTCGTTGGTTTCGAGCCCCACGTTGGGCG---  
>tdbD00006217 Drosophila\_melanogaster 7227 Lys CTT  
-GCCCGGTTAGCTCAGTC-GGT--AGAGCATGAGACTCTTAATCTCAGG-----GTCGTTGGTTTCGAGCCCCACGTTGGGCG---  
>tdbD00006219 Drosophila\_melanogaster 7227 Lys TTT  
-GCCCGGTTAGCTCAGTC-GGT--AGAGCATGAGACTCTTAATCCAAGG-----GTCCAGGGTTTCAGTCCCTGTTCCGGCG---  
>tdbD00006388 Gallus\_gallus 9031 Lys CTT

-GCCCCGGCTAGCTCAGTC-GGT--AGAGCATGAGACTCTTAATCTCAGG-----GTCGTGGGTTTCGAGCCCCACGTTGGGCG---  
>tdbD00001479 Homo\_sapiens 9606 Lys CTT  
-GCCCCGGCTAGCTCAGTC-GGT--AGAGCATGAGACTCTTAATCTCAGG-----GTCGTGGGTTTCGAGCCCCACGTTGGGCG---  
>tdbD00001478 Homo\_sapiens 9606 Lys TTT  
-GCCCCGGATAGCTCAGTC-GGT--AGAGCATCAGACTTTTAATCTGAGG-----GTCCAGGGTTCAAGTCCCTGTTCCGGGCG---  
>tdbD00006183 Homo\_sapiens 9606 Lys CTT  
-GCCCCGGCTAGCTCAGTC-GGT--AGAGCATGAGACTCTTAATCTCAGG-----GTCGTGGGTTTCGAGCCCCACGTTGGGCG---  
>tdbD00006184 Homo\_sapiens 9606 Lys CTT  
-GCCCCGGCTAGCTCAGTC-GGT--AGAGCATGGGACTCTTAATCCCAGG-----GTCGTGGGTTTCGAGCCCCACGTTGGGCG---  
>tdbD00006193 Homo\_sapiens 9606 Lys TTT  
-GCCCCGGATAGCTCAGTC-GGT--AGAGCATCAGACTTTTAATCTGAGG-----GTCCAGGGTTCAAGTCCCTGTTCCGGGCG---  
>tdbD00001476 Mus\_musculus 10090 Lys CTT  
-GCCCCGGCTAGCTCAGTC-GGT--AGAGCATGAGACTCTTAATCTCAGG-----GTCGTGGGTTTCGAGCCCCACGTTGGGCG---  
>tdbD00006415 Pan\_troglodytes 9598 Lys CTT  
-GCCCCGGCTAGCTCAGTC-GGT--AGAGCATGAGACTCTTAATCTCAGG-----GTCGTGGGTTTCGAGCCCCACGTTGGGCG---  
>tdbD00006416 Pan\_troglodytes 9598 Lys CTT  
-GCCCCGGCTAGCTCAGTC-GGT--AGAGCATGGGACTCTTAATCCCAGG-----GTCGTGGGTTTCGAGCCCCACGTTGGGCG---  
>tdbD00006424 Pan\_troglodytes 9598 Lys TTT  
-GCCTGGATAGCTCAGTC-GGT--AGAGCATCAGACTTTTAATCTGAGG-----GTCCAGGGTTCAAGTCCCTGTTCCAGGCG---  
>tdbD00006425 Pan\_troglodytes 9598 Lys TTT  
-GCCCCGGATAGCTCAGTC-GGT--AGAGCATCAGACTTTTAATCTGAGG-----GTCCAGGGTTCAAGTCCCTGTTCCGGGCG---  
>tdbD00006426 Pan\_troglodytes 9598 Lys TTT  
-GCCTGGATAGCTCAGTC-GGT--AGAGCATCAGACTTTTAATCTGAGG-----GTCCAGGGTTCAAGTCCCTGTTCCAGGCA---  
>tdbD00001477 Rattus\_norvegicus 10116 Lys CTT  
-GCCCCGGCTAGCTCAGTC-GGT--AGAGCATGAGACTCTTAATCTCAGG-----GTCGTGGGTTTCGAGCCCCACGTTGGGCG---  
>tdbD00001464 Saccharomyces\_cerevisiae 4932 Lys CTT  
-GCCTTGTGGCGCAATC-GGT--AGCGCGTATGACTCTTAATCATAAG-----GTTAGGGGTTTCGAGCCCCCTACAGGGCT---  
>tdbD00001463 Saccharomyces\_cerevisiae 4932 Lys TTT  
-TCCTTGTAGCTCAGTC-GGT--AGAGCGTTCGGCTTTTAACCGAAAT-----GTCAGGGGTTTCGAGCCCCCTATGAGGAG---  
>tdbD00006214 Saccharomyces\_cerevisiae 4932 Lys CTT  
-GCCTTGTGGCGCAATC-GGT--AGCGCGTATGACTCTTAATCATAAG-----GTTAGGGGTTTCGAGCCCCCTACAGGGCT---  
>tdbD00006215 Saccharomyces\_cerevisiae 4932 Lys TTT  
-TCCTTGTAGCTCAGTC-GGT--AGAGCGTTCGGCTTTTAACCGAAAT-----GTCAGGGGTTTCGAGCCCCCTATGAGGAG---  
>tdbD00006216 Saccharomyces\_cerevisiae 4932 Lys TTT  
-TCCTTGTAGCTCAGTC-GGT--AGAGCGTTCGGCTTTTAACCGAAAT-----GTCAGGGGTTTCGAGCCCCCTATGAGGAG---  
>tdbD00006221 Schizosaccharomyces\_pombe 4896 Lys CTT  
-TCCCAGTGGCTCAATC-GGTTTAGAGCGTCTGACTCTTAATCAGAAG-----GTTGCGAGTTCGAGTCTCGCCTGGGAG---  
>tdbD00006222 Schizosaccharomyces\_pombe 4896 Lys CTT  
-TCCCAGTGGCTCAATC-GGTTTAGAGCGTCTGACTCTTAATCAGAAG-----GTTGCGAGTTCGAGTCTCGCCTGGGAG---  
>tdbD00006223 Schizosaccharomyces\_pombe 4896 Lys CTT  
-TCCCAGTGGCTCAATC-GGTTTAGAGCGTCTGACTCTTAATCAGAAG-----GTTGCGAGTTCGAGTCTCGCCTGGGAG---  
>tdbD00006396 Takifugu\_rubripes 31033 Lys CTT  
-GCCCCGGCTAGCTCAGTC-GGT--AGAGCATGAGACTCTTAATCTCAGG-----GTCGTGGGTTTCGAGCCCCACGTTGGGCG---  
>tdbD00007908 Caenorhabditis\_elegans 6239 Asn GTT  
-GCTCCGTGGCGCAATA-GGC--AGCGCGTTCGGCTGTTAACCGAAAG-----GTTGGTGGTTCGAGCCCACCCGGGAGCG---  
>tdbD00007912 Drosophila\_melanogaster 7227 Asn GTT  
-GCCTCCGTGGCGCAATT-GGTT-AGCGCGTTCGGCTGTTAACCGAAAG-----GTTGGTGGTTCGAGTCCACCCGGGGGCG---  
>tdbD00002084 Homo\_sapiens 9606 Asn GTT  
-GTCTCTGTGGCGCAATC-GGTT-AGCGCGTTCGGCTGTTAACCGAAAG-----ATTGGTGGTTCGAGCCCACCCAGGGACG---  
>tdbD00007893 Homo\_sapiens 9606 Asn GTT  
-GTCTCTGTGGCGCAATG-GGTT-AGCGCGTTCGGCTGTTAACCGAAAG-----GTTGGTGGTTCGAGCCCATCCAGGGACG---  
>tdbD00007894 Homo\_sapiens 9606 Asn GTT  
-GTCTCTGTGGCGCAATC-GGTT-AGCGCGTTCGGCTGTTAACCGAAAG-----GTTGGTGGTTCGAGCCCACCCAGGGACG---  
>tdbD00007895 Homo\_sapiens 9606 Asn GTT  
-GTCTCTGTGGCGCAATC-GGTT-AGCGCGTTCGGCTGTTAACCGAAAG-----ATTGGTGGTTCGAGCCCACCCAGGGACG---  
>tdbD00007896 Homo\_sapiens 9606 Asn GTT  
-GTCTCTGTGGCGCAATC-GGTT-AGCGCGTTCGGCTGTTAACCGAAAG-----GTTGGTGGTTCGAGCCCACCCAGGGACG---  
>tdbD00008059 Pan\_troglodytes 9598 Asn GTT  
-GTCTCTGTGGCGCAATG-GGTT-AGCGCGTTCGGCTGTTAACCGAAAG-----GTTGGTGGTTCGAGCCCACCCAGGGACG---  
>tdbD00008060 Pan\_troglodytes 9598 Asn GTT  
-GTCTCTGTGGCGCAATC-GGTT-AGCGCGTTCGGCTGTTAACCGAAAG-----GTTGGTGGTTCGAGCCCACCCAGGGACG---  
>tdbD00007909 Saccharomyces\_cerevisiae 4932 Asn GTT  
-GACTCCATGGCCAAGTT-GGTT-AAGGCGTGCAGACTGTTAATCGCAAG-----ATCGTGAGTTCAACCTCACTGGGGTTCG---  
>tdbD00007914 Schizosaccharomyces\_pombe 4896 Asn GTT  
-GGTCCGGTAGCATAGTT-GGTT-ATGCGCAGACTGTTAATCGTGAG-----GTCGAGGGTTCGAGTCCCTCCCTGACCG---  
>tdbD00008050 Takifugu\_rubripes 31033 Asn GTT  
-GTCTCTGTGGCGCAATC-GGTT-AGCGCGTTCGGCTGTTAACCGAAAG-----GTTGGTGGTTCGAGCCCACCCAGGGACG---  
>tdbD00002082 Xenopus\_laevis 8355 Asn GTT  
-GTCTCTGTGGCGCAATC-GGTT-AGCGCGTTCGGCTGTTAACCGAAAG-----GTTGGTGGTTCGAGCCCACCCAGGGACG---  
>tdbD00004999 Arabidopsis\_thaliana 3702 Phe GAA  
-GCGGGGATAGCTCAGTT-GGG--AGAGCGTTCAGACTGAAGATCTGAAG-----GTCGCGTGTTCGATCCACGCTCACCAGCA---  
>tdbD00005011 Drosophila\_melanogaster 7227 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTTCAGACTGAAGATCTAAAG-----GTCCCGGTTCAATCCCGGGTTTCGGCA---  
>tdbD00005119 Gallus\_gallus 9031 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTTCAGACTGAAGATCTAAAG-----GTCCCGGTTTCGATCCCGGGTTTCGGCA---

>tdbD00004997 Homo\_sapiens 9606 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTTAGACTGAAGATCTAAAG-----GTCCCTGGTTTCGATCCC GGTTTCGGCA---  
>tdbD00005134 Pan\_troglodytes 9598 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTTAGACTGAAGATCTAAAG-----GTCCCTGGTTCAATCCC GGTTTCGGCA---  
>tdbD00005135 Pan\_troglodytes 9598 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTTAGACTGAAGATCTAAAG-----GTCCCTGGTTTCGATCCC GGTTTCGGCA---  
>tdbD00005006 Saccharomyces\_cerevisiae 4932 Phe GAA  
-GCGGATTTAGCTCAGTT-GGG--AGAGCGCCAGACTGAAGATCTGGAG-----GTCCCTGTGTTTCGATCCACAGAAATTCGCA---  
>tdbD00005007 Saccharomyces\_cerevisiae 4932 Phe GAA  
-GCGGATTTAGCTCAGTT-GGG--AGAGCGCCAGACTGAAGATCTGGAG-----GTCCCTGTGTTTCGATCCACAGAAATTCGCA---  
>tdbD00005008 Saccharomyces\_cerevisiae 4932 Phe GAA  
-GCGGATTTAGCTCAGTT-GGG--AGAGCGCCAGACTGAAGATCTGGAG-----GTCCCTGTGTTTCGATCCACAGAAATTCGCA---  
>tdbD00005009 Saccharomyces\_cerevisiae 4932 Phe GAA  
-GCGGACTTAGCTCAGTT-GGG--AGAGCGCCAGACTGAAGATCTGGAG-----GTCCCTGTGTTTCGATCCACAGAGATTCGCA---  
>tdbD00005012 Schizosaccharomyces\_pombe 4896 Phe GAA  
-GTCGCAATGTGTAGTT-GGG--AGCATGACAGACTGAAGATCTGTTG-----GTCATCGGTTTCGATCCC GGTTTGTGACA---  
>tdbD00005013 Schizosaccharomyces\_pombe 4896 Phe GAA  
-GTCGCGATGTGTAGTT-GGG--AGCATGACAGACTGAAGATCTGTTG-----GTCATCGGTTTCGATCCC GGTTTCGTGACA---  
>tdbD00005126 Takifugu\_rubripes 31033 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTTAGACTGAAGATCTAAAG-----GTCCCTGGTTCAATCCC GGTTTCGGCA---  
>tdbD00005128 Takifugu\_rubripes 31033 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTTAGACTGAAGATCTAAAG-----GTCCCTGGTTTCGATCCC GGTTTCGGCA---  
>tdbD00000794 Xenopus\_laevis 8355 Phe GAA  
-GCCGAAATAGCTCAGTT-GGG--AGAGCGTTAGACTGAAGATCTAAAG-----GTCCCTGGTTTCGATCCC GGTTTCGGCA---  
>tdbD00003870 Arabidopsis\_thaliana 3702 Ala TGC  
-GGGGATGTAGCTCATAT-GGT--AGAGCGCTCGCTTTCGATGCGGAGAG-----GCACAGGGTTTCGATTCCTGCATCTCCA---  
>tdbD00003877 Caenorhabditis\_elegans 6239 Ala AGC  
-GGGGGTATAGCTCAGT--GGT--AGAGCGCTCCCTTAGCATGGGAGAG-----GGCTGGGGTTCAATCCCCATACCTCCA---  
>tdbD00003883 Caenorhabditis\_elegans 6239 Ala TGC  
-GGGGGTATAGCTCAGG--GGT--AGAGCGCTCGCTTTCGATGCGGAGAA-----GTCTGGGGTTTCGATTCCTCATACCTCCA---  
>tdbD00004057 Candida\_glabrata CBS\_138 284593 Ala TGC  
-GGGCACATGGCGCAGTT-GGT--AGCGCGTTCCTTGCAGGAAGAG-----GTCATCGGTTTCGATTCGGTTGCGTCCA---  
>tdbD00003887 Drosophila\_melanogaster 7227 Ala AGC  
-GGGGATGTAGCTCAGAT-GGT--AGAGCGCTCGCTTAGCATGTGAGAG-----GTACGGGGATCGATGCCCCGCATCTCCA---  
>tdbD00004099 Gallus\_gallus 9031 Ala TGC  
-GGGGATGTAGCTCAGC--GGT--AGAGCGCATGCTTTCGATGTATGAG-----GTCCCGGGTTCAATCCC CGGCATCTCCA---  
>tdbD00000234 Mus\_musculus 10090 Ala CGC  
-GGGGATGTAGCTCAGT--GGT--AGAGCGCATGCTTTCGATGTATGAG-----GCCCCGGGTTTCGATCCCCGGCATCTCCA---  
>tdbD00004122 Pan\_troglodytes 9598 Ala AGC  
-GGGGAATTAGCTCAAAT-GGT--AGAGCGCTCGCTTAGCATGCGGAGAG-----GTAGCGGGATCGATGCCCGCATCTCCA---  
>tdbD00004124 Pan\_troglodytes 9598 Ala AGC  
-GGGGATTAGCTCAAAT-GGT--AGAGCGCTCGCTTAGCATGCGGAGAG-----GTAGCGGGATCGATGCCCGCATCTCCA---  
>tdbD00004135 Pan\_troglodytes 9598 Ala CGC  
-GGGGATGTAGCTCAGT--GGT--AGAGCGCGCTTTCGATGTGTGAG-----GTCCCGGGTTCAATCCC CGGCATCTCCA---  
>tdbD00004136 Pan\_troglodytes 9598 Ala CGC  
-GGGGATGTAGCTCAGT--GGT--AGAGCGCATGCTTTCGATGTATGAG-----GCCCCGGGTTTCGATCCCCGGCATCTCCA---  
>tdbD00004137 Pan\_troglodytes 9598 Ala CGC  
-GGGGATGTAGCTCAGT--GGT--AGAGCGCATGCTTTCGATGTATGAG-----GTCCCGGGTTTCGATCCCCGGCATCTCCA---  
>tdbD00004140 Pan\_troglodytes 9598 Ala TGC  
-GGGGGTGTAGCTCAGT--GGT--AGAGCGCATGCTTTCGATGTATGAG-----GCCTCGGGTTTCGATCCCCGACACCTCCA---  
>tdbD00004141 Pan\_troglodytes 9598 Ala TGC  
-GGGGATGTAGCTCAGT--GGT--AGAGCGCATGCTTTCGATGTATGAG-----GCCCCGGGTTCAATCCC CGGCATCTCCA---  
>tdbD00004143 Pan\_troglodytes 9598 Ala TGC  
-GGGGATGTAGCTCAGT--GGT--AGAGCGCATGCTTTCGATGTATGAG-----GCCCCGGGTTTCGATCCCCGGCATCTCCA---  
>tdbD00004144 Pan\_troglodytes 9598 Ala TGC  
-GGGGATGTAGCTCAGT--GGT--AGAGCGCATGCTTTCGATGTATGAG-----GTCCCGGGTTTCGATCCCCGGCATCTCCA---  
>tdbD00000218 Saccharomyces\_cerevisiae 4932 Ala TGC  
-GGGCACATGGCGCAGTT-GGT--AGCGCGTTCCTTGCAGGAAGAG-----GTCATCGGTTTCGATTCGGTTGCGTCCA---  
>tdbD00003885 Saccharomyces\_cerevisiae 4932 Ala AGC  
-GGGCGTGTGGCGTAGTC-GGT--AGCGCGTTCCTTAGCATGGGAGAG-----GTCTCCGGTTTCGATTCGGACTCGTCCA---  
>tdbD00003886 Saccharomyces\_cerevisiae 4932 Ala TGC  
-GGGCACATGGCGCAGTT-GGT--AGCGCGTTCCTTGCAGGAAGAG-----GTCATCGGTTTCGATTCGGTTGCGTCCA---  
>tdbD00004102 Takifugu\_rubripes 31033 Ala AGC  
-GGGGAATTAGCTCAAAT-GGT--AGAGCGCTCGCTTAGCATGCGGAGAG-----GTAGCGGGATCGATGCCCGCATCTCCA---  
>tdbD00004103 Takifugu\_rubripes 31033 Ala AGC  
-GGGGATTAGCTCAAAT-GGT--AGAGCGCTCGCTTAGCATGCGGAGAG-----GTAGCGGGATCGATGCCCGCATCTCCA---  
>tdbD00004110 Takifugu\_rubripes 31033 Ala TGC  
-GGGGATGTAGCTCAGT--GGT--AGAGCGCATGCTTTCGATGTATGAG-----GCCCCGGGTTCAATCCC CGGCATCTCCA---

**Archaea - non redundant**

>WENV069866|AACY023786699|Marine microbial communities from Global Ocean Sampling (GOS)||124|45|Ile|GAT|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
 TGGGCTCGTAGCTCAGCTTGGCT--GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCATCTT  
 >SRA1008758|SRR020491.16741|Microbial community gene content and expression in the Central North Pacific Gyre, Station ALOHA, HOT186 (SRP001041)||25|99|Ile|GAT|0|0|||||  
 -GGGCTCGTAGCTCAGCTTGGCT--GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
 >ENV004148|DQ397552|Environmental sample from ENV division of INSDC||26558|26479|Ile|GAT|0|0|||||  
 ENV division in DDBJ/EMBL/GenBank|  
 TGGGCTCGTAGCTCAGCTTGGCT--GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCATCCG  
 >At0675|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|484321|484248|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCATAGCCCGGT--GGTGCACCCGGCTGATAACCGGGAG-----GTCATGCGTTTGAATCGCATCGGGCCCA----  
 >At1632|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|2609678|2609605|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCATAGCCAGGT--GGTGCACCCGGCTGATAACCGGGAG-----GTCATGCGTTTGAATCGCATCGGGCCCA----  
 >At1212|Mlab\_Z|Euryarchaeota|Methanocorpusculum labreanum Z|1674125|1674198|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCATAGCTAGGT--GGTGCACCCGGCTGATAACCGGGAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
 >At0977|Mbur\_DSM6242|Euryarchaeota|Methanococcoides burtonii DSM 6242|2383540|2383613|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCTTAGCTAGGT--GGAGCGCACGGCTGATAACCGTGAG-----GCCATGAGTTCGAATCTCATCGGGCCCA----  
 >At1421|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|3889984|3889908|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCTTAGCTTGGT--GGAGCGCACGGCTGATAACCGTGAG-----GTCCTGCGTTTGAATCGCAGCGGGCCACCA--  
 >At1505|Mmaz\_GOE1|Euryarchaeota|Methanosarcina mazei Go1|493238|493311|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCTTAGCTTGGT--GGAGCGCACGGCTGATAACCGTGAG-----GTCCTGCGTTTGAATCGCAGCGGGCCCA----  
 >At1446|Mbar\_FUSARO\_01|Euryarchaeota|Methanosarcina barkeri str. Fusaro|2435508|2435584|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCTTAGCTTGGT--GGAGCGCACGGCTGATAACCGTGAG-----GTCCTGCGTTTGAATCGCAGCGGGCCACCA--  
 >At1363|Mthe\_PT|Euryarchaeota|Methanosaeta thermophila PT|915515|915442|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCTCGTAGCTTAGCTTGGC--GGAGCGCACGGCTGATAACCGTGAG-----GTCACGCGTTTGAATCGCGTCGGGCCCA----  
 >At2079|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I|2821338|2821433|Ile|GAT|2821363|2821383|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCTTAGCCAGGTC--GGAGCGCTCGGCTGATAACCGAGAG-----GTCCTGCGTTTCAAATCGCAGCGGGCCCA----  
 >At0460|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|1079156|1079083|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCTTAGCTTGGT--AGAGCGTCCGGCTGATAACCGGAG-----GCCGTGGGTTCAAATCCCACCGGGCCCA----  
 >At0009|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|606038|606114|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCTCAGCTTGGT--AGAGCGCCCGGCTGATAACCGGGAG-----GTCGGGGGTTTGAATCCCCCGGGCCACCA--  
 >At0404|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|1163786|1163859|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCTTAGCTTGGT--GGAGCGCCCGGCTGATAACCGGGAG-----GTCGGGGGTTTGAATCCCCCGGGCCCA----  
 >At0106|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|1033612|1033688|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCTCAGCCCGGC--GGAGCGCCCGGCTGATAACCGGGAG-----GTCGGGGGTTTCAAATCCCCCGGGCCACCA--  
 >At0511|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|913775|913690|Ile|GAT|913737|913726|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCTTAGCTTGGT--GGAGCGCCCGGCTGATAACCGGGAG-----GTCACGGGTTCAAATCCCGTCGGGCCCA----  
 >At0528|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|936179|936268|Ile|GAT|936217|936232|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCTTAGCTTGGT--AGAGCGCCCGGCTGATAACCGGGAG-----GTCGGGGGTTTCAAGTCCCGCCGGGCCCA----  
 >At0179|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|1735237|1735150|Ile|GAT|1735198|1735186|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCCGTAGCTTAGCATGGTT--AGAGCGCCCGGCTGATAACCGGGAG-----GTCGAGGGTTCAAATCCCTCCGGGCCCA----  
 >ENV000759|AM114193|Environmental sample from ENV division of INSDC||961849|961928|Met|CAT|0|0|||||tRNA-Met(elongator).|ENV division in DDBJ/EMBL/GenBank|  
 TGGGGTGTAGCTTAGCCAGGTC--AGAGCGCCCGGCTCATAACCGGGCG-----GCCATGGGTTTGAATCCCTTCAACCCCATGAT  
 >At2064|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I|961850|961924|Met|CAT|0|0|||||The tRNA gene was obtained from SPLITSdb. tRNA-Met(Ile) whose CAU anticodon is enzymatically converted to read AUA codons.|GIB in DDBJ|  
 -GGGGTGTAGCTTAGCCAGGTC--AGAGCGCCCGGCTCATAACCGGGCG-----GCCATGGGTTTGAATCCCTTCAACCCCA----  
 >At1990|Taci\_DSM1728|Euryarchaeota|Thermoplasma acidophilum DSM 1728|341284|341210|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGGTGTAGCTTAGACAGGCT--ATAGCACTCGGCTGATAACCGAGAG-----GTCACCGGTTTGAATCCGGTCAACCCCA----  
 >At1471|Mbar\_FUSARO\_01|Euryarchaeota|Methanosarcina barkeri str. Fusaro|200979|200905|Met|CAT|0|0|||||The tRNA gene was obtained from SPLITSdb. tRNA-Met(Ile) whose CAU anticodon is enzymatically converted to read AUA codons.|GIB in DDBJ|  
 -GGGCCTAGCTCAGTCAGGTT--AGAGCGCTCGGCTCATAACCGAGCG-----GTCACCGGTTTCAAATCCGGTCAGGCCCA----  
 >At1396|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|4781878|4781952|Met|CAT|0|0|||||The tRNA gene was obtained from SPLITSdb. tRNA-Met(Ile) whose CAU anticodon is enzymatically converted





268073|268045||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTAGCTAGCTCAGCCAGGT--AGAGCACTCGGCTGATAACCGAGGG-----GTCGCCGGTTCAAATCCCGGCGGGCCACCA-  
>At0649|Aful\_DSM4304|Euryarchaeota|Archaeoglobus fulgidus DSM 4304|2024579|2024505|Met|CAT|0|0|0|||  
The tRNA gene was obtained from SPLITSdb. tRNA-Met(Ile) whose CAU anticodon is enzymatically  
converted to read AUA codons.|GIB in DDBJ|  
-GGGCCGTAGCTTAGCCAGGTC-AGAGCGCCCGGCTCATAACCGGGCG-----GTCGAGGGTTCAATCCCTCCGGGCCA----  
>At1270|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|2415125|2415199|Met|CAT|0|0|0|||The  
tRNA gene was obtained from SPLITSdb. tRNA-Met(Ile) whose CAU anticodon is enzymatically converted  
to read AUA codons.|GIB in DDBJ|  
-GGGCCGTAGCTTAGCTCAGGTC-AGAGCGCCCGGCTCATAACCGGGCG-----GTCGTTGGGTTCAATCCCTCCGGGCCA----  
>WENV078538|AAQK01000498|Gut microbiome of Human (healthy human stool sample 7)|2551|2475|Lys|TTT|  
0|0|0|||ENV division in DDBJ/EMBL/GenBank|  
-GGGCCGTAGCTCAGTCTGGC--AGAGCGCTTGGCTTTTAACCAAGCG-----GCCGCGGGTTCAAATCCCGTCGGGCCCGTTT-  
>At0906|Msmi\_ATCC35061|Euryarchaeota|Methanobrevibacter smithii ATCC 35061|878292|878219|Lys|TTT|0|  
0|||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTAGCTCAGTCTGGC--AGAGCGCTTGGCTTTTAACCAAGCG-----GCCGCGGGTTCAAATCCCGTCGGGCCCG----  
>At1660|Mthe\_DELTAH|Euryarchaeota|Methanothermobacter thermautotrophicus str. Delta H|954430|954503|  
Lys|TTT|0|0|0|||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTAGCTCAGTCTGGC--AGAGCGCTTGGCTTTTAACCAAGTG-----GTCGCGGGTTCAAATCCCGTCGGGCCCG----  
>At1587|Msta\_DSM3091|Euryarchaeota|Methanosphaera stadtmanae DSM 3091|1550305|1550232|Lys|TTT|0|  
0|||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTCGTAGCTCAGTCTGGG--AGAGCGCTGGCTTTTAACCAAGCG-----GTCGCGGGTTCAACTCCCGTCGGGCCCG----  
>At0940|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|863816|863889|Lys|TTT|0|  
0|||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTAGCTCAGTCTGGC--AGAGCGCTGGCTTTTAACCAAGTG-----GTCGAGGGTTCAAATCCCTTCGGGCCCG----  
>At1037|Maeo\_Nankai3|Euryarchaeota|Methanococcus aeolicus Nankai-3|1377817|1377744|Lys|TTT|0|0|0|||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTAGCTTAGTCTGGT--AGAGCGCTGACTTTTAATCAGGCG-----GTCGAGGGTTCGAATCCCTTCGGGCCCG----  
>ENV000788|AM114193|Environmental sample from ENV division of INSDC||2932335|2932259|Lys|TTT|0|  
0|||ENV division in DDBJ/EMBL/GenBank|  
-GGGCTCATAGCTCAGTTAGT--AGAGCGCTGGCTTTTAACCAAGCG-----GCCTGGGGTTCAAATCCCATGAGCCCGCTC-  
>At2108|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I|2932335|2932262|Lys|TTT|0|  
0|||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTCATAGCTCAGTTAGT--AGAGCGCTGGCTTTTAACCAAGCG-----GCCTGGGGTTCAAATCCCATGAGCCCG----  
>At1245|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|273652|273725|Lys|TTT|0|0|0|||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTCTATAGCTCAGTTAGT--AGAGCGCTGGCTTTTAACCAAGTG-----GTCGGGGTTCAAATCCCTTCGGGCCCG----  
>At1327|Mthe\_PT|Euryarchaeota|Methanoseta thermophila PT|23457|23544|Lys|TTT|23495|23508|||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTCGTAGCTCAGTTAGC--AGAGCGCTGGCTTTTAACCAAGTG-----GCCGAGGGTTCAAATCCCCCGAGCCCG----  
>At1596|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|66705|66778|Lys|TTT|0|0|0|||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTCGTAGCTCAGTTAGC--AGAGCGCTGGCTTTTAACCAAGTG-----GTCGGGGTTCAAATCCCTTCGAGCCCG----  
>At0691|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|2002199|2002126|Lys|TTT|0|0|0|||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTCGTAGCTCAGTTAGC--AGAGCGCTGGCTTTTAACCAAGTG-----GTCGGGGTTCAAATCCCTTCGGGCCCG----  
>At1753|Ptor\_DSM9790|Euryarchaeota|Picrophilus torridus DSM 9790|296263|296190|Lys|TTT|0|0|0|||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTCGTAGCTCAGTCTAGT--AGAGCGCTGGCTTTTAACCAAGCG-----GTCAGGGTTCAAATCCCTTCGGACCCG----  
>At0872|Hwal\_DSM16790|Euryarchaeota|Haloquadratum walsbyi|1077666|1077591|Lys|TTT|0|0|0|||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTGGTAGCTTAGATTGGCCAAAGCATCTGGCTTTTAACCAAGAGG-----ATCGAGGGTTCAAATCCCTCCGGGCCCG----  
>At0790|Hmar\_ATCC43049|Euryarchaeota|Haloarcula marismortui ATCC 43049|2650861|2650788|Lys|TTT|0|  
0|||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTAGCTCAGTCTAGC--AGAGCGCTGGCTTTTAACCAAGATG-----GTCGGGGTTCAAATCCCTCCGGGCCCG----  
>At0838|Halo\_NRC1|Euryarchaeota|Halobacterium sp. NRC-1|1882136|1882063|Lys|TTT|0|0|0|||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGATAGCTCAGCCGGC--AGAGCGTCTGGCTTTTAACCAAGAGC-----GTCGAGGGTTCAAATCCCTCTCGGCCCG----  
>At1691|Npha\_DSM2160|Euryarchaeota|Natronomonas pharaonis DSM 2160|560890|560963|Lys|TTT|0|0|0|||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGATAGCTCAGCCGGC--AGAGCGTCTGGCTTTTAACCAAGATG-----GTCGGGGTTCAAATCCCTCTCGGCCCG----  
>At1700|Npha\_DSM2160|Euryarchaeota|Natronomonas pharaonis DSM 2160|1789864|1789937|Lys|CTT|0|0|0|||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGATAGCTCAGCCGGC--AGAGCGTCTGGCTTTTAACCAAGAGC-----GTCGGGGTTCAAATCCCTCTCGGCCCG----  
>At1413|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|1509797|1509721|Lys|TTT|0|0|0|||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTAGCTCAGTCTAGC--AGAGCGACTGGCTTTTAACCAAGTGC-----GCCTAGGGTTCAAATCCCTACGGGCCCGCCA-  
>At1495|Mbar\_FUSARO\_01|Euryarchaeota|Methanosarcina barkeri str. Fusaro|4759576|4759500|Lys|TTT|0|  
0|||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTAGCTCAGTCTAGC--AGAGCGTCTGGCTTTTAACCAAGAGC-----GCCTAGGGTTCAAATCCCTACGGGCCCGCCA-  
>At0997|Mbur\_DSM6242|Euryarchaeota|Methanococcoides burtonii DSM 6242|1271469|1271393|Lys|TTT|0|  
0|||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTGTAGCTTAGTCTAGC--AGAGCGTCTGGCTTTTAACCAAGAGC-----GTCTAGGGTTCAAATCCCTACAAGCCCGCCA-  
>ENV000771|AM114193|Environmental sample from ENV division of INSDC||1654069|1653991|Lys|CTT|0|  
0|||ENV division in DDBJ/EMBL/GenBank|





>At0888|Msmi\_ATCC35061|Euryarchaeota|Methanobrevibacter smithii ATCC 35061|1105878|1105951|Arg|TCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCCTAGCT-GGAT-AGGGCGTCGGACTTCTAATCCGAAG-----ACCCCGGGTTCAAATCCCGCGGGTCCG----  
>At1663|Mthe\_DELTAH|Euryarchaeota|Methanothermobacter thermotrophicus str. Delta H|1181056|1181130|Arg|TCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCCTAGCAGGAT-AGGGCGTCGGACTTCTAATCCGAAG-----GTCCCGGGTTCAAATCCCGCGGGTCCG----  
>At1664|Mthe\_DELTAH|Euryarchaeota|Methanothermobacter thermotrophicus str. Delta H|1181154|1181228|Arg|CCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCCTAGCAGGAT-AGGGCATCAGACTCCTAATCTGAAG-----GTCCCGGGTTCAAATCCCGCGGGTCCG----  
>WENV078805|AAQL01000501|Gut microbiome of Human (healthy human stool sample 8)|5215|5293|Arg|CCT|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGGGCTGTAGCCTAGTCTGGGA--AGGGCGTAAGACTCCTAATCTTAAAG-----ATCGAGGGTTCAAATCCCTCCAAGTCCGTATT  
>At0889|Msmi\_ATCC35061|Euryarchaeota|Methanobrevibacter smithii ATCC 35061|1106013|1106086|Arg|CCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTGTAGCCTAGTCTGGGA--AGGGCGTAAGACTCCTAATCTTAAAG-----ATCGAGGGTTCAAATCCCTCCAAGTCCG----  
>At1593|Msta\_DSM3091|Euryarchaeota|Methanosphaera stadtmanae DSM 3091|1703847|1703773|Arg|CCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTTGTAGCCTAGTCTGGGA--AGGGCACAGACTCCTAATCTGGAG-----ACCGAGGGTTCAAATCCCTCCAATCCG----  
>At1288|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|1695747|1695673|Arg|CCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTGTGGCCTAGCCCGGAC-ATGGCGTCAGCCTCCTAAGCTGAAT-----GCCGGGGTTCAAATCCCCCAAGCCCG----  
>At1625|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|722724|722650|Arg|CCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGACGTGTGGCCTAGTCTGGGA--ATGGCGTCAGCCTCCTAAGCTGAAT-----GCCGGGGTTCAAATCCCTCCAAGTCCG----  
>At1428|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|5346094|5346020|Arg|CCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGCTGGCCTAGCCCGGAT-ATGGCGGCAGCCTCCTAAGCTGTAA-----ATCGGGGGTTCAAATCCCTTCGCGCCCG----  
>At1437|Mbar\_FUSARO\_01|Euryarchaeota|Methanosarcina barkeri str. Fusaro|704447|704521|Arg|CCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGCTGGCCTAGCCCGGAT-ATGGCGGCAGCCTCCTAAGCTGTAA-----ATCGGGGGTTCAAATCCCTTCGCGCCCG----  
>At0960|Mbur\_DSM6242|Euryarchaeota|Methanococcoides burtonii DSM 6242|38091|38168|Arg|CCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGCGTGTGGCCTAGCCAGGAT-ATGGCGGCAGCCTCCTAAGCTGTAA-----ATCAGGGTTCAAATCCCTTCACGCCGCCA-  
>At1777|Ptor\_DSM9790|Euryarchaeota|Picrophilus torridus DSM 9790|1323417|1323343|Arg|CCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGACGTTGGCCTAGCCTAGGAT-ATGGCAACAGCCTCCTAAGCTGTAG-----ATCGGGGGTTCAAATCCCTCGTGCCCG----  
>At1225|Mlab\_Z|Euryarchaeota|Methanocorpusculum labreanum Z|777608|777534|Arg|CCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGACATGTAGCCAAAGCCAGGAT-ATGGCATCAGCCTCCTAAGCTGAAG-----ATCTAGGGTTCGAATCCCTACATGCCCG----  
>At1594|Msta\_DSM3091|Euryarchaeota|Methanosphaera stadtmanae DSM 3091|1703981|1703907|Arg|TCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGCCCTGTAGCCTAGACTGGAT-AGGGCGTTGGACTTCTAATCCAAAG-----GCCGGGGTTCAAATCCCCCAGGTCCG----  
>At0607|Aful\_DSM4304|Euryarchaeota|Archaeoglobus fulgidus DSM 4304|367982|368055|Arg|CCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGACCCGTAGCCTAGC-AGGAC-AGGGCGTGGCCTCCTAAGCCCAAG-----GTCGCGGGTTCGAATCCCGCCGGGTCCG----  
>At1842|Pfur\_DSM3638|Euryarchaeota|Pyrococcus furiosus DSM 3638|1844702|1844779|Arg|TCG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGCCCGTGGCCTAGCCTAGGAT-AGGGCGTCGGCCTTCGGAGCCGAAG-----GTCCCGGGTTCAAATCCCGCCGGCCCGCCA-  
>At1932|Tkod\_KOD1|Euryarchaeota|Thermococcus kodakaraensis KOD1|1499113|1499190|Arg|TCG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTTGGCCTAGTCTGGAC-AGGGCGTCGGCCTTCGGAGCCGAAG-----GTCCCGGGTTCAAATCCCGCCGGCCCGCCA-  
>At1927|Tkod\_KOD1|Euryarchaeota|Thermococcus kodakaraensis KOD1|1240853|1240930|Arg|CCG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGCCCGTGGCCTAGTCTGGAC-AGGGCGTCGGCCTTCGGAGCCGAAG-----GTCGCGGGTTCGAATCCCGCCGGCCCGCCA-  
>At1824|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|1761997|1761923|Arg|TCG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTGGCCTAGTCTGGAG-AGGGCGTCGGCCTTCGGAGCCGAAG-----GTCGCGGGTTCAAATCCCGCCGGCCCG----  
>ENV000748|AM114193|Environmental sample from ENV division of INSDC|215564|215485|Arg|TCT|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGGGCTCGTGGCTTAGTCTAGGAT-ATAGCACCGCCTTCTAAGCCGGGG-----GTCGTTGGTTTCAAATCCACCGGGCCCGCTAA  
>At2085|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I|215563|215489|Arg|TCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTCGTGGCCTTAGTCTAGGAT-ATAGCACCGCCTTCTAAGCCGGGG-----GTCGTTGGTTTCAAATCCACCGGGCCCG----  
>At1015|Maeo\_Nankai3|Euryarchaeota|Methanococcus aeolicus Nankai-3|1029211|1029285|Arg|TCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTGGCCTAGTCTGGAT-ACGGCACCGCCTTCTAAGCCGGGG-----ATCGGGGGTTCAAATCCCTCTGGGTCCG----  
>At1172|Mvan\_SB|Euryarchaeota|Methanococcus vannielii SB|1376175|1376249|Arg|TCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTGGCCTAGTCTGGAT-ACGGCACCGCCTTCTAAGCCGGGG-----ATCGGGGGTTCAAATCCCTCCGGGTCCG----  
>At1071|Mmar\_C5|Euryarchaeota|Methanococcus maripaludis C5|1283171|1283094|Arg|TCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTGGCCTAGTCTGGAT-ACGGCACCGCCTTCTAAGCCGGGG-----ATCGGGGGTTCAAATCCCTCCGGGTCCG----  
>At1773|Ptor\_DSM9790|Euryarchaeota|Picrophilus torridus DSM 9790|1144489|1144415|Arg|TCT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTCGTGGCCTAGCCTAGGAT-AGGGCACCGTCTCTAAGTCTGGTG-----ATCGTTGGTTTCAAATCCACCGAGCCCG----

>At0970|Mbur\_DSM6242|Euryarchaeota|Methanococcoides burtonii DSM 6242|1631638|1631712|Arg|TCT|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTGGCTTAGCCAGGAT-ATAGCACCGGGCTTCTAACCCGGGG-----GTCGTGGGTTCAACTCCACCCGGGTCCG----  
>At1368|Mthe\_PT|Euryarchaeota|Methanosaeta thermophila PT|1457298|1457224|Arg|TCT|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTGGCTTAGCCAGGAT-ATAGCACCGGGCTTCTAACCCGGGG-----GTCGTGGGTTTCAGTCCCGCGGGTCCG----  
>At0926|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|358768|358845|Arg|TCT|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCCTAGCCTGGAT-AGGGCACCGGCCTTCTAAGCCGGGG-----GTCGGGGGTTCAAATCCCTCGGGTCCGCCA->ENV000784|AM114193|Environmental sample from ENV division of INSDC|2695132|2695211|Arg|CCT|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
TGGGGGGTGCCTTAGCCAGGAC-ATAGCGCCGGCCTCTAAGCCGGAT-----ACCGTGGGTTCAATCCACCTCGCCCGCTGG  
>At2077|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I|2695133|2695207|Arg|CCT|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTGGCTTAGCCAGGAT-ATAGCGCCGGCCTCTAAGCCGGAT-----ACCGTGGGTTCAATCCACCTCGCCCG----  
>At0396|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|1056248|1056322|Arg|TCT|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTGGCTTAGCCTGGAT-AGGGCGCCGGCCTTCTAAGCCGGAG-----ACCGGGGTTCAATCCCGCGGGCCCG----  
>At0415|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|1101838|1101742|Arg|CCT|1101799|1101778|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCCTAGCCAGGAT-AGGGCGCCGGCCTCTAAGCCGGAG-----ACCGGGGTTCAATCCCGCGGGCCCG----  
>At1815|Paby\_OR5AY|Euryarchaeota|Pyrococcus abyssi|1261400|1261323|Arg|CCT|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCCTAGCCAGGAC-AGGGCGCCGGCCTCTAAGCCGGAG-----GTCGGGGGTTCAAATCCCGCGGGTCCGCCA->At1852|Pfur\_DSM3638|Euryarchaeota|Pyrococcus furiosus DSM 3638|556240|556163|Arg|CCT|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCCTAGCCAGGAT-AGGGCGCCGGCCTCTAAGCCGGAG-----GTCGGGGGTTCAAATCCCGCGGGTCCGCCA->At0116|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|1612557|1612634|Arg|TCT|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCCTAGCCAGGAT-AGGGCGCCGGCCTCTAAGCCGGAG-----GTCGGGGGTTCAAATCCCGCGGGCCCGCCA->At2204|Ihos\_KIN4I|Crenarchaeota|Ignicoccus hospitalis KIN4/I|498947|499024|Arg|TCT|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTGCCTAGCCAGGAT-AGGGCGCCGGCCTCTAAGCCGGTA-----GTCCCGGTTCAAATCCCGCGGGGCCACCA->At0138|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|1277540|1277463|Arg|GCG|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGTCTAGCCAGGAT-AGGACGCGCCGCTCGGAGCCGGTA-----GTCGGGGGTTCAAATCCCGCGGGCCCGCCA->At2218|Ihos\_KIN4I|Crenarchaeota|Ignicoccus hospitalis KIN4/I|1289353|1289431|Arg|GCG|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTGGCTAGCCTGGACTAGGGCGCCGGCCTGCGGAGCCGGAG-----GTCCCGGTTCAAATCCCGCGGGGCCCGCCA->At0378|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|563835|563910|Arg|TCG|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCCTAGCCAGGAT-AGGGCGCCGGCCTCGGAGCCGGAG-----ACCGGGGTTCAAATCCCGCGGGCCCG---->At0413|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|911866|911771|Arg|GCG|911827|911807|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCCTAGCCTGGAT-AGGGCGCCGGCCTGCGGAGCCGGAG-----GCCCCGGTTCAAATCCCGCGGGCCCG---->At0374|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|394378|394452|Arg|CCG|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCCTAGCCAGGAA-AGGGCGCCGGCCTCCGGAGCCGGAG-----ATCCCGGTTCAAATCCCGCGGGCCCG---->At0137|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|1187274|1187197|Arg|TCG|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCCTAGCCAGGAT-AGGGCGCCGGCCTCGGAGCCGGAG-----GTCCGGGTTCAAATCCCGCGGGCCCGCCA->ENV004152|DQ397558|Environmental sample from ENV division of INSDC|41022|41101|Arg|GCG|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
CGGGCTCGTTGCATAGCATGGAT-AGTGCATCGCTTGCAGGCGATAG-----GTCGCCGGTTCAATCCGGTCCGGCCCGCACA>At0077|Csym|Crenarchaeota|Cenarchaeum symbiosum|168851|168777|Arg|GCG|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTCGTTGCATAGCATGGAT-AGTGCATCGCTTGCAGGCGATAG-----GTCGCCGGTTCAATCCGGTCCGGCCCG---->At0690|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|1923324|1923250|Arg|CCT|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCGAGTGGCTTAGTCCGGAT-AGAGCGTTAGCTCCTAAGCTAATG-----GTCGGGGGTTCAAATCCCCCTCGCCCG---->At0837|Halo\_NRC1|Euryarchaeota|Halobacterium sp. NRC-1|1838642|1838568|Arg|TCT|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCGGTAGCTCAGTCCGGAC-AGAGCGTTCGGCTTCTAACCGAAAT-----GTCGGGGGTTCAATCCCTCGTGCCCG---->At0849|Hwal\_DSM16790|Euryarchaeota|Haloquadratum walsbyi|1078863|1078937|Arg|TCG|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCGCTTAGCTCAGTTGGAC-AGAGTGCTTGGCTTCGGACCAAGCT-----GTCGGGGGTTCAAATCCTGCAGCGCCCA---->At1729|Npha\_DSM2160|Euryarchaeota|Natronomonas pharaonis DSM 2160|2172895|2172821|Arg|TCG|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCGCTTAGCTCAGTCTGGAC-AGAGTACTTGGCTTCGGACCAAGCT-----GTCGGGGGTTCAAATCCTGCAGCGCCCA---->At0798|Halo\_NRC1|Euryarchaeota|Halobacterium sp. NRC-1|463914|463988|Arg|TCG|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCGCTTAGCTCAGCTTGGAC-AGAGCACTTGGCTTCGGACCAAGAT-----GCCCGGGTTCAAATCCTGCAGCGCCCA---->At0752|Hmar\_ATCC43049|Euryarchaeota|Haloarcula marismortui ATCC 43049|1197384|1197458|Arg|TCG|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCGCTTAGCTCAGCTTGGAC-AGAGTGCTTGGCTTCGGACCAAAAC-----GTCGGGGGTTCAAATCCCTCAGCGCCCG----



>At1590|Msta\_DSM3091|Euryarchaeota|Methanosphaera stadmanae DSM 3091|1550685|1550611|Pro|TGG|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGACCATAGGGTAGCTTGGTCGATCCTTTGGGCTTTGGGAGCCTGAG-----A-CTCCGGTTCAAATCCGGGTGGTCCCA----  
 >At1657|Mthe\_DELTAH|Euryarchaeota|Methanothermobacter thermautotrophicus str. Delta H|954020|954094|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGACCATAGGGTAGCTTGGTCGATCCTTTGGGCTTTGGGAGCCTGAG-----A-CCCGGTTCAAATCCGGGTGGTCCCA----  
 >WENV078810|AAQL01000509|Gut microbiome of Human (healthy human stool sample 8)|943|864|Pro|TGG|0|0|0||||ENV division in DDBJ/EMBL/GenBank|  
 TGGGACCGTAGGGTAGCTTGGTCGATCCTTTGGGCTTTGGGAGCCTGAG-----A-CTCCGGTTCAAATCCGGGCGGTCCCATTTT  
 >At0909|Msmi\_ATCC35061|Euryarchaeota|Methanobrevibacter smithii ATCC 35061|878691|878617|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGACCGTAGGGTAGCTTGGTCGATCCTTTGGGCTTTGGGAGCCTGAG-----A-CTCCGGTTCAAATCCGGGCGGTCCCA----  
 >At1077|Mmar\_C5|Euryarchaeota|Methanococcus maripaludis C5|1517796|1517720|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCTGTGGGGTAGCTTGGTC-ATCCTTTGGGATTTGGGATCCTGAA-----A-CCCAGTTCGAATCTGGGAGGCCACCA----  
 >At1041|Maeo\_Nankai3|Euryarchaeota|Methanococcus aeolicus Nankai-3|1378374|1378297|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCTGTGGGGTAGCTTGGTCATCCTTTGGGATTTGGGATCCTGAG-----A-CCCAGTTCGAATCTGGGCAAGCCCACCA----  
 >At1164|Mvan\_SB|Euryarchaeota|Methanococcus vannielii SB|1127062|1127139|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCTGTGGGGTAGCTTGGTCATCCTTTGGGATTTGGGATCCTGAG-----A-CCCAGTTCGAATCTGGGAGGCCACCA----  
 >At0938|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|863570|863647|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCTGTGGGGTAGCTTGGTCATCCTTTGGGATTTGGGATCCTGAG-----A-CCCAGTTCGAATCTGGGAGGCCACCA----  
 >At1308|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|1640532|1640609|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCGGTGGGGTAGCTTGGTCATCCTTCCGGCTTTGGGGCCGGAG-----A-CCCGGTTCAAATCCGGGCGGCCACCA----  
 >At1953|Tkod\_KOD1|Euryarchaeota|Thermococcus kodakaraensis KOD1|1325061|1324984|Pro|GGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCGGTGGGGTAGCTTGGTCATCCTTCCGGCTTTGGGGCCGGAG-----A-CCCGGTTCAAATCCGGGCGGCCACCA----  
 >At1960|Tkod\_KOD1|Euryarchaeota|Thermococcus kodakaraensis KOD1|1727255|1727178|Pro|CGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCGGTGGGGTAGCTTGGTCATCCTTCCGGCTTTGGGGAGCCGGAG-----A-CCCGGTTCAAATCTGGGCGGCCACCA----  
 >At1787|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|507939|508015|Pro|GGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCGGTGGGGTAGCTTGG-CTATCCTCCGGCTTTGGGGCCGGTG-----A-CCCGGTTCAAATCCGGGCGGCCACCA----  
 >At1864|Pfur\_DSM3638|Euryarchaeota|Pyrococcus furiosus DSM 3638|1464211|1464134|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCGGTGGGGTAGCTTGGCCATCCTGCGGGCTTTGGGAGCCCGTG-----A-CCCGGTTCAAATCCGGGCGGCCACCA----  
 >At1870|Pfur\_DSM3638|Euryarchaeota|Pyrococcus furiosus DSM 3638|1831351|1831274|Pro|CGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCGGTGGGGTAGCTTGGCCATCCTGCGGGCTTTGGGAGCCCGTG-----A-CCCGGTTCAAATCCGGGCGGCCACCA----  
 >At1871|Phor\_OT3|Euryarchaeota|Pyrococcus horikoshii OT3|6125|6202|Pro|CGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCGGTGGGGTAGCTTGGCCATCCTGCGGGCTTTGGGGAGCCCGTG-----A-CCCGGTTCAAATCCGGGCGGCCACCA----  
 >At1779|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|4930|5007|Pro|CGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCGGTGGGGTAGCTTGGCCATCCTGCGGGCTTTGGGAGCCCGTG-----A-CCCGGTTCAAATCCGGGCGGCCACCA----  
 >At1789|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|578219|578296|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCGGTGGGGTAGCTTGGTCATCCTGCGGGCTTTGGGAGCCCGTG-----A-CCCGGTTCAAATCCGGGCGGCCACCA----  
 >At1929|Tkod\_KOD1|Euryarchaeota|Thermococcus kodakaraensis KOD1|1249406|1249483|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGCGGTGGGGTAGCTTGGTCATCCTGCGGGCTTTGGGAGCCCGTG-----A-CCCGGTTCAAATCCGGGCGGCCACCA----  
 >ENV000774|AM114193|Environmental sample from ENV division of INSDC||1806069|1806146|Pro|TGG|0|0|0||||ENV division in DDBJ/EMBL/GenBank|  
 -GGGACAATGGGGTAGCTTGGTCATCCTCGAGCGTTTGGGAGCCTTGG-----A-CCCAGTTCGAATCTGGGTGTCCCATAA----  
 >At2072|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I|1806069|1806143|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGACAATGGGGTAGCTTGGTCATCCTCGAGCGTTTGGGAGCCTTGG-----A-CCCAGTTCGAATCTGGGTGTCCCACCA----  
 >At1628|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|1184126|1184052|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGTAATAGGGTAGCTTGGTCATCCTCGAGCGTTTGGGAGCCTTGG-----A-CCGCGTTCGAATCTGGGTACCCCA----  
 >At1412|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|829936|829862|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGATAGTAGGGTAGCTTGGTCATCCTCGAGCGTTTGGGAGCCTTGG-----A-CCGCGTTCGAATCCGCGCTATCCCA----  
 >At0968|Mbur\_DSM6242|Euryarchaeota|Methanococcoides burtonii DSM 6242|1499488|1499564|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGATAGTAGGGTAGCTTGGTC-ATCCTCGAGCGTTTGGGAGCCTTGG-----A-CTCGGTTCAAATCCGCGCTATCCCACCA----  
 >At1351|Mthe\_PT|Euryarchaeota|Methanosarcina thermophila PT|1583822|1583896|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGACAGTAGGGTAGCTTGGTCATCCTCGAGCGTTTGGGAGCCTTGG-----A-CCGCGTTCGAATCCGCGCTGTCCCA----  
 >At0655|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|730470|730544|Pro|TGG|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GGGTAAGTAGGGTAGCTTGGTCATCCTAGAGCGTTTGGGAGCCTTGG-----A-CCGCGTTCGAATCCGCCCTACCCCA----

>At1253|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|1019514|1019588|Pro|TGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCAGTAGGGTAGCCTGGTCCATCCTAGAGCGTTGGGACGCTTTG-----A-CGGCAGTTCGAATCTGCCCTGCCCA---->At1205|Mlab\_Z|Euryarchaeota|Methanocorpusculum labreanum Z|1004827|1004901|Pro|TGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGTGGTAGGGTCCCTGGTCCATCCTAGAGCGTTGGGACGCTTTG-----A-CCCGAGTTCGAATCTGGGCCACCCCA---->ENV000787|AM114193|Environmental sample from ENV division of INSDC||2882933|2883012|Pro|CGG|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGGGATCGTGGGGTAGCCTGGTCCATCCTTCGCGTTCGGGACGGGAA-----A-CCTGAGTTCGAATCTCAGCGATCCACCAA>At2081|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I|2882934|2883011|Pro|CGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGATCGTGGGGTAGCCTGGTCCATCCTTCGCGTTCGGGACGGGAA-----A-CCTGAGTTCGAATCTCAGCGATCCACCAA->At1483|Mbar\_FUSARO\_01|Euryarchaeota|Methanosarcina barkeri str. Fusaro|1756181|1756107|Pro|CGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGACCGTAGGGTAGCTTGGTCCATCCTTCGCGTTCGGGACGGGAA-----A-CCTGAGTTCGAATCTCAGCGGTCCCA---->At1373|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|702737|702811|Pro|CGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGACCGTAGGGTAGCCTGGTCCATCCTTCGCGTTCGGGACGGGTA-----A-CCTGAGTTCGAATCTCAGCGGTCCCA---->At0697|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|2292778|2292704|Pro|CGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGTCGTGGGGTAGCCTGGACTATCCTATTGCGTTCGGGACGCAGTG-----A-CCTGAGTTCGAATCTCAGCGACCCCA---->At1233|Mlab\_Z|Euryarchaeota|Methanocorpusculum labreanum Z|1270034|1269960|Pro|CGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGTCGTGGGGTAGCCTGGACCATCCTATTACGTTTCGGGACGTAGTG-----A-CCTGAGTTCGAATCTCAGCGACCCCA---->At1356|Mthe\_PT|Euryarchaeota|Methanosarcina thermophila PT|495551|495477|Pro|CGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGTGTAGGGTAGCCTGGTCCATCCTACAGCGTTCGGGACGCTGTG-----A-CCTGAGTTCGAATCTCAGCAACCCCA---->At1262|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|1796583|1796656|Pro|CGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGTCGTGGGGTAGCCTGG-CCATCCTATGGCGTTCGGGACGTGTG-----A-CCTGAGTTCGAATCTCAGCGACCCCA---->At1642|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|3176723|3176649|Pro|CGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGTCGTGGGGTAGCCTGGACCATCCTAGGGCGTTCGGGACGCTGTG-----A-CCTGAGTTCGAATCTCAGCGACCCCA---->At0616|Aful\_DSM4304|Euryarchaeota|Archaeoglobus fulgidus DSM 4304|1006371|1006444|Pro|CGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCCGTGGGGTAGCCTGG-TGATCCTGCGGCGTTCGGGACGCGGTG-----A-CCCGAGTTCGAATCTCGGCGGCCCA---->At0645|Aful\_DSM4304|Euryarchaeota|Archaeoglobus fulgidus DSM 4304|1810428|1810355|Pro|TGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCCGTGGGGTAGCCTGG-TGATCCTGCGGCTTCGGGACGCGGTG-----A-CCCGAGTTCGAATCTCGGCGGCCCA---->At0665|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|2004798|2004871|Pro|GGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCCATAGGGTAGCCTGG-CCATCCTAGGAGACTGGGGTCTTCTG-----A-CTGCGTTCAAATCGCGATGGGCCCA---->At1272|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|270542|270469|Pro|GGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCCATAGGGTAGCCTGG-CCATCCTAGGAGACTGGGGTCTTCTG-----A-CCTGCGTTCAAATCGCGATGGGCCCA---->At1409|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|612549|612472|Pro|GGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCCGTAGGGTAGCTTGGTCCATCCTGCAAGGCTGGGGTCTTTCG-----A-CTTGAATTCGAATCTCAGCGGCCCCACCA->At1543|Mmaz\_GOE1|Euryarchaeota|Methanosarcina mazei Go1|2027573|2027496|Pro|GGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCCGTAGGGTAGCTTGGTCCATCCTGCAAGACTGGGGTCTTTCG-----A-CTTGAATTCGAATCTCAACGGCCCCACCA->At1004|Mbur\_DSM6242|Euryarchaeota|Methanococcoides burtonii DSM 6242|1810391|1810317|Pro|GGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCCGTAGGGTAGCCTGGTCCATCCTGCAAGGCTGGGGTCTTTCG-----A-CTTGAATTCGAATCTCAGCGGCCCA---->At0923|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|190832|190908|Pro|GGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCCGTGGGGTAGCCTGGA-TATCCTGTGCGCTGGGGGGCGTGCG-----A-CCCGGGTTCGAATCCCGCGGCCCCACCA->At1306|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|1499268|1499357|Pro|GGG|1499308|1499322|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCCGTGGGGTAGCCTGGTCTATCCTCCGCGGTGGGGGCCGCGGG-----A-CCCGGGTTCGAATCCCGCGGCCCCCA---->At1055|Mmar\_C5|Euryarchaeota|Methanococcus maripaludis C5|1672014|1672177|Trp|CCA|1672054|1672142|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGAGTATGGTGTAGCTTGGTCTATCATCGGGGACTCCAAATCCCTGG-----A-CCTGGGTTCGAATCCCGACTACTTCCA---->At1189|Mvan\_SB|Euryarchaeota|Methanococcus vannielii SB|1004623|1004459|Trp|CCA|1004583|1004494|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGAGTATAGTGTAGCTAGCCATCATCGGGGACTCCAAATCCCTGG-----A-CCTGGGTTCGAATCCCGACTACTTCCA---->At1043|Maeo\_Nankai3|Euryarchaeota|Methanococcus aeolicus Nankai-3|1449341|1449227|Trp|CCA|1449301|1449262|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGATATGGTGTAGCCTGGCCTATCATGGGGACTCCAAATCCCTAG-----A-CCTGGGTTCGAATCCCGACTACTTCCA---->At0945|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|1189945|1190055|Trp|CCA|1189985|1190017|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGTGTGGTGTAGCCAGGCTATCATCGGGGACTCCAGATCCCTGG-----A-CCTGGGTTCGAATCCCGACTACTTCCA---->At1854|Pfur\_DSM3638|Euryarchaeota|Pyrococcus furiosus DSM 3638|937515|937367|Trp|CCA|937475|937405|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCCGTGGTGTAGCCTGGTCCATCATCGGGGACTCCAGACCGCGG-----A-CCCGGGTTCGAATCCCGCGGCCCCACCA-



>At1816|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|1330624|1330476|Trp|CCA|1330584|1330514|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCGTGGTGTAGCCTGGTCTATCATCGCGGGCTCCAGACCCGCGG-----A-CCGGGTTCAAATCCCGCGCCCCACCA-  
>At1294|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|55068|55221|Trp|CCA|55108|55183|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCGCGTGGTGTAGCCTGGTCTATCATCGCGGGCTCCAGACCCGCGG-----A-CCCGGTTCAAATCCCGCGGGCCCCACCA-  
>ENV000778|AM114193|Environmental sample from ENV division of INSDC||2190428|2190350|Arg|TCG|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGGACTCGTGGGGTAGCCAGG-ATATCCTACCGGGCTTCGGACCCGCGG-----A-CCCGGTTCAAATCCCGCGAGTCCGCTGA  
>At2102|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I|2190427|2190354|Arg|TCG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGACTCGTGGGGTAGCCAGG-ATATCCTACCGGGCTTCGGACCCGCGG-----A-CCCGGTTCAAATCCCGCGAGTCCG-----  
>At1417|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|3031244|3031151|Arg|TCG|3031205|3031186|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTCGTGGGGTAGCCAGG-ATATCCTAATGGGCTTCGAACCCATTG-----A-CTCGTGTTCGAATCCCGCGGGCCCCG-----  
>At1492|Mbar\_FUSARO\_01|Euryarchaeota|Methanosarcina barkeri str. Fusaro|3995529|3995436|Arg|TCG|3995490|3995471|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTCGTAGGGTAGCCAGG-ATATCCTAATGGGCTTCGAACCCATTG-----A-CTCGTGTTCGAATCCCGCGGGCCCCG-----  
>At0963|Mbur\_DSM6242|Euryarchaeota|Methanococcoides burtonii DSM 6242|436719|436814|Arg|TCG|436758|436779|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTCGTAGGGTAGCCAGG-ACATCCTCATGGGCTTCGAACCCATTG-----A-CCCGGTTCAAATCCCGCGGGCCCCG-----  
>At1751|Ptor\_DSM9790|Euryarchaeota|Picropilus torridus DSM 9790|201417|201344|Arg|TCG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCGGTGGGGTAGTTAGG-ACATCCTGTGGCCTTCGAAGCCGAGG-----A-CCCGGTTCAAATCCCGCGGGCCCCG-----  
>ENV004189|DQ397615|Environmental sample from ENV division of INSDC||7356|7432|Pro|CGG|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
-GGGGACGTGGGTTAGCTTGG--TATACTGCCAGCCTCGGGCGCTGGAG-----ATCATGGGTTCAAATCCCATCGTCCCCATGC-  
>ENV004240|DQ397865|Environmental sample from ENV division of INSDC||24228|24150|Pro|CGG|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGGGGACGTGGGTTAGCTTGG--TATACTGCCAGCCTCGGGCGCTGGAG-----ATCATGGGTTCAAATCCCATCGTCCCCATGAA  
>At0070|Csym|Crenarchaeota|Cenarchaeum symbiosum|1706771|1706844|Pro|CGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGACGTGGGTTAGCTTGG--TATACTGCCAGCCTCGGGCGCTGGAG-----ATCATGGGTTCAAATCCCATCGTCCCCA-----  
>ENV004145|DQ397546|Environmental sample from ENV division of INSDC||7290|7366|Pro|TGG|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
-GGGACCGTAGTCTAGCTTGG-C-ATGATTCTGGTTTTGGGTACCAGAG-----GCCGAGGTTCAAATCCTGCCGGTCCCACCA-  
>ENV004166|DQ397575|Environmental sample from ENV division of INSDC||24123|24200|Pro|GGG|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
-GGGACCGTCTAGCTTGG--CCATGATGCTAGCCTGGGGTGTAGAG-----GTCCGAGGTTCAAATCCTGCCGGTCCCACCA-  
>At0552|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|914044|913951|Pro|GGG|914004|913987|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGACCGTCTAGCTTGG--T-AGGATGCCAGCCTGGGGCGCTGGTG-----GTCCCGGTTCAAATCCCGCGGGTCCCACCA-----  
>At0040|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|1161734|1161620|Pro|GGG|1161695|1161659|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCGTCTAGCTTGG--CTAGGATGCCAGCCTGGGGCGCTGGTG-----GTCCCGGTTCAAATCCCGCGGGCCCCACCA-  
>At0112|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|1171412|1171523|Pro|GGG|1171450|1171484|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCGTCTAGCTTGG--C-AGGATGCCAGCCTGGGGCGCTGGTG-----GTCCCGGTTCAAATCCCGCGGGCCCCACCA-  
>At0579|Tpen\_HRK5|Crenarchaeota|Thermophilum pendens Hrk 5|643667|643802|Pro|GGG|643693|643705||643743|643769|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCGTCTAGCTTGG--T-AGGATGCCAGCCTGGGGCGCTGGTG-----GTCCCGGTTCAAATCCCGCGGGCCCCACCA-  
>At0433|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|1096644|1096740|Pro|GGG|1096684|1096704|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCGTCTAGCTTGG--GACTAGGATGCCAGCCTGGGGCGCTGGTG-----GTCCCGGTTCAAATCCCGCGGGCCCCA-----  
>At0178|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|1724960|1724864|Pro|GGG|1724920|1724900|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCGTCTAGCTTGG--ATTAGGATGCCAGCCTGGGGCGCTGGTG-----GTCCCGGTTCAAATCCCGCGGGCCCCA-----  
>At0441|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|48109|48034|Pro|TGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCGTCTAGCTTGG--GACTAGGATGCCAGCCTGGGGCGCTGGTG-----GTCCCGGTTCAAATCCCGCGGGCCCCA-----  
>At0203|Paer\_IM2|Crenarchaeota|Pyrobaculum aerophilum str. IM2|1798211|1798301|Pro|GGG|1798250|1798265|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCGTCTAGCTTGG--T-AGGATGCCAGCCTGGGGCGCTGGTG-----ATCCCGGTTCAAATCCCGCGGGCCCCA-----  
>At0321|Pcal\_JCM11548|Crenarchaeota|Pyrobaculum calidifontis JCM 11548|1601212|1601090|Pro|GGG|1601128|1601113|1601173|1601145|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCGTCTAGCTTGG--CTAGGATGCCAGCCTGGGGCGCTGGTG-----ATCCCGGTTCAAATCCCGCGGGCCCCACCA-  
>At0183|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|2052864|2052789|Pro|TGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCGTCTAGCTTGG--T-AGGATGCCAGCCTGGGGCGCTGGTG-----ATCCCGGTTCAAATCCCGCGGGCCCCA-----  
>At0467|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|48739|48814|Pro|TGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCGTCTAGCTTGG--GACTAGGACGCCAGCCTGGGGCGCTGGTG-----ATCCCGGTTCAAATCCCGCGGGCCCCA-----  
>At0535|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|2105122|2105197|Pro|TGG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGCGTCTAGCTTGG--GACTAGGACGCCAGCCTGGGGCGCTGGTG-----GTCCGAGGTTCAAATCCCGCGGGCCCCA-----





>At0754|Hmar\_ATCC43049|Euryarchaeota|Haloarcula marismortui ATCC 43049|1355959|1356033|Val|GAC|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTTCTGGTCTAGGTCGGT-TATGACACCTCCTTGACATGGAGGAG-----GCCGGCGGTTCAAATCCGCCGGAACCCA----  
>At1722|Npha\_DSM2160|Euryarchaeota|Natronomonas pharaonis DSM 2160|1599658|1599584|Val|GAC|0|0||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTTCTGGTCTAGGTCGGT-TATGACACCTCCTTGACATGGAGGAG-----GCCGGCAGTTCAAATCTGCCGGAACCCA----  
>At0753|Hmar\_ATCC43049|Euryarchaeota|Haloarcula marismortui ATCC 43049|1302449|1302523|Val|CAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTTGGTGATCTAGTTCGGT-TATGATACCTCCTTACACGGAGGAA-----GTCGGCGGTTCAATCCGCCGGAACCCA----  
>At1717|Npha\_DSM2160|Euryarchaeota|Natronomonas pharaonis DSM 2160|1240239|1240165|Val|CAC|0|0|0||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTTCTGGTCTAGGTCGGT-TATGACACCTCCTTACACGGAGGAA-----GCCGGCGGTTCAAATCCGCCGGAACCCA----  
>At0862|Hwal\_DSM16790|Euryarchaeota|Haloquadratum walsbyi|2554497|2554571|Val|CAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTTGGTGGTCTAGCCCGG-TATGACGGCTCCTTACACGGAGCAG-----GTCGGCGGTTCAATCCGCCGGAACCCA----  
>At0830|Halo\_NRC1|Euryarchaeota|Halobacterium sp. NRC-1|1154096|1154022|Val|CAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTTCTGGTCTAGTCCGGT-TATGACGGCTCCTTACACGGAGCAG-----GTCGGCGGTTCAACTCCGCCGGAACCCA----  
>At0758|Hmar\_ATCC43049|Euryarchaeota|Haloarcula marismortui ATCC 43049|2063268|2063341|Val|TAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTTCTGGTCTAGT-TGGT-TATGACGTCGCTTACAAGGCGGAG-----GCCGGTGGTTCAATCCGCCGGAACCCA----  
>At0819|Halo\_NRC1|Euryarchaeota|Halobacterium sp. NRC-1|103431|103358|Val|TAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTTCTGGTCTAGT-TGGT-TATGACGTCGCTTACAAGGCGGAG-----GTCGGTGGTTCAATCCGCCGGAACCCA----  
>ENV004176|DQ397587|Environmental sample from ENV division of INSDC|25831|25908|Val|TAC|0|0|0||||  
ENV division in DDBJ/EMBL/GenBank|  
-GGGTCATAGTCCAGTTCGGT-CATGACGTCGCCCTTACACGGCGAAG-----ATCCGGGTTCAAATCCCGTGGGCCCATGT-  
>At0059|Csym|Crenarchaeota|Cenarchaeum symbiosum|257294|257368|Val|TAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTCATAGTCCAGTTCGGT-CATGACGTCGCCCTTACACGGCGAAG-----ATCCGGGTTCAAATCCCGTGGGCCCACCA----  
>At1278|Mmar\_JR1|Euryarchaeota|Methanococcus marisnigri JR1|638194|638121|Val|TAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGTTGTGGTCTAGC-CGGT-CATGACGTCGCCCTTACACGGCGAAG-----ATCCCGGTTCAATCCGGGCAGGCCCA----  
>At1014|Mao\_Nankai3|Euryarchaeota|Methanococcus aeolicus Nankai-3|978297|978370|Val|TAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGACCATGTTCTAGT-TGGC-TATGACATCGCCCTTACAAGGCGGAG-----GTCGGCGGTTCAATCCGGCTGGGTCCA----  
>At1182|Mvan\_SB|Euryarchaeota|Methanococcus vannielii SB|811493|811420|Val|TAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGACTCATGTTCTAGT-TGGC-TATGACATCGCCCTTACAAGGCGGAG-----GTCGGCGGTTCAATCCGGCTGGGTCCA----  
>At1046|Mmar\_C5|Euryarchaeota|Methanococcus maripaludis C5|97098|97174|Val|TAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGACCTAGTCTAGT-TGGC-TATGACATCGCCCTTACAAGGCGGAG-----GTCGGCGGTTCAATCCGGCTAGTCCACCA-  
>At1598|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|548757|548830|Val|TAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTATGTTCTAGT-TGGT-TATGACACCGCCTTACACGGCGGAG-----GTCGGCGGTTCAATCCGGCTGGGCCCACCA----  
>At0942|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|883681|883754|Val|TAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCATGTTCTAGC-TGGC-TATGACGTCGCCCTTACAAGGCGAAG-----GTCGGCGGTTCAATCCGGCTGGGCCCACCA----  
>At1782|Paby\_OR SAY|Euryarchaeota|Pyrococcus abyssi|415004|415080|Val|TAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTGGTCTAGT-TGGT-TATGACGTCGCCCTTACGAGGCGGAG-----GTCCGGGTTCAATCCCGCGGGCCACCA-  
>At1940|Tkod\_KOD1|Euryarchaeota|Thermococcus kodakaraensis KOD1|86293|86216|Val|CAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTGGTCTAGACTGGT-TATGACGTCGCCCTTACGAGGCGGAG-----GTCCGGGTTCAATCCCGCGGGCCACCA-  
>At1784|Paby\_OR SAY|Euryarchaeota|Pyrococcus abyssi|463515|463592|Val|CAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTGGTCTAGACTGGT-TATGACGTCGCCCTTACAAGGCGGAG-----GTCCGGGTTCAATCCCGCGGGCCACCA-  
>At1840|Pfur\_DSM3638|Euryarchaeota|Pyrococcus furiosus DSM 3638|1611698|1611775|Val|CAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTGGTCTAGACTGGT-TATGACGTCGCCCTTACAAGGCGGAG-----GTCCGGGTTCAATCCCGCGGGCCACCA-  
>At1801|Paby\_OR SAY|Euryarchaeota|Pyrococcus abyssi|1315623|1315700|Val|GAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTGGTCTAGACTGGT-TATGACGTCGCCCTTACAAGGTTGAG-----GTCCGGGTTCAAATCCCGCGGGCCACCA-  
>At1920|Tkod\_KOD1|Euryarchaeota|Thermococcus kodakaraensis KOD1|424241|424318|Val|GAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTGGTCTAGACTGGT-TATGACGCCACCTGACAAGGTTGAG-----GTCCGGGTTCAATCCCGCGGGCCACCA-  
>At1217|Mlab\_Z|Euryarchaeota|Methanococcus labreanum Z|375982|375909|Val|TAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGACTCGTGGTCTAGG-TGGT-TATGACGTCGCCCTTACATGCTGGAG-----GTCAGGGTTCAATCCCTTGGGTCCA----  
>At0007|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|542607|542684|Val|TAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTGGTCTAGCTGGT-TAGGACGTCGCCCTTACGAGGCGGAG-----GTCCGGGTTCAAATCCCGCGGGCCACCA-  
>At0015|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|1277182|1277259|Val|GAC|0|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTGGTCTAGCTGGT-TAGGACGTCGCCCTTACGAGGCGGAG-----GTCCGGGTTCAAATCCCGCGGGCCACCA-

>At0097|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|65064|65141|Val|GAC|0|0|||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTGACACGGCGGAG-----GTCCGGGGTTCAAATCCCCGCGGGCCACCA-  
>At0025|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|330242|330165|Val|CAC|0|0|||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTGACACGGCGGAG-----GTCCGGGGTTCAAATCCCCGCGGGCCACCA-  
>At0382|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|719035|719112|Val|CAC|0|0|||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTGACACGGCGGAG-----GTCCGGGGTTCAAATCCCCGCGGGCCACCA-  
>At0149|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|195938|196012|Val|CAC|0|0|||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTGACACGGCGGAG-----GTCCGGGGTTCAAATCCCCGCGGGCCACCA-  
>At0451|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|515780|515706|Val|GAC|0|0|||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTGACACGGCGGAG-----ATCCTGGGTTCAAGTCCCAGCGGGCCCA----  
>At0548|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|362002|361928|Val|GAC|0|0|||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTGACACGGCGGAG-----GTCCGGGGTTCAAAGTCCCAGCGGGCCCA----  
>At0469|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|114659|114733|Val|CAC|0|0|||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTGACACGGCGGAG-----ATCCTGGGTTCAAGTCCCAGCGGGCCCA----  
>At0543|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|224532|224458|Val|CAC|0|0|||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTGACACGGCGGAG-----ATCCGGGGTTCAAGTCCCAGCGGGCCCA----  
>At0497|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|227569|227495|Val|GAC|0|0|||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTGACACGGCGGAG-----GTCCGGGGTTCAAATCCCAGCGGGCCCA----  
>At0186|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|2154485|2154411|Val|GAC|0|0|||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGATGCCGCTGACACAGCGGAG-----GTCCGGGGTTCAAATCCCAGCGGGCCCA----  
>At0518|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|355127|355201|Val|TAC|0|0|||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTTACAAGGCGGAG-----GTCCGGGGTTCAAAGTCCCAGCGGGCCCA----  
>ENV09004243|ADKL01000479|Hot springs metagenome ctg\_1106426165452||17804|17728|Val|TAC|0|0|||||ENV  
division in DDBJ/EMBL/GenBank|  
TGGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTTACAAGGCGGAG-----GTCCGGGGTTCAAAGTCCCAGCGGGCCCA----  
>At0450|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|507601|507527|Val|TAC|0|0|||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTTACAAGGCGGAG-----GTCCGGGGTTCAAATCCCAGCGGGCCCA----  
>At0481|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|646823|646897|Val|TAC|0|0|||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTTACGAGGCGAG-----GTCCGGGGTTCAAATCCCAGCGGGCCCA----  
>At0398|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|1066315|1066408|Val|GAC|1066354|  
1066372|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTGACGAGGCGGAG-----GTCCGGGGTTCAAATCCCCGCGGGCCCA----  
>At0407|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|633113|633007|Val|TAC|633074|633043|||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTTACGAGGCGGAG-----GTCCGGGGTTCAAATCCCCGCGGGCCCA----  
>At0454|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|594546|594472|Val|CAC|0|0|||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTGACACGGCGGAG-----GTCCGGGGTTCAAATCTCGGCGGGCCCA----  
>At0166|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|2180910|2180984|Val|TAC|0|0|||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTCGTCTAGCCTGGT-TAGGACGCCGCCCTTACAAGCCAGAG-----GTCTGGGGTTCAAATCCCAACGGGGCCCA----  
>At0556|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|1429759|1429685|Arg|CCG|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCTTAGCCAGGACAAAGCA-CGGGTCCTCCGGAACCCGAG-----ATCCCGGGTTCAAATCCCGGCGGGCCCG----  
>At0008|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|584144|584222|Arg|GCG|0|0|||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCTCAGCCAGGACCAGAGCGCGCCCTGCGGAGCCGAG-----GTCCGGGGTTCAAATCCCGGCGGGCCCGCCA-  
>At0113|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|1173683|1173760|Arg|CCG|0|0|||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCTCAGCCAGGAC-AGAGCGCCGCCCTCCGGAGCCGAG-----GTCCGGGGTTCAAATCCCGGCGGGCCCGCCA-  
>At0016|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|1665596|1665674|Arg|TCG|0|0|||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCTCAGCCAGGACCAGAGCGCGCCCTCGGAGCCGCG-----GTCCGGGGTTCAAATCCCGGCGGGCCCGCCA-  
>At0001|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|198449|198526|Arg|CCG|0|0|||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGTAGCTCAGCCAGGAT-AGAGCGCCGCCCTCCGGAGCCGAG-----GTCCGGGGTTCAAATCCCGGCGGGCCCGCCA-  
>At1300|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|584970|585046|Val|TAC|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGCAGTTCAGCCCGG-C-AGAACGCCGCCCTTACGAGCCGGTG-----GTCCGGGGTTCAAATCCCGGCGGGCCCGCCA-  
>At1314|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|299603|299530|Val|GAC|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGCAGTTCAGCCCGG-C-AGAACGCCGCCCTGACGAGCCGGTG-----GTCCGGGGTTCAAATCCCGGCGGGCCCA----





>At0419|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|1415757|1415658|Ala|CGC|1415719|1415697|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGCTGGAA--GAGCGCCGCCCTCGCAAGCGGGAG-----GTCCCGGGTTCAAATCCCGCCGGTCCACCA-  
>ENV004175|DQ397587|Environmental sample from ENV division of INSDC|20775|20851|Ala|TGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTGATAGCTATAGACTGGTA--GTATACCCGCCCTGCACGCGGGG-----GTCCCGGGTTCAAATCCCGCTCAGTCCACCA-  
>ENV004188|DQ397615|Environmental sample from ENV division of INSDC|6169|6093|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTAGTCTGGTA--GGATGCGCCCTTGGCATGGGCGAG-----ATCGAGGGTTCAAATCCCGCTCAGTCCACCA-  
>At1050|Mmar\_C5|Euryarchaeota|Methanococcus maripaludis C5|492159|492232|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTGATAGCTCAGACTGGGA--GAGTACCGCATTGGCTATGCGGAA-----GCCCGGGTTCAAATCCCGCTCAGTCCACCA-  
>At1102|Mmar\_C7|Euryarchaeota|Methanococcus maripaludis C7|326141|326068|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTGATAGCTCAGACTGGGA--GAGTGC CGCATTGGCTATGCGGAA-----GCCCGGGTTCAAATCCCGCTCAGTCCACCA-  
>At1144|Mmar\_S2|Euryarchaeota|Methanococcus maripaludis S2|1049964|1049891|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTGATAGCTCAGACTGGGA--GAGTGC CGCATTGGCTATGCGGAT-----GCCCGGGTTCAAATCCCGCTCAGTCCACCA-  
>At1026|Maeo\_Nankai3|Euryarchaeota|Methanococcus aeolicus Nankai-3|838331|838258|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTGATAGCTCAGCTGGGA--GAGTGC CGCATTGGCTATGCGGAA-----GCCCGGGTTCAAATCCCGCTCAGTCCACCA-  
>At0950|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|227780|227704|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTGGTGTAGCTCAGACTGGGA--GAGCGCCGCATTGGCTGTGCGGAG-----GCCCGGGTTCAAATCCCGCCAGTCCACCA-  
>At1649|Mthe\_DELTAH|Euryarchaeota|Methanothermobacter thermautotrophicus str. Delta H|708805|708878|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTGGTGTAGCTCAGCTGGTA--GAGCGTCGCCTTGGCATGGCGGAG-----GCCCGGGTTCAAATCCCGCCAGTCCACCA-  
>At1585|Msta\_DSM3091|Euryarchaeota|Methanosphaera stadtmanae DSM 3091|1403944|1403871|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTAGTGTAGCTCAGCTGGTA--GAGTGTGCGCCTTGGCATGGCGGAG-----GCCTCGGGTTCAACTCCCGACTAGTCCACCA-  
>At0621|Aful\_DSM4304|Euryarchaeota|Archaeoglobus fulgidus DSM 4304|1884704|1884777|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGTCTGGTA--GAGCGTCGCCTTGGCATGGCGGAG-----GCCTGGGGTTCAAATCCCGCCAGTCCACCA-  
>At1292|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|51546|51622|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGCAGCTCAGCTGGGA--GAGCGCGCCCTTGGCGGGCCGTG-----GCCCGGGTTCAAATCCCGCCGGTCCACCA-  
>At1297|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|464925|465001|Ala|TGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCCGCAGCTCAGTCTGGGA--GAGCGCGCCCTTGGCGAGCCGTG-----GCCCGGGTTCAAATCCCGCCGGTCCACCA-  
>At0031|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|455727|455651|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGCTGGGA--GAGCGCCCGTTGGCATCCGGGAG-----GCCCGGGTTCAAATCCCGCCGGTCCACCA-  
>At0043|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|1194213|1194137|Ala|TGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGCTGGGA--GAGCGCCCGCTTGCACCCGGGAG-----GCCCGGGTTCAAATCCCGCCGGTCCACCA-  
>At0189|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|2191299|2191226|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGCTGGGA--GAGTGC CGGTTGGCATCCCGGAG-----GTCCCGGGTTCAAATCCCGCCGGTCCACCA-  
>At0429|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|579685|579758|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGCTGGGA--GAGTGC CGTGGTTGGCATCCACGAG-----GTCCCGGGTTCAAATCCCGCCGGTCCACCA-  
>At0154|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|1542915|1542988|Ala|CGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGCTGGGA--GAGTGCCTGGTTGCACCCAGGAG-----GTCCCGGGTTCAAATCCCGCCGGTCCACCA-  
>At0107|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|1062352|1062428|Ala|TGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGCTGGGA--GAGCGCTCGGCTTGCACCCGAGAG-----GTCCCGGGTTCAAATCCCGCCGGTCCACCA-  
>At0132|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|598843|598767|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGCTGGGA--GAGCGCTCGGTTGGCATCCGAGAG-----GTCCCGGGTTCAAATCCCGCCGGTCCACCA-  
>At0470|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|222725|222798|Ala|TGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGCTGGGA--GAGTGCCTCGGTTGCACCCGAGAG-----GTCCCGGGTTCAAATCCCGCCGGTCCACCA-  
>ENV09004257|ADKL01000514|Hot springs metagenome ctg\_1106426165452|11645|11722|Ala|TGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGCTGGGA--GAGTGCCTCGGTTTGCACCCGAGAG-----GTCCCGGGTTCAAATCCCGCCGGTCCATCA-  
>At0485|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|915708|915781|Ala|CGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGCTGGGA--GAGTGCCTCGGTTGCACCCGAGAG-----GTCCCGGGTTCAAATCCCGCCGGTCCACCA-  
>ENV09004261|ADKL01000514|Hot springs metagenome ctg\_1106426165452|3678|3602|Ala|CGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGCTGGGA--GAGTGCCTCGGTTTGCACCCGAGAG-----GTCCCGGGTTCAAATCCCGCCGGTCCACCT-  
>At0473|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|333447|333520|Ala|GGC|0|0|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTGTAGCTCAGCTGGGA--GAGTGCCTCGGTTGGCATCCGAGAG-----GTCCCGGGTTCAAATCCCGCCGGTCCACCA-





-GCGGCCGTCGTCTAGTCTGGATTAGGACGCTGGCCTCCCAAGCCAGCA-----ATCCCGGGTTCAATCCCGCGGCCGCA----  
>At0465|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|2160161|2160071|Gly|TCC|2160121|  
2160107|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGTCTGGATTAGGACGCTGGCCTCCCAAGCCAGCA-----TCCCGGGTTCAATCCCGCGGCCGCA----  
>At0538|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|2204279|2204354|Gly|TCC|0|0|The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGTCTGGATTAGGACGCTGGCCTCCCAAGCCAGTA-----TCCCGGGTTCAATCCCGCGGCCGCA----  
>At0524|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|418363|418438|Gly|CCC|0|0|The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGTCTGGATTAGGACGCGCGCCTCCCAAGCCGGTA-----TCCCGGGTTCAATCCCGCGGCCGCA----  
>At0503|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|590292|590217|Gly|CCC|0|0|The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGTCTGGATTAGGACGCGCGCCTCCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGCA----  
>At0474|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|338925|339000|Gly|TCC|0|0|The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGTCTGGATTAGGACGCGCGCCTCCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGCA----  
>At0379|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|624851|624954|Gly|GCC|624891|624915|The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGACTAGGACGCGCGCCTGCCACGCCGGAG-----TCCCGGGTTCAATCCCGCGGCCGACCA--  
>At0126|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|123181|123103|Gly|GCC|0|0|The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGACTAGGACGCGCGCCTGCCAAGCCGGCG-----TCCCGGGTTCAATCCCGCGGCCGACCA--  
>At2219|Ihos\_KIN4I|Crenarchaeota|Ignicoccus hospitalis KIN4/I|1290865|1290787|Gly|TCC|0|0|The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGACTAGGATGCCCGCCTCCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGACCA--  
>At2232|Ihos\_KIN4I|Crenarchaeota|Ignicoccus hospitalis KIN4/I|1030645|1030567|Gly|CCC|0|0|The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGACTAGGATGCCCGCCTCCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGACCA--  
>At0131|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|510728|510650|Gly|TCC|0|0|The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGACTAGGACGCGCGCCTCCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGACCA--  
>At0032|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|467913|467835|Gly|GCC|0|0|The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGACTAGGACGCGCGCCTGCCAAGCCGGAG-----TCCCGGGTTCAATCCCGCGGCCGACCA--  
>At0038|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|986027|985949|Gly|CCC|0|0|The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGACTAGGACGCGCGCCTCCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGACCA--  
>At0051|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|1528663|1528585|Gly|TCC|0|0|The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGACTAGGACGCGCGCCTCCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGACCA--  
>At0202|Paer\_IM2|Crenarchaeota|Pyrobaculum aerophilum str. IM2|1740444|1740534|Gly|TCC|1740484|  
1740498|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGACTAGGATGGCGGCCTCCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGCA----  
>At0235|Paer\_IM2|Crenarchaeota|Pyrobaculum aerophilum str. IM2|1960241|1960166|Gly|CCC|0|0|The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGACTAGGATGGCGGCCTCCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGCA----  
>At0258|Pars\_DSM13514|Crenarchaeota|Pyrobaculum arsenaticum DSM 13514|895710|895620|Gly|TCC|895670|  
895656|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGACTAGGATGGCGGCCTCCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGCA----  
>At0330|Pisl\_DSM4184|Crenarchaeota|Pyrobaculum islandicum DSM 4184|471455|471566|Gly|CCC|471477|  
471513|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGTTAGGATGGCGGCCTCCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGCA----  
>At0265|Pars\_DSM13514|Crenarchaeota|Pyrobaculum arsenaticum DSM 13514|1479953|1479841|Gly|GCC|  
1479929|1479896|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGTTAGGATGGCGGCCTGCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGACCA--  
>At0304|Pcal\_JCM11548|Crenarchaeota|Pyrobaculum calidifontis JCM 11548|1687978|1688071|Gly|GCC|  
1688010|1688027|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGTTAGGATGGCGGCCTGCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGCA----  
>At0359|Pisl\_DSM4184|Crenarchaeota|Pyrobaculum islandicum DSM 4184|459148|459041|Gly|GCC|459126|  
459097|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGTTAGGATGGCGGCCTGCCAAGCCGGTG-----TCCCGGGTTCAATCCCGCGGCCGACCA--  
>At0583|Tpen\_HRK5|Crenarchaeota|Thermofilum pendens Hrk 5|796113|796209|Gly|GCC|796159|796178|The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGT--AGGATGGCGGCCTGCCACGCCGAG-----A-CCCGGGTTCAATCCCGCGGCCGACCA--  
>At0596|Tpen\_HRK5|Crenarchaeota|Thermofilum pendens Hrk 5|528662|528566|Gly|TCC|528616|528597|The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGT--AGGATGGCGGCCTGCCACGCCGAG-----A-CCCGGGTTCAATCCCGCGGCCGACCA--  
>At0565|Tpen\_HRK5|Crenarchaeota|Thermofilum pendens Hrk 5|360726|360820|Gly|CCC|360772|360789|The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCCGTCGTCTAGCTGGT--AGGATGGCGGCCTCCCAAGCCGGAG-----A-CCCGGGTTCAATCCCGCGGCCGACCA--  
>ENV004153|DQ397560|Environmental sample from ENV division of INSDC|27469|27545|Gly|CCC|0|0|The  
ENV division in DDBJ/EMBL/GenBank|  
-GCGGAGTTAGTCCAGCCCGT--AGGACGTCAGCTCCCAAGCTGAAG-----TCGCGTGTTCATCCCGCACTCCGCACTG--  
>At0092|Csym|Crenarchaeota|Cenarchaeum symbiosum|1898649|1898576|Gly|CCC|0|0|The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|



-GCCTCGGTGGCTCAGACCGGC--AGAGCAAACGCCTCGTAAGCGTTAG-----CCGTGGGTTCAAATCCCACCCGAGGCTTCA-  
>At0065|Csym|Crenarchaeota|Cenarchaeum symbiosum|1120854|1120930|Thr|CGT|0|0|||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCCTCGGTGGCTCAGACCGGC--AGAGCAAACGCCTCGTAAGCGTTAG-----CCGTGGGTTCAAATCCCACCCGAGGCTCCA-  
>At0778|Hmar\_ATCC43049|Euryarchaeota|Haloarcula marismortui ATCC 43049|1247215|1247142|Thr|CGT|0|  
0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGACTGGC--AGAGCGAATCCTTCGTAAGGATTAG-----CCGAGGGTTCAAATCCCTCCACCGGCT---  
>At0684|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|1320489|1320416|Thr|GGT|0|0|||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCTAAGTGACTCAGCCCGGC--AGAGTACCTCCTTGTAAGGAGGAA-----TCGCGAGTTCAAATCTCGCCTTAGGCT---  
>At1348|Mthe\_PT|Euryarchaeota|Methanoseta thermophila PT|1392025|1392099|Thr|GGT|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCTCGGTAGCAAAGCTCGGTC-ATTGCGCGTCTTGTAAGGACGAG-----CCGCGGGTTCGAATCCCGCCCGAGGCT---  
>At0101|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|444135|444211|Thr|GGT|0|0|||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCTGGC--GGAGCGCGCCCTGGTAAGCGGAG-----TCCCGGGTTCAAATCCCGCGCGGCTCCA-  
>At0403|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|1116245|1116333|Thr|GGT|1116284|  
1116297|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCTGGT--GGAGCGCGCCCTGGTAAGCGGAG-----TCCCGGGTTCGAATCCCGCGCGGCT---  
>At0152|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|1535617|1535703|Thr|GGT|1535656|  
1535667|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCTGGC--GGAGCGCGCCCTGGTAAGGACGAG-----CCCGGGTTCAAATCCCGCGCGGCT---  
>At0486|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|2538937|2539011|Thr|GGT|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCTGGC--AGAGCGGTGCCCTGGTAAGGACGAG-----TCCCGGGTTCGAATCCCGCGCGGCT---  
>At0459|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|1071144|1071070|Thr|GGT|0|0|||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCTGGT--AGAGCGTTCCTGGTAAGGCAAAG-----TCCCGGGTTCGAATCCCGCGCGGCT---  
>At1304|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|1020437|1020514|Thr|GGT|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCTGGT--AGAGCGCGCCTTGTAAGCGGTG-----TCCCGGGTTCGAATCCCGCGCGGCTCCA-  
>At0296|Pcal\_JCM11548|Crenarchaeota|Pyrobaculum caldifontis JCM 11548|1028707|1028799|Thr|GGT|  
1028745|1028760|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCTGGT--GGAGCGCCTCACTGGTAGTGGAG-----TCCCGGGTTCGAATCCCGCGCGGCTCCA-  
>At0352|Pisl\_DSM4184|Crenarchaeota|Pyrobaculum islandicum DSM 4184|409363|409290|Thr|GGT|0|0|||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCTGGT--GGAGCGCCTCACTGGTAATGAGGAG-----TCCCGGGTTCGAATCCCGCGCGGCT---  
>At0228|Paer\_IM2|Crenarchaeota|Pyrobaculum aerophilum str. IM2|1792192|1792081|Thr|GGT|1792153|  
1792135|1792116|1792101|||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCTGGT--GGAGCGCCTCACTGGTAATGAGGAG-----TCCCGGGTTCGAATCCCGCGCGGCTCCA-  
>At0260|Pars\_DSM13514|Crenarchaeota|Pyrobaculum arsenaticum DSM 13514|1141743|1141651|Thr|GGT|  
1141704|1141686|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCTGGT--GGAGCGCCTCACTGGTAATGAGGAG-----TCCCGGGTTCGAATCCCGCGCGGCT---  
>At1788|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|578139|578215|Thr|TGT|0|0|||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCCTAGCCTGGT--GGGCGGGGACTTGTAATCCCCAG-----TCGCGGGTTCGAATCCCGCGCGGCTCCA-  
>At1795|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|894672|894748|Thr|CGT|0|0|||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCCTAGCCTGGT--GGGCGGGGACTCGTAATCCCCAG-----TCCCGGGTTCGAATCCCGGTCCCGGCTCCA-  
>At1313|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|272692|272615|Thr|TGT|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGCGAGCTTAGCCTGGT--AGAGCGCGGACTTGTAATCCCGTG-----TCCCGGGTTCGAATCCCGCGCGGCTCCA-  
>At0272|Pars\_DSM13514|Crenarchaeota|Pyrobaculum arsenaticum DSM 13514|1693504|1693410|Thr|TGT|  
1693473|1693454|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCCGGTC--GGAGCGCGCCCTGTAAGCGGAG-----TCCCGGGTTCGAATCCCGCGCGGCT---  
>At0196|Paer\_IM2|Crenarchaeota|Pyrobaculum aerophilum str. IM2|1239015|1239132|Thr|TGT|1239046|  
1239065|1239096|1239115|||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCCGGTC--GGAGCGCGCCCTGTAAGCGGAG-----TCCCGGGTTCGAATCCCGCGCGGCTCCA-  
>At0213|Paer\_IM2|Crenarchaeota|Pyrobaculum aerophilum str. IM2|2039014|2039108|Thr|CGT|2039045|  
2039064|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCCGGTC--GGAGCGCGCCCTCGTAAGCGGAG-----TCCCGGGTTCGAATCCCGCGCGGCT---  
>At0309|Pcal\_JCM11548|Crenarchaeota|Pyrobaculum caldifontis JCM 11548|168716|168604|Thr|CGT|168692|  
168674|168658|168643|||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCCGGTC--GGAGCGCGCCCTCGTAAGCGGAG-----TCCCGGGTTCGAATCCCGCGCGGCTCCA-  
>At0318|Pcal\_JCM11548|Crenarchaeota|Pyrobaculum caldifontis JCM 11548|987244|987115|Thr|TGT|987220|  
987202|987154|987138|||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGCTCAGCCCGGTC--AGAGCGCGCCCTGTAAGCGGCG-----CCCGGGTTCGAATCCCGCGCGGCTCCA-  
>ENV005253|EF584002|Environmental sample from ENV division of INSDC||15271|15347|Phe|GAA|0|0|||||  
ENV division in DDBJ/EMBL/GenBank|  
-GCCGCTTAGCTCAGACTGGG--AGAGCACTCGACTGAAGATCGAGCT-----TCCCGGGTTCGAATCCCGGAGGCGGCATCC-  
>At1707|Npha\_DSM2160|Euryarchaeota|Natronomonas pharaonis DSM 2160|153907|153834|Phe|GAA|0|0|||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCTTAGCTCAGACTGGG--AGAGCACTCGACTGAAGATCGAGCT-----TCCCGGGTTCGAATCCCGGAGGCGGCA---  
>At0818|Halo\_NRC1|Euryarchaeota|Halobacterium sp. NRC-1|95300|95227|Phe|GAA|0|0|||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|

-GCCGCCCTTAGCTCAGACTGGG--AGAGCACTCGACTGAAGATCGAGCT-----TCCCTGGTTCAAATCCGGGAGGGCGGCA----  
>At0782|Hmar\_ATCC43049|Euryarchaeota|Haloarcula marismortui ATCC 43049|1796729|1796656|Tyr|GTA|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-CCGCCCTTAGCTCAGACTGGT--AGAGCAGTCGACTGTAGATCGACTT-----TCCCCGTTCAAATCCGGGAGGGCGGGA----  
>At0795|Halo\_NRC1|Euryarchaeota|Halobacterium sp. NRC-1|167315|167388|Tyr|GTA|0|0||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-CCGCCCTTAGCTCAGACTGGT--AGAGCAGTCGACTGTAGATCGACTT-----CCCCCGTTCAAATCCGGGAGGGCGGGA----  
>At0853|Hwal\_DSM16790|Euryarchaeota|Haloquadratum walsbyi|1778178|1778251|Tyr|GTA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-CCGCCCTTAGCTCAGACTGGT--AGAGCAGTCGACTGTAGATCGACTT-----CCCCCGTTCAAATCCGGGAGGGCGGGA----  
>At1287|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|1674306|1674200|Tyr|GTA|1674268|  
1674236||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-CCGCCCTTAGCTCAGACTGGT--AGAGTGC GCGGCTGTAGACCGCGAT-----TCCCCGTTCAAATCCGGGAGGGCGGGA----  
>At1637|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|2881854|2881749|Tyr|GTA|2881816|  
2881785||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-CCGCCCTTAGCTCAGACTGGT--AGAGTGC GCGGCTGTAGACCGCGAT-----TCCCCGTTCAAATCCGGGAGGGCGGGA----  
>At1359|Mthe\_PT|Euryarchaeota|Methanosaeta thermophila PT|551859|551752|Tyr|GTA|551821|551788||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-CCGCCCTTAGCTCAGACTGGT--AGAGTGC GCGGCTGTAGACCGCGAT-----TCCCCGTTCAAATCCGGGAGGGCGGGA----  
>At1078|Mmar\_C5|Euryarchaeota|Methanococcus maripaludis C5|1517711|1517638|Tyr|GTA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-CCCGGATAGTTCAGACTGGTA-G-AACGGCGGACTGTAGATCCGCAT-----TCGCTGGTTCAAATCCGGCTCGCGGGA----  
>At1165|Mvan\_SB|Euryarchaeota|Methanococcus vannielii SB|1127147|1127220|Tyr|GTA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-CCCGGATAGTTCAGACTGGTA-G-AACGGCGGACTGTAGATCCGCAT-----TCGCTGGTTCAAATCCGGCTCGCGGGA----  
>At0939|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|863656|863732|Tyr|GTA|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-CCCGGCTAGTTCAGACTGGTA-G-AACGGCGGACTGTAGATCCGCAT-----TCGCTGGTTCAAATCCGGCCCGCGGACCA-  
>At1883|Phor\_OT3|Euryarchaeota|Pyrococcus horikoshii OT3|909699|909776|Tyr|GTA|0|0||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-CCCGGCTAGCTCAGACTGGG--GTGGCGGCGGACTGTAGATCCGCAG-----TCCCCGTTCAAATCCGGGCGCGGACCA-  
>At1810|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|941806|941729|Tyr|GTA|0|0||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-CCCGGCTAGCTCAGACTGGTA-GTGGCGGCGGACTGTAGATCCGCAG-----TCCCCGTTCAAATCCGGGCGCGGACCA-  
>At0569|Tpen\_HRK5|Crenarchaeota|Thermofilum pendens Hrk 5|424782|424890|Phe|GAA|424826|424855||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGTAGCTCAGCT-GGG--AGAGCGCTCGGCTGAAGACCGAGTA-----GTCCCCGTTCAAATCCGGCCCCGGCACCA-  
>At0647|Aful\_DSM4304|Euryarchaeota|Archaeoglobus fulgidus DSM 4304|1977911|1977838|Phe|GAA|0|0||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGTAGCTCAGCCAGGG--AGAGCGTGC GCGGCTGAAGACCGCATA-----TCCCCGTTCAAATCCGGGTCCGGGCA----  
>At0681|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|779946|779873|Phe|GAA|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCTAGTACTCAGACTGGG--AGAGCGCCAGACTGAAGATCTGGTT-----TCCCCGTTCAAATCCGGGCTGGGGCA----  
>At1639|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|3100268|3100195|Phe|GAA|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCTCAGTACTCAGACTGGG--AGAGCGCCAGACTGAAGATCTGGTT-----TCCCCGTTCAAATCCGGGCTGAGGCA----  
>At1265|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|2005461|2005534|Phe|GAA|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCTGTAGCTCAGACTGGG--AGAGCGCCAGACTGAAGATCTGGTT-----TCCCCGTTCAAATCCGGGCGGGGCA----  
>At1081|Mmar\_C5|Euryarchaeota|Methanococcus maripaludis C5|1699854|1699781|Phe|GAA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCAAGGTAGTTCAGCTGGG--AGAACGCTGGACTGAAGATCCAGTT-----TCGGGTGTTCAATCACCCCTTGGCA----  
>At1034|Maeo\_Nankai3|Euryarchaeota|Methanococcus aeolicus Nankai-3|1293476|1293403|Phe|GAA|0|0||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGTGGTAGTTCAGCTGGG--AGAACGCTGGACTGAAGATCCAGTT-----TCGGGTGTTCAATCACCCCCACGGCA----  
>At0928|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|637583|637659|Phe|GAA|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTAGTTCAGCTGGG--AGAACGCTGGACTGAAGATCCAGTT-----TCGGGTGTTCAATCACCCCCCGGCACCA-  
>At1319|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|864537|864460|His|GTG|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGCGAGCTCAGCTGGT--AGAGCGCCGCTGTGGAGCCGGTG-----CCCCGGTTCAAATCCGGGCGCGGCCCA-  
>At1307|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|1560286|1560363|Tyr|GTA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-CCGGCCGAGCTCAGTCTGGCT--AGAGCGCGGACTGTAGATCCCGTG-----TCCCCGTTCAAATCCGGGCGCGGACCA-  
>ENV004177|DQ397588|Environmental sample from ENV division of INSDC|15370|15292|Asn|GTT|0|0||||  
ENV division in DDBJ/EMBL/GenBank|  
TCCCGCCTAGCTCAGCCCGT--AGAGCGTGC GACTGTAAATCCGTG-----TCGCCAGTTCAAGTCTGGTGGGCGCGCCAA  
>At0063|Csym|Crenarchaeota|Cenarchaeum symbiosum|890144|890220|Asn|GTT|0|0||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCCTAGCTCAGCCCGT--AGAGCGTGC GACTGTAAATCCGTG-----TCGCCAGTTCAAGTCTGGTGGGCGCGCCA-  
>At0142|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|1616934|1616806|Met|CAT|1616895|  
1616845||||The tRNA gene was obtained from SPLITSdb. tRNA-Met (elongator).|GIB in DDBJ|  
-GCCCGCTAGCTCAGCGCGTC--AGAGCGCGGACTCATAATCCCGTG-----TCCCCGTTCAAGTCCCGCGCGGCACCA-  
>At0214|Paer\_IM2|Crenarchaeota|Pyrobaculum aerophilum str. IM2|2099023|2099110|Asn|GTT|2099062|  
2099074||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCCGCCGTAGCTCAGCCCGGTT-AGAGCGCGGGCTGTTAACCCGTAG-----TCCCGGGTTCAAATCCCGCGCGCGGCG----  
>At0361|Pisl\_DSM4184|Crenarchaeota|Pyrobaculum islandicum DSM 4184|713260|713145|Asn|GTT|713228|  
713206|713190|713173||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCCCGGTT-AGAGCGCGGGCTGTTAACCCGTAG-----TCCCGGGTTCAAATCCCGCGCGCGGCG----  
>At0247|Pars\_DSM13514|Crenarchaeota|Pyrobaculum arsenaticum DSM 13514|1755536|1755610|Asn|GTT|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCCCGGTC-AGAGCGCGGGCTGTTAACCCGTAG-----TCCCGGGTTCAAATCCCGCGCGCGGCG----  
>At0319|Pcal\_JCM11548|Crenarchaeota|Pyrobaculum calidifontis JCM 11548|1088212|1088102|Asn|GTT|  
1088165|1088150||1088135|1088119||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCCCGGTC-AGAGCGCGGGCTGTTAACCCGTAG-----TCCCGGGTTCAAATCCCGCGCGCGGCGCA-  
>At0157|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|1598625|1598713|Thr|TGT|1598664|  
1598677||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCTGTAGCTCAGCCTGGCC-AGAGCGCCGGCCTGTAAGCCGGCG-----TCGCGGGTTCAAATCCCGCCAGCGGCT----  
>At0530|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|1201508|1201599|Thr|TGT|1201547|1201563||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCTGTAGCTCAGCCTGGTT-AGAGCGCCGGCCTGTAAGCCGGCG-----TCCGGGGTTCAAATCCCGCAGCGGCT----  
>At0496|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|206424|206337|Thr|CGT|206385|206373||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCCTGGTT-AGAGCGCCGGCCTGTAAGCCGGCG-----TCGCGGGTTCAAATCCCGCCAGCGGCT----  
>At0509|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|789766|789677|Thr|TGT|789727|789713||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCCTGGTT-AGAGCGCCGGCCTGTAAGCCGGCG-----TCGCGGGTTCAAATCCCGCCAGCGGCT----  
>At0405|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|427592|427465|Thr|TGT|427554|427501||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCCCGGT--AGAGCGCCGGCCTGTAAGCCGGTG-----TCGCGGGTTCAAATCCCGCCAGCGGCT----  
>At0411|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|883502|883401|Thr|CGT|883464|883437||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCTCGGT--AGAGCGCCGGCCTGTAAGCCGGTG-----TCGCGGGTTCAAATCCCGCCAGCGGCT----  
>At0453|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|563615|563514|Thr|CGT|563576|  
563550||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCACGGTC-AGAGCGCCGGCCTGTAAGCCGGTG-----TCCCGGGTTCAAATCCCGCGCGCGGCT----  
>At0462|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|1188479|1188389|Thr|TGT|1188440|  
1188425||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCACGGCC-AGAGCGCTGGCCTGTAAGCCAGTG-----TCCCGGGTTCAAATCCCGCGCGCGGCT----  
>At0506|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|642552|642464|Tyr|GTA|642512|642500||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCCCGGTTAGAGCGCCGGCTGTAGACCCGGTG-----TCCGGGGTTCAAGTCCCGCGCGCGGGA----  
>At0520|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|361250|361342|Tyr|GTA|361288|361306||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-CCCGCCGTAGCTCAGCCCGGT--GGAGCGCCGGCTGTAGACCCGGTG-----TCCGGGGTTCAAGTCCCGCGCGCGGGA----  
>At0163|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|2152523|2152611|Tyr|GTA|2152563|  
2152575||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-CCCACCGTAGCTCAGCCCGGTTTACAGCGCCGGCTGTAGACCCGGTG-----TCCGGGGTTCAAGTCCCGCGCGGTGGGA----  
>At0449|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|458927|458836|Phe|GAA|458889|  
458872||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCCCGG--AGAGCGCCGGCTGAAGACCCGGTG-----TCCGGGGTTCAAGTCCCGCGCGCGCA----  
>At0169|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|99766|99769|Phe|GAA|99728|  
99715||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCCCGG--AGAGCACCCGGCTGAAGACCCGGTT-----TCCGGGGTTCAAGTCCCGCGCGCGCA----  
>At0414|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|1021027|1020954|Phe|GAA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCCTGGG--AGAGCGCCGGCTGAAGACCCGGTT-----TCCGGGGTTCAAATCCCGCGCGCGCA----  
>At0435|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|1166821|1166915|Met|CAT|1166860|  
1166879||||The tRNA gene was obtained from SPLITSdb. tRNA-Met(elongator).|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCCTGGTT-AGAGCGCCGGACTCATAATCCGGTT-----TCCGGGGTTCAAATCCCGCGCGCGCA----  
>At0156|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|1598318|1598408|Met|CAT|1598357|  
1598369||||The tRNA gene was obtained from SPLITSdb. tRNA-Met(elongator).|GIB in DDBJ|  
-GCCGCCGTAGCTCAGCCTGGCC-AGAGCGCCGGACTCATAATCCGGTC-----TCCGGGGTTCAAATCCCGCGCGCGCACCA-  
>At0547|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|306779|306682|Thr|CGT|306741|306718||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTAGCTCAGTCTGGT--AGAGCGCCGGCCTGTAAGCCGGTG-----TCCGGGGTTCAAGTCCCGCGCGCGGCT----  
>At0445|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|387747|387673|His|GTG|0|0||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCTCGGGTAGCTCAGCCTGGTT-AGAGCGATGGGCTGTGGACCCATAG-----TCCCGGGTTCAAGTCCCGGCCGAGCC----  
>At0545|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|274313|274239|His|GTG|0|0||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GCTCGGGTAGCTCAGCCTGGTT-AGAGCGACGGGCTGTGGACCCGTAG-----TCCCGGGTTCAAGTCCCGGCCGAGCC----  
>At0171|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|115550|115476|His|GTG|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCTCAGGTAGCTCAGCTCGGTT-AGAGCGCTGGGCTGTGGACCCAGTG-----TCCCGGGTTCAAATCCCGGCCGAGCC----  
>At0492|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|179553|179480|His|GTG|0|0||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GCTCGGGTAGCTCAGCCTGGA--AGAGCGCCGGGCTGTGGACCCGAA-----TCCCGGGTTCAAATCCCGGCCGAGCC----  
>At0048|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|1422799|1422722|His|GTG|0|0||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|

-GCCCCGGGTAGCTCAGCCTGGAT-AGAGCGCCGGACTGTGGATCCGGAG-----TCCCGGGTTCAAATCCCGGCCGGGCCCA-  
>At0212|Paer\_IM2|Crenarchaeota|Pyrobaculum aerophilum str. IM2|2028602|2028700|Cys|GCA|2028661|  
2028682||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCCGGGTAGCTCAGTCCGGC--AGAGCGCGGGCTGCAGACCCGTAG-----TCCCGGGTTCAAATCCCGGCCGGGCTCCA-  
>At0276|Pars\_DSM13514|Crenarchaeota|Pyrobaculum arsenaticum DSM 13514|1786437|1786342|Cys|GCA|  
1786414|1786393||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCCGGGTAGCTCAGTCCGGC--AGAGCGCGGGCTGCAGACCCGTAG-----TCCCGGGTTCAAATCCCGGCCGGGCT----  
>At0308|Pcal\_JCM11548|Crenarchaeota|Pyrobaculum calidifontis JCM 11548|160958|160848|Cys|GCA|160934|  
160915|160891|160876||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCCGGGTAGCTCAGCCTGGAT-AGAGCGCGGGCTGCAGACCCGTAG-----TCCCGGGTTCAAATCCCGGCCGGGCT----  
>At1821|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|1466472|1466395|Arg|GCG|0|0||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCCGGTGGCTAGCCTGGAT-AGGGCGCGAGGCTGCGGACCTCGAG-----TCCGGGGTTCAAATCCCGGCCGGGCGCCA-  
>At1850|Pfur\_DSM3638|Euryarchaeota|Pyrococcus furiosus DSM 3638|361280|361204|Arg|GCG|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCCGGTGGCTAGCCTGGAT-AGGGCGCGAGGCTGCGGACCTCGAG-----TCCGGGGTTCAAATCCCGGCCGGG-CGCCA-  
>At1930|Tkod\_KOD1|Euryarchaeota|Thermococcus kodakaraensis KOD1|1311255|1311332|Arg|GCG|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCCGGTGGCTAGTCTGGAT-AGGGCGCGAGGCTGCGGACCTCGAG-----TCCGGGGTTCAAATCCCGGCCGGGCGCCA-  
>WENV077513|AAFX01050855|Soil microbial communities from Minnesota Farm|112|201|Ser|GCT|0|0||||  
ENV division in DDBJ/EMBL/GenBank|  
TGACGAGATAGCCAAGCCCGT--ATGGCGCGGGATTGCTAATCCCGTG-----CCGGGGTTTCGAGTCCCCTCTCGTCTTTC  
>At1532|Mmaz\_GOE1|Euryarchaeota|Methanosarcina mazei Go1|1111332|1111248|Ser|GCT|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GACGAGATAGCCAAGCCCGT--ATGGCGCGGGATTGCTAATCCCGTG-----CCGGGGTTTCGAGTCCCCTCTCGTCTG----  
>At1001|Mbur\_DSM6242|Euryarchaeota|Methanococcoides burtonii DSM 6242|1589860|1589776|Ser|GCT|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GACGAGATAGCCAAGCCCGT--ATGGCGCAGGATTGCTAATCCTGTG-----TCGGGGTTTCGAATCCCCTCTCGTCTG----  
>ENV000782|AM114193|Environmental sample from ENV division of INSDC|2572366|2572454|Ser|GCT|0|  
0||||ENV division in DDBJ/EMBL/GenBank|  
TGTCGCGGTATCCAAGCCTGGT--ATGGAGCAGGTTGCTAAACCTGTG-----TCCGGAGTTCAAATCTCCGCCGCGGCTTT  
>At2076|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I|2572367|2572450|Ser|GCT|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GTCCGCGTATCCAAGCCTGGT--ATGGAGCAGGTTGCTAAACCTGTG-----TCCGGAGTTCAAATCTCCGCCGCGGCG----  
>At1978|Taci\_DSM1728|Euryarchaeota|Thermoplasma acidophilum DSM 1728|1185299|1185383|Ser|GGA|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCTGGATAGCCTAGCCCGT--AAGGCGCAGGCTGGAAAACCTGTG-----TCGGGAGTTCAAATCTCCCTCCCAGCG----  
>At2038|Tvol\_GSS1|Euryarchaeota|Thermoplasma volcanium GSS1|436949|436866|Ser|GGA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCTGGATAGCCTAGCCTGGT--AAGGCGCAGGCTGGAAAACCTGTG-----TCGGGAGTTCAAATCTCCCTCCCAGCG----  
>At1769|Ptor\_DSM9790|Euryarchaeota|Picropilus torridus DSM 9790|909582|909500|Ser|GGA|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCTGGATAGCCTAGCCTGGT--AAGGCGCAGGCTGGAAAACCTGTG-----TCGGGAGTTCAAATCTCCCTCCCAGCG----  
>At0745|Hmar\_ATCC43049|Euryarchaeota|Haloarcula marismortui ATCC 43049|49406|49490|Ser|GCT|0|0||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GTCGTGGTAGCCAAGCCTGGCCCAAGGCGCAGGTTGCTAACTCTGTG-----TCCGGGGTTTCGAATCCCAGCCACGACG----  
>At1695|Npha\_DSM2160|Euryarchaeota|Natronomonas pharaonis DSM 2160|1364233|1364316|Ser|GCT|0|0||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GTCGTGGTAGCCAAGCATGGCCCAAGGCGCAGGTTGCTAACTCTGTG-----TCCGGGGTTCAAATCCCAGCCACGACG----  
>At0879|Hwal\_DSM16790|Euryarchaeota|Haloquadratum walsbyi|2243610|2243526|Ser|GCT|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GTTGCGGTAGCCAAGTCTGGCCCAAGGCGCTGGATTGCTAATCAGTG-----TCCGGGGTTTCGAATCCCAGCCCAAG----  
>At0803|Halo\_NRC1|Euryarchaeota|Halobacterium sp. NRC-1|860171|860253|Ser|GCT|0|0||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GTCGTGGTAGCCTAGCCTGGT--AAGGCGCAGGTTGCTAACTCTGTG-----TCCGGGGTTCAAATCCCAGCCACGACG----  
>At1261|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|1792799|1792883|Ser|GCT|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GTTGAGGTAGCCAAGCCTGGT--ATGGCGCAGGTTGCTAAACCTGTG-----TCGAGGGTTCAAATCCCTCCCTCAGCG----  
>ENV09001119|ABSQ01034865|Freshwater sediment metagenome lwMethenol\_C1|273|360|Ser|GCT|0|0||||ENV  
division in DDBJ/EMBL/GenBank|  
-GTTGAGGTAGCCAAGCCTGGT--ATGGCGCAGGTTGCTAAACCTGTG-----TCGAGGGTTCAAATCCCTCCCTCAGCGCTA-  
>At1234|Mlab\_Z|Euryarchaeota|Methanocorpusculum labreanum Z|1273905|1273821|Ser|GCT|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GTAGACGTAGCCAAGCCTGGT--ATGGCGCAGGTTGCTAAACCTGTG-----TCGAGGGTTCAAATCCCTCCCTCAGCG----  
>At1643|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|3180519|3180436|Ser|GCT|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GTTGAGGTAGCCAAGCAGGT--ATGGCGCAGGTTGCTAAACCTGTG-----TCGGGGTTCAAATCCCTCCCTCAACG----  
>At1331|Mthe\_PT|Euryarchaeota|Methanosaeta thermophila PT|339791|339875|Ser|GCT|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GTCGAGGTAGCCTAGCCAGT--AGGGCGCAGGTTGCTAAACCTGTT-----TCGAGGGTTTCGAATCCCTCCCTCAGCG----  
>At0895|Msmi\_ATCC35061|Euryarchaeota|Methanobrevibacter smithii ATCC 35061|1705326|1705411|Ser|GCT|  
0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GTTGGGGTAGCCTAGCCTGGT--AGGGCGTGTAGCTGCTAATCTAATG-----G-CAGGGTTCAAATCCCTCCCAATG----  
>WENV078782|AAQL01000095|Gut microbiome of Human (healthy human stool sample 8)|2041|2129|Ser|GCT|  
0|0||||ENV division in DDBJ/EMBL/GenBank|

TGTCGGGATGGCCAGCCTGGT--ACGGCGTCGGACTGCTAATCCGATG-----CACGGGTTCAAATCCCGTCCCGGGCTTTT  
>At0902|Msmi\_ATCC35061|Euryarchaeota|Methanobrevibacter smithii ATCC 35061|753185|753102|Ser|GCT|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GTCGGGATGGCCAGCCTGGT--ACGGCGTCGGACTGCTAATCCGATG-----A-CACGGGTTCAAATCCCGTCCCGGGCG----  
>At1672|Mthe\_DELTAH|Euryarchaeota|Methanothermobacter thermautotrophicus str. Delta H|1718338|  
1718422|Ser|GCT|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGTGGCCAGCTGGT--ACGGCGTTGGCCTGCTAAGCCAATG-----TCGCGGGTTCAAATCCCGTCCCGGGCG----  
>At1131|Mmar\_S2|Euryarchaeota|Methanococcus maripaludis S2|454031|454115|Ser|GCT|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGAGATGGCCAGCTGGT--ACGGCGCGGGACTGCTAATCCCGTT-----A-CCCAGGTTCAAATCTCGGTCTCCGCG----  
>At1118|Mmar\_C7|Euryarchaeota|Methanococcus maripaludis C7|1469379|1469295|Ser|GCT|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGAGATGGCCAGCCTGGT--ACGGCGCGGGACTGCTAATCCCGTT-----A-CCCAGGTTCAAATCTCGGTCTCCGCG----  
>At0946|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|1313165|1313249|Ser|GCT|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGTGGCCAGCCTGGT--ACGGCGTGGACTGCTAATCCCATG-----G-CCCAGGTTCAAGTCCCGGCCCGCG----  
>At1565|Msta\_DSM3091|Euryarchaeota|Methanosphaera stadtmanae DSM 3091|602745|602828|Ser|GCT|0|0||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GTCGAGGTGGCCAGCCTGGT--ACGGCGTGGCCTGCTAAGCCACTG-----A-CCCAGGTTCAAGTCCCGGCCCGCG----  
>WENV078529|AAQK01000339|Gut microbiome of Human (healthy human stool sample 7)|1818|1729|Ser|GGA|  
0|0||||ENV division in DDBJ/EMBL/GenBank|  
TGCCGAGATAGTCTAGCTGGT--AAGGCGGAGACTGGAAATCTCGTG-----CTCCTGGGTTCAAATCCAGTCTCGGGCTTTA  
>At0891|Msmi\_ATCC35061|Euryarchaeota|Methanobrevibacter smithii ATCC 35061|1454656|1454740|Ser|GGA|  
0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGATAGTCTAGCTGGT--AAGGCGGAGACTGGAAATCTCGTG-----CTCCTGGGTTCAAATCCAGTCTCGGGCG----  
>WENV078536|AAQK01000495|Gut microbiome of Human (healthy human stool sample 7)|207|120|Ser|TGA|0|  
0||||ENV division in DDBJ/EMBL/GenBank|  
TGCCGAGATAGTCTAGCTGGT--AAGGCGCAGACTTGAAATCTCGTG-----G-CCTGGGTTCAAATCCAGTCTCGGGCTTCT  
>At2301|Msmi\_ATCC35061|Euryarchaeota|Methanobrevibacter smithii ATCC 35061|858702|858620|Ser|TGA|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGATAGTCTAGCTGGT--AAGGCGCAGACTTGAAATCTCGTG-----G-CCTGGGTTCAAATCCAGTCTCGGGCG----  
>WENV078537|AAQK01000495|Gut microbiome of Human (healthy human stool sample 7)|345|258|Ser|TGA|0|  
0||||ENV division in DDBJ/EMBL/GenBank|  
TGCCGAGATAGTCTAGCTGGT--AAGGCGCAGACTTGAAATCTCGTG-----G-CCTGGGTTCAAATCCAGTCTCGGGCTTAT  
>At1583|Msta\_DSM3091|Euryarchaeota|Methanosphaera stadtmanae DSM 3091|1002836|1002753|Ser|GGA|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGATAGTCTAGCTGGT--AAGGCGCAAGACTGGAAATCTTGTG-----TCCTGGGTTCAAATCCAGTCTCGGGCG----  
>At1646|Mthe\_DELTAH|Euryarchaeota|Methanothermobacter thermautotrophicus str. Delta H|17473|17557|  
Ser|GGA|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGATAGCTTAGCCAGGT--AAGGCGCAAGACTGGAAATCTTGTG-----TCCTGGGTTCAAATCCAGTCCCGGGCG----  
>At1586|Msta\_DSM3091|Euryarchaeota|Methanosphaera stadtmanae DSM 3091|1534991|1534908|Ser|TGA|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGATAGCTTAGCCAGGT--AAGGCGCGGGACTTGAGATCCCGTG-----TCATGGGTTCAAATCCCATCTCGGGCG----  
>At1661|Mthe\_DELTAH|Euryarchaeota|Methanothermobacter thermautotrophicus str. Delta H|967977|968061|  
Ser|TGA|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGATAGCTTAGCCAGGT--AAGGCGCGGGACTTGAGATCCCGTG-----G-CCTGGGTTCAAATCCAGTCCCGGGCG----  
>At0925|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|303992|304081|Ser|TGA|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCAGGGTAGCCAGCCAGGACTACGGCGTGGACTTGAGATCCAGTG-----G-CCTGGGTTCAAATCCAGCCCCTGCGCCA-  
>At1785|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|503940|504026|Ser|TGA|0|0||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGATAGCTTAGCCAGGT--AAGGCGCGGGCCTTGAGAGCCCGTG-----G-CCGGGTTCAAATCCCGTCCCGGGCGCCA-  
>At1792|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|638589|638675|Ser|GGA|0|0||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGTAGCTTAGCCAGGGA--AGGCCGCGGGCCTGGAGAGCCCGTG-----A-CCGGGTTCAAATCCCGGCCCGGGCGCCA-  
>At1802|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|1376125|1376211|Ser|CGA|0|0||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGTAGCTTAGCCAGGGA--AGGCCGCGGGACTCGAGATCCCGTG-----A-CCGGGTTCAAATCCCGGCCCGGGCGCCA-  
>At1829|Pfur\_DSM3638|Euryarchaeota|Pyrococcus furiosus DSM 3638|561295|561381|Ser|CGA|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGTAGCTTAGCCAGGGA--AGGCCGCGGGACTCGAGATCCCGTG-----G-CCGGGTTCAAATCCCGGCCCGGGCGCCA-  
>At1905|Phor\_OT3|Euryarchaeota|Pyrococcus horikoshii OT3|1326096|1326010|Ser|GGA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGTAGCTTAGCCAGGGA--AGGCCGCGGGCCTGGAGAGCCCGTG-----A-CCGGGTTCAAATCCCGGCCCGGGCGCCA-  
>At1942|Tkod\_KOD1|Euryarchaeota|Thermococcus kodakaraensis KOD1|262163|262077|Ser|GGA|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGTAGCTTAGCCAGGGA--AGGCCGCGGGCCTGGAGAGTCCCGTG-----G-CCAGGTTCAAATCCCTGCCCGGGCGCCA-  
>At1877|Phor\_OT3|Euryarchaeota|Pyrococcus horikoshii OT3|522870|522956|Ser|CGA|0|0||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGTAGCTTAGCCAGGGA--AGGCCGCGGGACTCGAGATCCCGTG-----A-CCGGGTTCAAATCCCGGCCCGGGCGCCA-  
>At1947|Tkod\_KOD1|Euryarchaeota|Thermococcus kodakaraensis KOD1|1040863|1040777|Ser|CGA|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGTAGCTTAGCCAGGGA--AGGCCGCGGGACTCGAGATCCCGTG-----A-CCAGGTTCAAATCCCTGCCCGGGCGCCA-  
>ENV000755|AM114193|Environmental sample from ENV division of INSDC|638134|638046|Ser|GGA|0|0||||  
ENV division in DDBJ/EMBL/GenBank|



TGCCGGGGTAGTCTAGT--GGT--AAGCGCGAAGCCTGGAAGCTTGTG-----CTCAGGAGTTCAAGTCTCTCCCGGGCGCTTT  
>At2090|Umet\_RC1|Euryarchaeota|uncultured methanogenic archaeon RC-I|638133|638050|Ser|GGA|0|0|||||The  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTAGTCTAGT--GGT--AAGCGCGAAGCCTGGAAGCTTGTG-----CTCAGGAGTTCAAGTCTCTCCCGGGCG----  
>At1613|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|2532857|2532940|Ser|GGA|0|0|||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCTGAGGTAGTCTAGTCTGGG--AAGCGCGAAGATTGGAATCTTGTG-----CTCGGGAGTTCAAATCTCCCCCTTAGCG----  
>At1468|Mbar\_FUSARO\_01|Euryarchaeota|Methanosarcina barkeri str. Fusaro|99955|99873|Ser|GGA|0|0|||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGGTAGTCTAGT--GGT--AGGGCGCAAGCCTGGAAGCTTGTG-----CTCGGGAGTTCAATCTCCCCCTCGGCG----  
>At1377|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|1308692|1308774|Ser|GGA|0|0|||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGGTAGTCTAGC--GGT--AGGGCGCAAGCCTGGAAGCTTGTG-----CTCGGGAGTTCAAATCTCCCCCTCGGCG----  
>At0671|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|2466900|2466984|Ser|CGA|0|0|||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGGTAGTCTAGCCCGG--AAGCGCGTAGCCTCGAAAGCTACTG-----CTCGGGAGTTCAAATCTCCCCCTCGGCG----  
>ENV09000431|ABSNO1068318|Freshwater sediment metagenome lwFormaldehyde\_C1||110|24|Ser|CGA|0|0|||||  
ENV division in DDBJ/EMBL/GenBank|  
TGCCGAGGTAGTCTAGCCCGG--AAGCGCGTAGCCTCGAAAGCTACTG-----CTCGGGAGTTCAAATCTCCCCCTCGGCGT---  
>At1603|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|960738|960821|Ser|TGA|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGATAGTCTAGTCCGGG--AAGCGCGTGGTCTTGAAGCAACTG-----CTCGGGAGTTCAAATCTCCCTTTCGGCG----  
>At1627|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|1088896|1088813|Ser|CGA|0|0|||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGGTAGTCTAGTCCGGG--AAGCGCGTGGTCTCGAAACCCTG-----CTCGGGAGTTCAAATCTCCCCCTCGGCG----  
>At1215|Mlab\_Z|Euryarchaeota|Methanocorpusculum labreanum Z|344812|344726|Ser|TGA|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGATAGTCTAGTCCGGA--AAGCGCGTGGCCTTGAAGCCCTG-----CTCGGGAGTTCAAATCTCCCTCTCGGCGCCA-  
>At1282|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|1436443|1436359|Ser|TGA|0|0|||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGATAGTCTAGTCCGGG--AAGCGCGTGGCCTTGAAGCCACTG-----CTCGGGAGTTCAAATCTCCCTCCCGGCG----  
>At1224|Mlab\_Z|Euryarchaeota|Methanocorpusculum labreanum Z|752303|752220|Ser|CGA|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGGTAGTCTAGTCCGGA--AGGGCGTGGCCTCGAAAGCCACTG-----CTCGGGAGTTCAAATCTCCCCCTCGGCG----  
>At1271|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|248553|248469|Ser|CGA|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGGTAGTCTAGTCCGGG--AAGCGCGTGGCCTCGAAAGCCACTG-----CTCGGGAGTTCAAATCTCCCCCTCGGCG----  
>At0660|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|1441465|1441549|Ser|TGA|0|0|||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTAGTCTAGTCCGGT--AAGCGCGTGGCCTTGAAGCCACTG-----CTCAAGAGTTCAAATCTCTTCCCGGGCG----  
>At0780|Hmar\_ATCC43049|Euryarchaeota|Halosarcina marismortui ATCC 43049|1517540|1517456|Ser|CGA|0|  
0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGGTAGCTAGCTAGCCTGGCC--AAGCGCGTGGTCTCGAGAGCAACTG-----CTCAGGAGTTCAAATCTCCTCTCGGCG----  
>At1711|Npha\_DSM2160|Euryarchaeota|Natronomonas pharaonis DSM 2160|327596|327512|Ser|CGA|0|0|||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGGTAGCTAGCCTAGCCTGGCC--AAGCGCGTGGTCTCGAGAGCAACTG-----CTCGTGAGTTCAAATCTCACCTCGGCG----  
>At0866|Hwal\_DSM16790|Euryarchaeota|Halosarcina walsbyi|386951|386867|Ser|CGA|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGGTAGCCTAGCCTGGTC--AAGCGCGCAGATTGGAATCTGTG-----A-CGTGAGTTCAAATCTCACCTCGGCG----  
>At2008|Taci\_DSM1728|Euryarchaeota|Thermoplasma acidophilum DSM 1728|1477335|1477253|Ser|CGA|0|  
0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GTCGGGGTAGCCTAGCCTGGGT--AAGCGGTAGACTCGAGATCTACTG-----CTCGGGAGTTCAAATCTCCCCCGGAGC----  
>At1411|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|754369|754290|Ser|CGA|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGGTAGTCTAGT--GGT--AAGCGCGCAGGTCTCGAAACCCTTT-----G-CGCAGGTTCAAATCTGCCCCTGGGCG----  
>At1487|Mbar\_FUSARO\_01|Euryarchaeota|Methanosarcina barkeri str. Fusaro|1927445|1927362|Ser|CGA|0|  
0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGGTAGTCTAGT--GGT--AAGCGCGCAGGTCTCGAAACCCTTT-----G-CGCAGGTTCAAATCTGCCCCTGGGCG----  
>At1545|Mmaz\_GOE1|Euryarchaeota|Methanosarcina mazei Go1|2154810|2154731|Ser|CGA|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGAGGTAGTCTAGC--GGT--ATGGCGACGGTCTCGAAACCCTTT-----ATCGCAGGTTCAAATCTGCCCCTGGGCG----  
>ENV004146|DQ397547|Environmental sample from ENV division of INSDC||5693|5605|Ser|TGA|0|0|||||ENV  
division in DDBJ/EMBL/GenBank|  
TGCAGAGGTGCGCTAGCCCGG--ATGGCGCGGCCTTGAGAGCCTGTG-----A-CGGGGTTCAAATCCCCCTCTCTGCGCCAA  
>At0090|Csym|Crenarchaeota|Cenarchaeum symbiosum|1717306|1717220|Ser|TGA|0|0|||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCAGAGGTGCGCTAGCCCGG--ATGGCGCGGCCTTGAGAGCCTGTG-----A-CGGGGTTCAAATCCCCCTCTCTGCGCCAA-  
>At1064|Mmar\_C5|Euryarchaeota|Methanococcus maripaludis C5|234332|234245|Ser|GGA|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCAGAGATAGTCTAGCTGGG--AAGCGGTACGGCTGGAACCGTATG-----G-CGGGGTTCAAATCCCCCTCTCTGCGCCAA-  
>At1157|Mvan\_SB|Euryarchaeota|Methanococcus vannielii SB|686363|686450|Ser|GGA|0|0|||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GCAGAGATAGTCTAGCTGGG--AAGCGGTACGGCTGGAACCGTATG-----G-CGGGGTTCAAATCCCCCTCTCTGCGCCAA-  
>At1134|Mmar\_S2|Euryarchaeota|Methanococcus maripaludis S2|1305759|1305846|Ser|GGA|0|0|||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCAGAGATAGTCTAGCCTGGG--AAGGCGTACGGCTGGAAACCGTATG-----CCCGGGGTTCAAATCCCCCTCTCTGCGCCA-  
 >At1031|Maeo\_Nankai3|Euryarchaeota|Methanococcus aeolicus Nankai-3|1146041|1145957|Ser|GGA|0|0||||  
 The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCAGAGATAGTCTAGCTCGGT--AAGGCGTGGGACTGGAAATCCCATG-----G-CGGGGGTTCAAATCCCCCTCTCTGCG----  
 >At0922|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|186978|187066|Ser|GGA|0|  
 0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCGGAGGTAGCCTAGCCCGCC--AAGGCGTGGGACTGGAGATCCCATG-----G-CGGGGGTTCAAATCCCCCTCCGCGCCA-  
 >At1066|Mmar\_C5|Euryarchaeota|Methanococcus maripaludis C5|619792|619706|Ser|TGA|0|0||||The tRNA  
 gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCAGAGGTAGTCTAGCCTGGCCAAAGGCGCGGACTTGAATCCGGTT-----G-CGGGGGTTCAAATCCCTCCTCTGCG----  
 >At1032|Maeo\_Nankai3|Euryarchaeota|Methanococcus aeolicus Nankai-3|1173128|1173042|Ser|TGA|0|0||||  
 The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCAGAGGTGGTCGAGCTGGACTATGGCGCGGACTTGAATCCGGTG-----G-CAAGGGTTCAAATCCCTCCTCTGCG----  
 >At0676|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|494636|494553|Ser|GGA|0|0||||The  
 tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCTGAGGTAGTCTAG--CGGT--AGGGCGCAGGCCTGGAAAGCCTGTG-----CTCGGGGTTCAATTCCTCCCTCAGCG----  
 >At1214|Mlab\_Z|Euryarchaeota|Methanocorpusculum labreanum Z|76148|76065|Ser|GGA|0|0||||The tRNA  
 gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCTGAGGTAGTCTAG--CGGT--AGGGCGCGGCTGGAAAGCCTGTG-----CTCGGGAGTTCAAATTCCTCCCTCAGCG----  
 >At1275|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|520620|520534|Ser|GGA|0|0||||The tRNA  
 gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCTGAGGTAGTCTAGCCGGT--AGGGCGCGGCTGGAAAGCCTGTG-----CTCGGGAGTTCAAATTCCTCCCTCAGCG----  
 >At0956|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|1038620|1038544|Arg|GCG|0|  
 0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCCGGGTCGCCTAGCCAGGAT--AGGGCGCTGGCCTGCGGAGCCAGTT-----TTCAGGGGTTCAAATCCCTCCCGGGCG----  
 >At0079|Csym|Crenarchaeota|Cenarchaeum symbiosum|271171|271071|Ser|GGA|271133|271120||||The tRNA  
 gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCCGGGTCGCCTAGCCTGGT--AGGGCGCGCCTGGAAAGCCTGTG-----ATCGGGAGTTCAATTCCTCCCTCCCGGGCCA-  
 >At0161|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|1960401|1960497|Ser|GCT|1960440|  
 1960451||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCCGGATCGCCTAGCCTGGT--AGGGCGCGCCTGCTAAGCCGTG-----G-CGTGGGTTCAAATCCACTCCCGGGCG----  
 >At2201|Ihos\_KIN4I|Crenarchaeota|Ignicoccus hospitalis KIN4/I|152550|152637|Ser|GCT|0|0||||The tRNA  
 gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCCGGGTCGCCTAGCCTGGCC--AGGGCGCGCCTGCTAAGCCGGTG-----G-CGCGGGTTCAAATCCCGCCCCGGCGCCA-  
 >At0390|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|864114|864198|Ser|GCT|0|0||||The tRNA gene  
 was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCCGGGTCGCCTAGCCTGGT--AGGGCGCGCCTGCTAAGCCGGTG-----G-CGCGGGTTCAAATCCCGCCCCGGCG----  
 >At0103|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|455560|455647|Ser|GCT|0|0||||The  
 tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCCGGGTCGCCTAGCCTGGT--AGGGCGCGCCTGCTAAGCCGGTG-----G-CGCGGGTTCAAATCCCGCCCCGGCGCCA-  
 >At0443|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|72657|72570|Ser|GCT|0|0||||The  
 tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCCGGGTCGCCTAGCCTGGT--AGGGCGGAGGCCTGCTAAGCCCTG-----G-CGCGGGTTCAAATCCCGCCCCGGCGCCA-  
 >At0557|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|2064049|2063961|Ser|GCT|0|0||||The tRNA  
 gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCCGGGTCGCCTAGCCTGGT--AGGGCGCGCCTGCTAAGCCGGTG-----G-CGCGGGTTCAAATCCCGCCCCGGCGCCA-  
 >At0487|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|49832|49748|Ser|GCT|0|0||||The tRNA gene  
 was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCAGGTCGCCTAGCCAGGT--AGGGCGCGCCTGCTAAGCCGGTG-----A-CGCGGGTTCAAATCCCGCCTCAGCG----  
 >At0020|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|192778|192691|Ser|GCT|0|0||||The tRNA gene was  
 obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCCGGGTCGCCTAGCCTGGCC--AGGGCGCGCCTGCTAAGCCGGTG-----G-CGCGGGTTCAAATCCCGCCCCGGCGCCA-  
 >At1796|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|894809|894895|Ser|GCT|0|0||||The tRNA gene was  
 obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCCGGGTCGCCTAGCCTGGT--AGGGCGCGCCTGCTAAGCCGGTG-----G-CCGGGTTCAAATCCCGCCGCGGGCCA-  
 >At1922|Tkod\_KOD1|Euryarchaeota|Thermococcus kodakaraensis KOD1|995072|995157|Ser|GCT|0|0||||The  
 tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCCGGGTCGCCTAGCCTGGT--AGGGCGCGCCTGCTAAGCCGGTG-----A-CCGGGTTCAAATCCCGCCGCGGGCCA-  
 >WENV078520|AAQK01000174|Gut microbiome of Human (healthy human stool sample 7)||606|521|Leu|TAG|0|  
 0||||ENV division in DDBJ/EMBL/GenBank|  
 -GCCGGGTTGCCGAGA--GGCCAAAGGGGACAGGCTTAGGACCTGTTG-----A-CCAGGGTTCAAATCCCTGCTCCCGCATTC-  
 >At0913|Msmi\_ATCC35061|Euryarchaeota|Methanobrevibacter smithii ATCC 35061|1050938|1050856|Leu|TAG|  
 0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCGGGTTGCCGAGA--GGCCAAAGGGGACAGGCTTAGGACCTGTTG-----A-CCAGGGTTCAAATCCCTGCTCCCGCA----  
 >At1560|Msta\_DSM3091|Euryarchaeota|Methanosphaera stadtmanae DSM 3091|337323|337406|Leu|TAG|0|0||||  
 The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCGGGTTGCCGAGCT--GGCCAAAGGGGACAGGCTTAGGACCTGTTG-----C-CCAGGGTTCAAATCCCTGCTCCCGCA----  
 >At1678|Mthe\_DELTAH|Euryarchaeota|Methanothermobacter thermautotrophicus str. Delta H|1160209|  
 1160126|Leu|TAG|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
 -GCCGGGTTGCCGAGCT--GGCCAAAGGGGACAGGCTTAGGACCTGTTG-----A-CCAGGGTTCAAATCCCTGCCCGCA----  
 >WENV078526|AAQK01000290|Gut microbiome of Human (healthy human stool sample 7)||1022|935|Leu|TAA|0|  
 0||||ENV division in DDBJ/EMBL/GenBank|  
 TGCAAGGGTTGCCGAGC--GGCCAAAGGGGAGGACTAAGATCCTCTG-----TTCGAGGGTTCAAATCCCTTCCCTGCACTAT  
 >At0900|Msmi\_ATCC35061|Euryarchaeota|Methanobrevibacter smithii ATCC 35061|554355|554273|Leu|TAA|0|  
 0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|





-GCGGGGGTGCCCGAGCCAGGTCAAAGGGGCAGGGTTCAGGTCCCTGTG-----G-CGTGGGTTCAAATCCCACCCCCGCACCA-  
>At0198|Paer\_IM2|Crenarchaeota|Pyrobaculum aerophilum str. IM2|1420272|1420359|Leu|GAG|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTGCCCGAGCCAGGTCAAAGGGGCAGGGTTCAGGTCCCTGTG-----G-CGTGGGTTCAAATCCCACCCCCGCACCA-  
>At0315|Pcal\_JCM11548|Crenarchaeota|Pyrobaculum calidifontis JCM 11548|603197|603113|Leu|CAA|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTGCCCGAGCCAGGCCAAAGGGGCAGGGCTCAAGACCCTGTG-----A-CGTGGGTTCAAATCCCACCCCCGCA----  
>At0367|Pisl\_DSM4184|Crenarchaeota|Pyrobaculum islandicum DSM 4184|1456990|1456906|Leu|CAA|0|0||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTGCCCGAGCCAGGCCAAAGGGGCAGGGCTCAAGACCCTGTG-----G-CGTGGGTTCAAATCCCACCCCCGCA----  
>ENV09004098|ADKH01001090|Hot springs metagenome ctg\_1106445186506|1120|1207|Leu|CAA|0|0||||ENV  
division in DDBJ/EMBL/GenBank|  
-GCGGGGGTGCCCGAGCCAGGCCAAAGGGGCAGGGCTCAAGACCCTGTG-----G-CGTGGGTTCAAATCCCACCCCCGCACCA-  
>At0269|Pars\_DSM13514|Crenarchaeota|Pyrobaculum arsenaticum DSM 13514|1531664|1531580|Leu|TAA|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTGCCCGAGCCAGGTCAAAGGGGCAGGGCTTAAGACCCTGTG-----G-CGTGGGTTCAAATCCCACCCCCGCA----  
>At0322|Pcal\_JCM11548|Crenarchaeota|Pyrobaculum calidifontis JCM 11548|1647452|1647368|Leu|TAA|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTGCCCGAGCCAGGTCAAAGGGGCAGGGCTTAAGACCCTGTG-----G-CGTGGGTTCAAATCCCACCCCCGCA----  
>At0208|Paer\_IM2|Crenarchaeota|Pyrobaculum aerophilum str. IM2|1959975|1960062|Leu|TAA|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTGCCCGAGCCAGGTCAAAGGGGCAGGGCTTAAGACCCTGTG-----G-CGTGGGTTCAAATCCCACCCCCGCACCA-  
>At0383|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|767378|767465|Leu|GAG|0|0||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTGCCCGAGCCAGGTCAAAGGGGCAGGGCTTAAGACCCTGTG-----G-CGTGGGTTCAAATCCCACCCCCGCACCA-  
>At0027|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|340125|340001|Ser|CGA|340087|340052||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGCCCGAGC--GGCCCAAGGCGGGCTCGAGACCCTGTG-----G-CGCGGGTTCAAATCCCACCCCCGCGCCA-  
>At0041|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|1163580|1163492|Ser|GGA|0|0||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGCCCGAGC--GGTCCAAGGGGCAGGGCTGAGACCCTGTG-----G-CGCGGGTTCAAATCCCACCCCCGCGCCA-  
>At0035|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|872084|871996|Ser|TGA|0|0||||The tRNA gene was  
obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGCCCGAGC--GGCCCAAGGCGGGCTTGAAGACCCTGTG-----G-CGCGGGTTCAAATCCCACCCCCGCGCCA-  
>At0164|Msed\_DSM5348|Crenarchaeota|Metallosphaera sedula DSM 5348|2154080|2154188|Ser|CGA|2154118|  
2154141||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGCCCGAGC--GGACCAAGGGGGTAGGCTCGAGACCTACTG-----A-CGCGGGTTCAAATCCCACCCCCGCGCG----  
>At0505|Ssol\_P2|Crenarchaeota|Sulfolobus solfataricus P2|641038|640931|Ser|CGA|641001|640978||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGCCCGAGC--GG-TCAAGGGGGTAGGCTCGAGACCTACTG-----A-CACGGGTTCAAATCCCCTCCCCGCGCG----  
>At0521|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|367006|367116|Ser|CGA|367044|367069||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGCCCGAGC--GGACTAAGGGGGTAGGCTCGAGACCTACTG-----A-CGCGGGTTCAAATCCCACCCCCGCGCG----  
>At0377|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|563621|563770|Ser|CGA|563659|563718||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGCCCGAGC--GGACTAAGGGGGTAGGCTCGAGACCTACTG-----G-CGCGGGTTCAAATCCCACCCCCGCGCGCCA-  
>At2222|Ihos\_KIN4I|Crenarchaeota|Ignicoccus hospitalis KIN4/I|1252098|1251982|Ser|CGA|1252060|  
1252034||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGCCCGAGC--GGCCCAAGGGGGTAGGCTCGAGACCCACTG-----G-CGCGGGTTCAAATCCCACCCCCGCGCGCCA-  
>At2243|Ihos\_KIN4I|Crenarchaeota|Ignicoccus hospitalis KIN4/I|62894|62806|Ser|GGA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGCCCGAGC--GGCCCAAGGGGGTAGGCTGAGAGCCACTC-----G-CGCGGGTTCAAATCCCACCCCCGCGCGCCA-  
>At2118|Nequ\_KIN4M|Nanoarchaeota|Nanoarchaeum equitans Kin4-M|308534|308618|Ser|TGA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTGCCCGAGC--GGACCAAGGGGGTTCGGCTGAGACCGAATC-----G-CGCGGGTTCAAATCCCACCCCCGCGCGCG----  
>At2138|Nequ\_KIN4M|Nanoarchaeota|Nanoarchaeum equitans Kin4-M|253445|253361|Ser|GGA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTGCCCGAGC--GGACCAAGGGGGTTCGGCTGAGACCGAATC-----G-CGCGGGTTCAAATCCCACCCCCGCGCGCG----  
>At2125|Nequ\_KIN4M|Nanoarchaeota|Nanoarchaeum equitans Kin4-M|486338|486422|Ser|CGA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGCCGTGCCCGAGC--GGCCCAAGGGGGTAGGCTCGAGACCCTCTC-----G-CGCGGGTTCAAATCCCACCCCCGCGCGCG----  
>At0387|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|810962|811050|Ser|GGA|0|0||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGCCCGAGC--GGACTAAGGGGGTTCGGCTGAGAGCCAGTG-----G-CGCGGGTTCAAATCCCACCCCCGCGCGCCA-  
>At0099|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|373519|373640|Ser|CGA|373557|  
373589||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGCCCGAGC--GGTCCAAGGCGGTTCGGCTCGAGACCCACTG-----G-CGCGGGTTCAAATCCCACCCCCGCGCGCCA-  
>At0575|Tpen\_HRK5|Crenarchaeota|Thermophilum pendens Hrk 5|536447|536563|Ser|CGA|536480|536493||  
536499|536513||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGCCCGAGC--GGACCAAGGCGGGTTCGAGATCCACTG-----G-CCC GGTTCAAATCCCACCCCCGCGCGCCA-  
>At0586|Tpen\_HRK5|Crenarchaeota|Thermophilum pendens Hrk 5|231236|231134|Ser|TGA|231203|231189||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGCCCGAGT--GGACTAAGGCGGTTCGAGATCCACTA-----G-CCC GGTTCAAATCCCACCCCCGCGCGCCA-  
>At0576|Tpen\_HRK5|Crenarchaeota|Thermophilum pendens Hrk 5|538958|539045|Ser|GGA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|



-GCCGGGGTGGCCGAGC--GGTCTAAGCGGGGGCTGCAGACCCCGTT-----ACCGGGGTTTCGAATCCCGCCCCGGCTCCA-  
>At0568|Tpen\_HRK5|Crenarchaeota|Thermofilum pendens Hrk 5|420870|421000|Cys|GCA|420900|420925||  
420933|420960||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGGCCGAGA--GGTC-AAGGCGTCGGGCTGCAGACCCGATA-----TTCCCGGGTTCGAGTCCCGGCCCGGCTCCA-  
>At2199|Ihos\_KIN4I|Crenarchaeota|Ignicoccus hospitalis KIN4/I|56438|56542|Cys|GCA|56476|56502||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGGCCGAGC--GGCTAAGGGGTCGGGCTGCAGACCCGATC-----CTCCCGGGTTCGAATCCCGGCCCGGCTCCA-  
>At0047|Aper\_K1|Crenarchaeota|Aeropyrum pernix K1|1391457|1391362|Cys|GCA|1391419|1391402||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGGCCGAGC--GGTCTAAGCGGGGGCTGCAGACCCGTTA-----TTCCCGGGTTCGAATCCCGGCCCGGCTCCA-  
>At0567|Tpen\_HRK5|Crenarchaeota|Thermofilum pendens Hrk 5|394845|394954|Ser|GCT|394879|394900||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGGCCGAGC--GGCCCAAGGCGGGGATTGCTAATCCGTTA-----G-CCCGGGTTCGAATCCCGGCCCGGCGCCA-  
>At1299|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|566035|566125|Ser|TGA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGCGCCGAGCCCGTCCAAGGCGGGACTTGAGATCCCGTG-----G-CCCGGGTTCGAATCCCGGCCCGGCGCCA-  
>At1322|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|1552920|1552830|Ser|GGA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGCGCCGAGCCCGTCCAAGGCGGGGATTGAGATCCCGTG-----G-CCCGGGTTCGAATCCCGGCCCGGCGCCA-  
>At1310|Mkan\_AV19|Euryarchaeota|Methanopyrus kandleri AV19|1670465|1670555|Ser|GCT|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGCGCCGAGCCCGTCCAAGGCGGGACTGCTAATCCCGTG-----G-CCCGGGTTCGAATCCCGGCCCGGCGCCA-  
>At2112|Nequ\_KIN4M|Nanoarchaeota|Nanoarchaeum equitans Kin4-M|161947|162030|Leu|TAG|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCGGTGCCGAGC--GGTCAAGGGGTCGGGCTTAGGACCCGATG-----GTCCGGGGTTCGAATCCCGCGGCCGCA----  
>At2117|Nequ\_KIN4M|Nanoarchaeota|Nanoarchaeum equitans Kin4-M|304059|304142|Leu|CAA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCGGTGCCGAGC--GGTCAAGGGGTCGGGCTCAAGACCCGATG-----GTCCGGGGTTCGAATCCCGCGGCCGCA----  
>At2124|Nequ\_KIN4M|Nanoarchaeota|Nanoarchaeum equitans Kin4-M|476845|476928|Leu|GAG|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCGGTGCCGAGC--GGACAAAGGGGCGAGTTGAGGTCCTGGTG-----G-CCGGGGTTCGAATCCCGCGGCCGCA----  
>At2141|Nequ\_KIN4M|Nanoarchaeota|Nanoarchaeum equitans Kin4-M|279015|278931|Leu|TAA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCGGTGCCGAGC--GGCCAAAGGGGTCGGGCTTAAGACCCGATG-----G-CCGGGGTTCGAATCCCGCGGCCGCA----  
>ENV004068|DQ314493|Environmental sample from ENV division of INSDC|31442|31520|Cys|GCA|0|0||||  
ENV division in DDBJ/EMBL/GenBank|  
-GCCAAGGTGGCAGAGCCTGGCCTAACGCGTCCGCCTGCAGAGCGGATC-----ATCGCCGGTTCGAATCCCGCCCTTGCTTCA-  
>At0842|Hwal\_DSM16790|Euryarchaeota|Haloquadratum walsbyi|73400|73475|Cys|GCA|0|0||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCAAGGTGGCAGAGCCTGGCCTAACGCGTCCGCCTGCAGAGCGGATC-----ATCGCCGGTTCGAATCCCGCCCTTGCTTCA-  
>At0814|Halo\_NRC1|Euryarchaeota|Halobacterium sp. NRC-1|1880755|1880830|Cys|GCA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCAAGGTGGCAGAGTTTCGGCCTAACGCGGCGCCTGCAGAGCGGCTC-----ATCGCCGGTTCGAATCCCGCCCTTGCTTCA-  
>At0766|Hmar\_ATCC43049|Euryarchaeota|Haloarcula marismortui ATCC 43049|2637802|2637877|Cys|GCA|0|  
0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCAAGGTGGCAGAGTCTGGCCTAACGCGGCGCCTGCAGAGCGGCC-----ATCGCCGGTTCGAATCCCGCCCTTGCTTCA-  
>At0771|Hmar\_ATCC43049|Euryarchaeota|Haloarcula marismortui ATCC 43049|99037|98954|Ser|TGA|0|0||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGTGGGATGGCAGAGC--GGCCTATTGCGCCTGCCTTGAAGCAGGTA-----TTCCTGGGTTTCGAATCCCGTCCCACCG----  
>At1720|Npha\_DSM2160|Euryarchaeota|Natronomonas pharaonis DSM 2160|1484046|1483965|Ser|TGA|0|0||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGTGGGATGGCAGAGT--GGCCATTGCGTCTGCCTTGAAGCAGATG-----CTCCTGGGTTTCGAATCCCGTCCCACCG----  
>At0881|Hwal\_DSM16790|Euryarchaeota|Haloquadratum walsbyi|2275833|2275750|Ser|TGA|0|0||||The tRNA  
gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGTGGGATGGCAGAGT--GGACTAAGCGCGCCTGCCTTGAGAGCAGGTG-----CTCCTGGGTTTCGAATCCCGTCCCACCG----  
>At0825|Halo\_NRC1|Euryarchaeota|Halobacterium sp. NRC-1|920358|920276|Ser|TGA|0|0||||The tRNA gene  
was obtained from SPLITSdb.|GIB in DDBJ|  
-GGTGAGGTGGCAGAGC--GGCCTATTGCGCGGCTTGAAGACCGGTG-----CTCCTGGGTTTCGAATCCCGTCCCACCG----  
>WENV078521|AAQK01000174|Gut microbiome of Human (healthy human stool sample 7)|738|659|Glu|TTC|0|  
0||||ENV division in DDBJ/EMBL/GenBank|  
TGCTCCGGTGGTGTAGTCCGGCCAATCATTTTCGGCCTTCGAGCCGAAG-----A-CTCGGGTTCGAATCCCGGCCGAGCATTTA  
>At1559|Msta\_DSM3091|Euryarchaeota|Methanosphaera stadtmanae DSM 3091|337144|337218|Glu|TTC|0|0||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCTCCGATAGTGTAGTCCGGCCAATCATTTTCGGCCTTCGAGCCGAAG-----A-CTCGGGTTCGAATCCCGGTCGGAGCA----  
>At0914|Msmi\_ATCC35061|Euryarchaeota|Methanobrevibacter smithii ATCC 35061|1051069|1050995|Glu|TTC|  
0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCTCCGGTGGTGTAGTCCGGCCAATCATTTTCGGCCTTCGAGCCGAAG-----A-CTCGGGTTCGAATCCCGGCCGAGCA----  
>At1679|Mthe\_DELTAH|Euryarchaeota|Methanothermobacter thermautotrophicus str. Delta H|1160328|  
1160254|Glu|TTC|0|0||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCTCCGGTGTAGTGTAGTCCGGCCAATCATTTTCGGCCTTCGAGCCGAAG-----A-CTCGGGTTCGAATCCCGGCCGAGCA----  
>At0989|Mbur\_DSM6242|Euryarchaeota|Methanococcoides burtonii DSM 6242|157872|157795|Glu|TTC|0|0||||  
The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCTCCGGTGTAGTGTAGTCCGGCCAATCATTTTCAGCCTTCGAGCTGAAA-----A-CTCGGGTTCGAATCCCGGCCGAGCACCA-  
>At1380|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|1681890|1681967|Glu|TTC|0|0||||The  
tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATTCGGCCTTTCGAGCCGAAG-----A-CTCGGGTTCGAATCCCGGCCGAGCACCA->ENV000764|AM114193|Environmental sample from ENV division of INSDC||1335580|1335657|Glu|TTC|0|0|||||ENV division in DDBJ/EMBL/GenBank|

-GCTCCGGTGTAGTCCGGCCAATCATGTCCGGCCTTTCGAGCCGACG-----A-CTCGGGTTCGAATCCCGACCAGGAGCATT->At2069|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I||1335580|1335654|Glu|TTC|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATGTCCGGCCTTTCGAGCCGACG-----A-CTCGGGTTCGAATCCCGACCAGGAGCA---->At0826|Halo\_NRC1|Euryarchaeota|Halobacterium sp. NRC-1|990847|990773|Glu|CTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATCTTGCCCTTCACGGCAAGG-----A-CTAGGGTTCAAATCCCTGACGGAGCA---->At1714|Npha\_DSM2160|Euryarchaeota|Natronomonas pharaonis DSM 2160|700944|700870|Glu|CTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATCTTGCCCTTCACGGCAAGG-----A-CCAGGGTTCGAATCCCTGACGGAGCA---->At0873|Hwal\_DSM16790|Euryarchaeota|Haloquadratum walsbyi|1689734|1689660|Glu|CTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATCTTGCCCTTCACGGCAAGG-----A-CTTGGGTTCAAATCCCAAACGGAGCA---->At0774|Hmar\_ATCC43049|Euryarchaeota|Haloarcula marismortui ATCC 43049|709124|709050|Glu|CTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATATCACCCCTTCACGGTGTAG-----A-CTAGGGTTCAAATCCCTGACGGAGCA---->At0777|Hmar\_ATCC43049|Euryarchaeota|Haloarcula marismortui ATCC 43049|970207|970133|Glu|TTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATCTTGCCCTTCGAGCCGAGG-----A-CCAGGGTTCAAATCCCTGACGGAGCA---->At0805|Halo\_NRC1|Euryarchaeota|Halobacterium sp. NRC-1|982991|983065|Glu|TTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATGTGGCCTTTCGAGCCGACG-----A-CCAGGGTTCAAATCCCTGACGGAGCA---->At0856|Hwal\_DSM16790|Euryarchaeota|Haloquadratum walsbyi|2299050|2299124|Glu|TTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATGTGGCCTTTCGAGCCGACG-----A-CAGGGTTCGAATCCCTACGGAGCA---->At1726|Npha\_DSM2160|Euryarchaeota|Natronomonas pharaonis DSM 2160|1941912|1941838|Glu|TTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATATTGGCCTTTCGAGCCGATG-----A-CAGGGTTCAAATCCCTAGCGAGCA---->At1732|Ptor\_DSM9790|Euryarchaeota|Picrophilus torridus DSM 9790|231309|231383|Glu|TTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAAGCATTCGGCCTTTCGAGCCGATG-----A-CTCGGGTTCAAATCCCGACCAGGAGCA---->At0927|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|358869|358943|Glu|TTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATGCGGGCCTTTCGAGCCCGCG-----A-CCCGGGTTCAAATCCCGCCGGAGCA---->At1016|Mao\_Nankai3|Euryarchaeota|Methanococcus aeolicus Nankai-3|1029319|1029393|Glu|TTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCAGTGTAGTCCGGCCAATCATGCAGGCCTTTCGAGCCTGCG-----A-CTCGGGTTCAAATCCCGGCTGGAGCA---->At1058|Mmar\_C5|Euryarchaeota|Methanococcus maripaludis C5|1700176|1700250|Glu|TTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCAGTGTAGTCCGGCCAATCATCCGGCCTTTCGAGCCGGG-----A-CTCGGGTTCAAATCCCGGCTGGAGCA---->At1173|Mvan\_SB|Euryarchaeota|Methanococcus vanniellii SB|1376273|1376347|Glu|TTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATGTGGCCTTTCGAGCCGACG-----A-CTCGGGTTCAAATCCCGCCGGAGCA---->At0614|Aful\_DSM4304|Euryarchaeota|Archaeoglobus fulgidus DSM 4304|788605|788695|Glu|TTC|788645|788660|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATTCGGCCTTTCGAGCCGCG-----A-CCCGGGTTCAAATCCCGCCGGAGCA---->ENV000764|AM114193|Environmental sample from ENV division of INSDC||141433|141354|Glu|CTC|0|0|0|||||ENV division in DDBJ/EMBL/GenBank|

TGCTCCGATAGTGTAGACCGCCAATCATGACGACTCTCACTCCGTCG-----A-CTGGGGTTCAAATCCCCATCGGAGCACTGA->At2082|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I||141432|141358|Glu|CTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGATAGTGTAGACCGCCAATCATGACGACTCTCACTCCGTCG-----A-CTGGGGTTCAAATCCCCATCGGAGCA---->At1399|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|5042745|5042819|Glu|CTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGATAGTGTAGTCCGGCCAATCATTCAGGACTCTCACTCCTGCG-----A-CTGGGGTTCAAATCCCCATCGGAGCA---->At1006|Mbur\_DSM6242|Euryarchaeota|Methanococcoides burtonii DSM 6242|2427741|2427664|Glu|CTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGATAGTGTAGCACCAGCCAATCATACAGGACTCTCACTCCTGCG-----A-CTGGGGTTCGAATCCCCATCGGAGCACCA->At1259|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|1698223|1698297|Glu|CTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTGCTATAGTGTAGACCGCCAATCATGCAGGACTCTCACTCCTGCG-----A-CTGGGGTTCGAATCCCCATAGCAGCA---->At1332|Mthe\_PT|Euryarchaeota|Methanosaeta thermophila PT|533761|533835|Glu|CTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTCCGGTGTAGTCCGGCCAATCATGAGGACTCTCACTCCTGCG-----A-CTAGGGTTCAAATCCCTACGGAGCA---->At0661|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|1451410|1451484|Glu|TTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTGCTATAGTGTAGACCGCCAATCATGCGGGCCTTTCACGCCGCG-----A-CTGGGGTTCAAATCCCCATAGCAGCA---->At0663|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|1927535|1927609|Glu|CTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|

-GCTGCTATAGTGTAGACCGCCAATCATGCAGGACTCTCACTCCTGCG-----A-CAGGGGTTTCAAATCCCTTAGCAGCA---->At1602|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|778389|778463|Glu|TTC|0|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|











>At0610|Aful\_DSM4304|Euryarchaeota|Archaeoglobus fulgidus DSM 4304|515561|515643|Leu|CAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTTGCCGAG--CGGACAAAGGCGCGGATTTCAGGGTCCCCTGTC-----TTCGAGGGTTCGAATCCCTCCCCCGCA----  
>At0629|Aful\_DSM4304|Euryarchaeota|Archaeoglobus fulgidus DSM 4304|319266|319184|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTTGCCGAG--CGGACAAAGGCGCGGATTTCAGGGTCCCCTGTC-----TTCGAGGGTTCGAATCCCTCCCCCGCA----  
>At0632|Aful\_DSM4304|Euryarchaeota|Archaeoglobus fulgidus DSM 4304|766944|766847|Leu|CAA|766906|766892|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTTGCCGAG--TGGCCAAAGGCGGTGACTCAAGATCCACTC-----TTCGAGGGTTCGAATCCCTCCCCCGCA----  
>At1760|Ptor\_DSM9790|Euryarchaeota|Picropophilus torridus DSM 9790|654775|654691|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGAGATTGCCGAGCCAGGCCAAAGGCGATGGATTTCAGGGTCCATT-----TTCGGGGTTCGAATCCCTCTCCGCA----  
>At1778|Ptor\_DSM9790|Euryarchaeota|Picropophilus torridus DSM 9790|1443023|1442939|Leu|CAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGAGATTGCCGAGCCAGGCCAAAGGCGATGGATTTCAGGGTCCATT-----TTCGGGGTTCGAATCCCTCTCCGCA----  
>At1969|Taci\_DSM1728|Euryarchaeota|Thermoplasma acidophilum DSM 1728|669964|670048|Leu|CAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGAGATTGCCGAGCCAGGCCAAAGGCGATGGATTTCAGGGTCCATT-----TTCGGGGTTCGAATCCCTCTCCGCA----  
>At1996|Taci\_DSM1728|Euryarchaeota|Thermoplasma acidophilum DSM 1728|656418|656334|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGAGTTGTCGAGACTGGCCAAAGGCGATGGATTTCAGGGTCCATT-----TTCGAGGGTTCGAATCCCTCTCCGCA----  
>At1987|Taci\_DSM1728|Euryarchaeota|Thermoplasma acidophilum DSM 1728|15112|15028|Leu|GAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGAGTTGTCGAGACTGGTCAAAGGCGCAGATTGAGGGTCTGGTT-----G-CGAGGGTTCGAATCCCTCTCCGCA----  
>At1742|Ptor\_DSM9790|Euryarchaeota|Picropophilus torridus DSM 9790|861295|861379|Leu|GAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCAGAGTTGCCGAGACTGGACAAAGGCGCTAGATTGAGGGTCTAGTT-----TCCGCGGGTTCGAATCCCGTCTCTGCA----  
>At1975|Taci\_DSM1728|Euryarchaeota|Thermoplasma acidophilum DSM 1728|1008253|1008337|Leu|CAA|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCAGAGTTGCCGAGACTGGTCAAAGGCGCAGACTCAAGATCTGCCT-----TTCGCGGGTTCGAATCCCGTCTCTGCA----  
>At2020|Tvol\_GSS1|Euryarchaeota|Thermoplasma volcanium GSS1|1139566|1139650|Leu|CAA|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCAGAGTTGCCGAGACTGGTCAAAGGCGCAGACTCAAGATCTGCCT-----TTCGCGGGTTCGAATCCCGTCTCTGCA----  
>At1771|Ptor\_DSM9790|Euryarchaeota|Picropophilus torridus DSM 9790|948816|948732|Leu|CAA|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGAGTTACCGAGTCAGGTTAAAGGTGACAGACTCAAGATCTGTTC-----TTCGCGGGTTCGAATCCCGTCTCTGCA----  
>At0685|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|1393977|1393893|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGATCGCCAGCTTGGTCAAAGGCGCTGGATTTCAGGGTCCAGTC-----TTCGCGGGTTCGAATCCCGTCTCTGCA----  
>At1624|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|677338|677254|Leu|CAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGATCGCCAGCCAGGTCAAAGGCGTTAGGTTTCAGGGCCTAATC-----TTCGCGGGTTCGAATCCCGTCTCTGCA----  
>At1614|Mhun\_JF1|Euryarchaeota|Methanospirillum hungatei JF-1|2548309|2548393|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGATCGCCAGCCAGGTCAAAGGCGCAGGATTTCAGGGTCCGTT-----TTCGCGGGTTCGAATCCCGTCTCTGCA----  
>At0920|Mjan\_DSM2661|Euryarchaeota|Methanocaldococcus jannaschii DSM 2661|97629|97716|Leu|GAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTCCCAAGCCAGGTCAAAGGCGCAGATTGAGGGTCTGGTC-----TTCGCGGGTTCGAATCCCGTCCCCCGACCA--  
>ENV000757|AM114193|Environmental sample from ENV division of INSDC|938696|938609|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTAGCCAGCCAGGTCAAAGGCGTAGGACTTAGGATCCTATC-----TTCGTGCGTTCGAATCCGACCCCCGCACTT--  
>At2092|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I|938696|938612|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTAGCCAGCCAGGTCAAAGGCGTAGGACTTAGGATCCTATC-----TTCGTGCGTTCGAATCCGACCCCCGCA----  
>At1425|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|5064696|5064612|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGGTTCGCCAGCTAGGTCAAAGGCGATGGGCTTAGGACCCATT-----TTCGTGCGTTCGAATCCGACCCCTCGCA----  
>At1511|Mmaz\_GOE1|Euryarchaeota|Methanosarcina mazei Go1|945437|945521|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGGTTCGCCAGCCAGGTCAAAGGCGATGGGCTTAGGACCCATT-----TTCGTGCGTTCGAATCCGACCCCTCGCA----  
>At0979|Mbur\_DSM6242|Euryarchaeota|Methanococcoides burtonii DSM 6242|2437020|2437107|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGGTTCGCCAGCCAGGTCAAAGGCGATGGGCTTAGGACCCATT-----TTCGTGCGTTCGAATCCGACCCCTCGCA----  
>ENV000754|AM114193|Environmental sample from ENV division of INSDC|633281|633194|Leu|TAA|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTAACCAAGTCAGGCCAAAGGTGCAGGACTTAAGATCCTGTC-----TTCAGGGGTTTCGAATCCCTTCCCCCGCACTT--  
>At2089|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I|633281|633197|Leu|TAA|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGGTAACCAAGTCAGGCCAAAGGTGCAGGACTTAAGATCCTGTC-----TTCAGGGGTTTCGAATCCCTTCCCCCGCA----  
>At0651|Mboo\_6A8|Euryarchaeota|Candidatus Methanoregula boonei 6A8|119615|119697|Leu|CAA|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGAATATCTAAGT--GGCCAACAGAGGCGGACTCAAGATCCGTTC-----TTCGAGGGTTCGACTCTGCTTCTCGCA----  
>At1213|Mlab\_Z|Euryarchaeota|Methanocorpusculum labreanum Z|1722192|1722273|Leu|CAA|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGGTATCCAAGT--GGCCAACGAGGCTGACTCAAGATCTGCTC-----TTCGCGGGTTCGAATCCCTCCCCCGCA----









Archaea - siblings

>SRA1008912|SRR020491.59429|Microbial community gene content and expression in the Central North Pacific Gyre, Station ALOHA, HOT186 (SRP001041)||121|47|Ile|GAT|0|0|||||  
-GGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
>ENV004163|DQ397571|Environmental sample from ENV division of INSDC|31894|31815|Ile|GAT|0|0|||||  
ENV division in DDBJ/EMBL/GenBank|  
TGGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCATCCG  
>SRA1008833|SRR020491.38199|Microbial community gene content and expression in the Central North Pacific Gyre, Station ALOHA, HOT186 (SRP001041)||145|219|Ile|GAT|0|0|||||  
-GGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
>SRA1009108|SRR020491.122298|Microbial community gene content and expression in the Central North Pacific Gyre, Station ALOHA, HOT186 (SRP001041)||184|110|Ile|GAT|0|0|||||  
-GGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
>SRA1009246|SRR020491.163158|Microbial community gene content and expression in the Central North Pacific Gyre, Station ALOHA, HOT186 (SRP001041)||98|172|Ile|GAT|0|0|||||  
-GGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
>SRA1009315|SRR020491.186207|Microbial community gene content and expression in the Central North Pacific Gyre, Station ALOHA, HOT186 (SRP001041)||97|171|Ile|GAT|0|0|||||  
-GGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
>SRA1009399|SRR020491.213434|Microbial community gene content and expression in the Central North Pacific Gyre, Station ALOHA, HOT186 (SRP001041)||150|76|Ile|GAT|0|0|||||  
-GGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
>SRA1009447|SRR020491.231579|Microbial community gene content and expression in the Central North Pacific Gyre, Station ALOHA, HOT186 (SRP001041)||85|11|Ile|GAT|0|0|||||  
-GGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
>SRA1009494|SRR020491.252752|Microbial community gene content and expression in the Central North Pacific Gyre, Station ALOHA, HOT186 (SRP001041)||190|116|Ile|GAT|0|0|||||  
-GGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
>SRA1009563|SRR020491.278827|Microbial community gene content and expression in the Central North Pacific Gyre, Station ALOHA, HOT186 (SRP001041)||15|89|Ile|GAT|0|0|||||  
-GGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
>SRA1010114|SRR020491.461938|Microbial community gene content and expression in the Central North Pacific Gyre, Station ALOHA, HOT186 (SRP001041)||101|175|Ile|GAT|0|0|||||  
-GGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
>SRA1010358|SRR020492.27148|Microbial community gene content and expression in the Central North Pacific Gyre, Station ALOHA, HOT186 (SRP001041)||59|133|Ile|GAT|0|0|||||  
-GGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
>SRA1010448|SRR020492.58559|Microbial community gene content and expression in the Central North Pacific Gyre, Station ALOHA, HOT186 (SRP001041)||137|211|Ile|GAT|0|0|||||  
-GGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
>At0064|Csym|Crenarchaeota|Cenarchaeum symbiosum|1081371|1081445|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCTCGTAGCTCAGCTTGGCT-GGAGCGTTCGACTGATAATCGAAAG-----GTCATGAGTTCGAATCTCATCGGGCCCA----  
>At1422|Mace\_C2A|Euryarchaeota|Methanosarcina acetivorans C2A|3890122|3890046|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTAGCTTAGCCTGGT--GGAGCGCACGGCTGATAACCGTGAG-----GTCCTGCGTTTCAATCGCAGCGGGCCACCA-  
>At1504|Mmaz\_GOE1|Euryarchaeota|Methanosarcina mazei Go1|493102|493178|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTAGCTTAGCCTGGT--GGAGCGCACGGCTGATAACCGTGAG-----GTCCTGCGTTTCAATCGCAGCGGGCCACCA-  
>At1447|Mbar\_FUSARO\_01|Euryarchaeota|Methanosarcina barkeri str. Fusaro|2435659|2435735|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTAGCTTAGCCTGGT--GGAGCGCACGGCTGATAACCGTGAG-----GTCCTGCGTTTCAATCGCAGCGGGCCACCA-  
>At2080|Umet\_RCI|Euryarchaeota|uncultured methanogenic archaeon RC-I|2821549|2821644|Ile|GAT|2821574|2821594|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGTAGCTTAGCCTGGT--GGAGCGCTCGGCTGATAACCGAGAG-----GTCCTGCGTTTCAATCGCAGCGGGCCCA----  
>At2037|Tvol\_GSS1|Euryarchaeota|Thermoplasma volcanium GSS1|433376|433302|Ile|GAT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGGTGTAGCTTAGACAGGCT-ATAGCACTCGGCTGATAACCGAGAG-----GTCACCGGTTTCAATCCGGTCAACCCCA----  
>At1507|Mmaz\_GOE1|Euryarchaeota|Methanosarcina mazei Go1|856272|856346|Met|CAT|0|0|||||The tRNA gene was obtained from SPLITSdb. tRNA-Met(Ile) whose CAU anticodon is enzymatically converted to read AUA codons.|GIB in DDBJ|  
-GGGCTGTAGCTCAGTCAGGTT-AGAGCGTTCGGCTCATAACCGAGCG-----GTCACCGGTTTCAATCCGGTCAAGGCCA----  
>At1111|Mmar\_C7|Euryarchaeota|Methanococcus maripaludis C7|893989|893915|Met|CAT|0|0|||||The tRNA gene was obtained from SPLITSdb. tRNA-Met(Ile) whose CAU anticodon is enzymatically converted to read AUA codons.|GIB in DDBJ|  
-GGGCCGTAGCTCAGGCTGGT--AGAGTGCCTCGGCTCATAACCGAGTG-----GTCATGGGTTTCAATCCCATCGGGCCCA----  
>At1153|Mmar\_S2|Euryarchaeota|Methanococcus maripaludis S2|1601263|1601189|Met|CAT|0|0|||||The tRNA gene was obtained from SPLITSdb. tRNA-Met(Ile) whose CAU anticodon is enzymatically converted to read AUA codons.|GIB in DDBJ|  
-GGGCCGTAGCTCAGGCTGGT--AGAGTGCCTCGGCTCATAACCGAGTG-----GTCATGGGTTTCAATCCCATCGGGCCCA----  
>At1855|Pfur\_DSM3638|Euryarchaeota|Pyrococcus furiosus DSM 3638|1287370|1287293|Met|CAT|0|0|||||The tRNA gene was obtained from SPLITSdb. tRNA-Met(Ile) whose CAU anticodon is enzymatically converted to read AUA codons.|GIB in DDBJ|  
-GGGCCGTAGCTCAGCCTGGT--AGAGCGCGGCTCATAACCGCGTG-----GTCCGGGTTTCAATCCCGCGGGCCACCA-











>At0386|Smar\_F1|Crenarchaeota|Staphylothermus marinus F1|798271|798347|Ala|GGC|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTAGCTCAGCCTGGAA--GAGCGCTCGGTTGGCATCCGAGAG-----GTCCCGGGTTCAAATCCCGGCCGGTCCACCA-  
>At0516|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|323746|323819|Ala|GGC|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTAGCTCAGCCTGGAA--GAGTGTCTCGGTTGGCATCCGAGAG-----GTCCCGGGTTCAAATCCCGGCCGGTCCACCA-  
>At0121|Hbut\_DSM5456|Crenarchaeota|Hyperthermus butylicus DSM 5456|2453|2377|Ala|CGC|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGGCCGGTAGCTCAGCCTGGAA--GAGCGCTCGGTTGCACCCGAGAG-----GTCCCGGGTTCAAATCCCGGCCGGTCCACCA-  
>WENV078784|AAQL01000161|Gut microbiome of Human (healthy human stool sample 8)|938|1016|Gly|GCC|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGCGGTGTAGTCCAGCCTGGTT-AAGACTCTAGCCTGCCAGCTTAGAG-----A-CCCGGGTTCAAATCCCGGCCGGCATTTA  
>WENV078785|AAQL01000161|Gut microbiome of Human (healthy human stool sample 8)|1017|1095|Gly|TCC|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGCAGTTGTGGTATAGTCTGGTT-ATTACTTGGGCCTTCCAAGCCTACA-----A-CCCGGGTTCAAATCCCGGCCAACTGCATTG  
>At1574|Msta\_DSM3091|Euryarchaeota|Methanosphaera stadtmanae DSM 3091|1391522|1391595|Gly|TCC|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGTGTAGTCTAGTCTGGCT-AGGACTTGGGCCTTCCAAGCCTACG-----A-CCCGGGTTCAAATCCCGGCCAGCCGCA-  
>ENV004185|DQ397603|Environmental sample from ENV division of INSDC|43372|43450|Gly|TCC|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGCAGTCATAGTATAGCTTGGTC-AGTATACGGGGTTTCCAACCCTGCG-----A-CGCGGGTTCAAATCCCGCTGACTGCATCTA  
>At1896|Phor\_OT3|Euryarchaeota|Pyrococcus horikoshii OT3|836701|836624|Gly|CCC|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGTGGTAGTCTAGCCTGGTCTAGGACGCGGCCTCCCAAGCCGGCG-----A-CCCGGGTTCAAATCCCGGCCACCGCACCA-  
>At1837|Pfur\_DSM3638|Euryarchaeota|Pyrococcus furiosus DSM 3638|1120311|1120388|Gly|CCC|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGTGGTAGTCTAGCCTGGTCTAGGACGCGGCCTCCCAAGCCGGCG-----A-CCCGGGTTCAAATCCCGGCCACCGCACCA-  
>At1844|Pfur\_DSM3638|Euryarchaeota|Pyrococcus furiosus DSM 3638|77737|77660|Gly|TCC|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGTGGTAGTCTAGCCTGGTCTAGGACGCGGCCTTCCGAGCCGGCG-----A-CCCGGGTTCAAATCCCGGCCACCGCACCA-  
>At1890|Phor\_OT3|Euryarchaeota|Pyrococcus horikoshii OT3|127167|127090|Gly|TCC|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGTGGTAGTCTAGCCTGGTCTAGGACGCGGCCTTCCGAGCCGGCG-----A-CCCGGGTTCAAATCCCGGCCACCGCACCA-  
>At1873|Phor\_OT3|Euryarchaeota|Pyrococcus horikoshii OT3|483198|483275|Gly|GCC|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGTGGTAGTCTAGCCTGGCTAGGACGCCACCCTGCCAAGGTGGAG-----A-CCCGGGTTCAAATCCCGGCCACCGCACCA-  
>At2202|Ihos\_KIN4I|Crenarchaeota|Ignicoccus hospitalis KIN4/I|289795|289873|Gly|GCC|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCGGTCTAGCCTGGACTAGGACGCGGCCTGCCACGCGGAG-----TCCCGGGTTCAAATCCCGGCCGCCACCA-  
>At0329|Pisl\_DSM4184|Crenarchaeota|Pyrobaculum islandicum DSM 4184|335212|335303|Gly|TCC|335252|335267|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCGGTAGTCTAGCCTGGTTTAGGATGGCGGCCTTCCAAGCCGTTG-----TCCCGGGTTCAAATCCCGGCCGCCGCA-  
>At0270|Pars\_DSM13514|Crenarchaeota|Pyrobaculum arsenaticum DSM 13514|1534612|1534537|Gly|CCC|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCGGTAGTCTAGCCTGGTTTAGGATGGCGGCCTCCCAAGCCGTTG-----TCCCGGGTTCAAATCCCGGCCGCCGCA-  
>At0303|Pcal\_JCM11548|Crenarchaeota|Pyrobaculum calidifontis JCM 11548|1647546|1647639|Gly|CCC|1647578|1647595|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCGGTAGTCTAGCCTGGTTTAGGATGGCGGCCTCCCAAGCCGTTG-----TCCCGGGTTCAAATCCCGGCCGCCGCA-  
>At0324|Pcal\_JCM11548|Crenarchaeota|Pyrobaculum calidifontis JCM 11548|1821412|1821305|Gly|TCC|1821380|1821363|1821354|1821341|1821341|The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCGGTAGTCTAGCCTGGTTTAGGATGGCGGCCTTCCAAGCCGTTG-----TCCCGGGTTCAAATCCCGGCCGCCGCA-  
>At0205|Paer\_IM2|Crenarchaeota|Pyrobaculum aerophilum str. IM2|1903980|1904119|Gly|GCC|1903983|1904043|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCGGTAGTCTAGCCTGGTTTAGGATGGCGGCCTGCCAAGCCGTTG-----TCCCGGGTTCAAATCCCGGCCGCCGCA-  
>ENV004165|DQ397574|Environmental sample from ENV division of INSDC|17020|17096|Gly|CCC|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
-GCGGAGTTAGTCCAGCCCGGT--AGGACGTCAGCTTCCCAAGCTGAAG-----TCGCGTGTCAAATCCCGCACTCCGCACTG-  
>ENV004208|DQ397830|Environmental sample from ENV division of INSDC|16950|16874|Gly|CCC|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
-GCGGAGTTAGTCCAGCCCGGT--AGGACGTCAGCTTCCCAAGCTGAAG-----TCGCGTGTCAAATCCCGCACTCCGCACTG-  
>At0447|Saci\_DSM639|Crenarchaeota|Sulfolobus acidocaldarius DSM 639|440438|440363|Gly|GCC|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGCGGTAGTCTAGCCTGGATTAGGACGCGCTGCCTGCCACGAGAG-----TCCCGGGTTCAAATCCCGGCCGGTTCGCA-  
>WENV078811|AAQL01000509|Gut microbiome of Human (healthy human stool sample 8)|1150|1074|Thr|TGT|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
-GCCTCGATAGCTCAGTCTGGT--GGAGCGGAGACTTGTAATCTCGTG-----TCGCGGGTTCAAATCCCGTTCCGGGCTTTC-  
>At1079|Mmar\_C5|Euryarchaeota|Methanococcus maripaludis C5|1517916|1517843|Thr|TGT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCTCGGTGGCTCAGCCTGGT--AGAGCGCCTGACTTGTAATCAGGTG-----TCGGGGTTCAAATCCCCCGGGGCT-  
>At1089|Mmar\_C7|Euryarchaeota|Methanococcus maripaludis C7|1071911|1071984|Thr|TGT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCTCGGTGGCTCAGCCTGGT--AGAGCGCCTGACTTGTAATCAGGTG-----TCGGGGTTCAAATCCCCCGGGGCT-  
>At1120|Mmar\_S2|Euryarchaeota|Methanococcus maripaludis S2|112878|112951|Thr|TGT|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCTCGGTGGCTCAGCCTGGT--AGAGCGCCTGACTTGTAATCAGGTG-----TCGGGGTTCAAATCCCCCGGGGCT-













>At0225|Paer\_IM2|Crenarchaeota|Pyrobaculum aerophilum str. IM2|1226102|1226004|Asp|GTC|1226099|1226079|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCCGGTAGTATAGCCCGGACTAGTATGCGGGCCTGTCGAGCCCGTG-----A-CCCGGGTTCAAATCCCGGCCGGGGCCCA-  
>At0278|Pars\_DSM13514|Crenarchaeota|Pyrobaculum arsenaticum DSM 13514|1804398|1804300|Asp|GTC|1804395|1804375|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCCGGTAGTATAGCCCGGACTAGTATGCGGGCCTGTCGAGCCCGTG-----A-CCCGGGTTCAAATCCCGGCCGGGGCCCA-  
>At0541|Stok\_7|Crenarchaeota|Sulfolobus tokodaii str. 7|191251|191161|Glu|TTC|191228|191213|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCGGTTAGTATAGCCCGGCAAGTATGCGGGCCTTTCGAGCCCGTG-----A-CCCGGGTTCAAATCCCGGCCGGGCA----  
>At0366|Pis1\_DSM4184|Crenarchaeota|Pyrobaculum islandicum DSM 4184|1447364|1447227|Glu|CTC|1447361|1447323|1447288|1447268|||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCCGGTAGTCTAGCCCGTCAAGGATGCGGGCCTCTCGAGCCCGTG-----A-CCCGGGTTCAAATCCCGGCCGGGGCACC-  
>At1100|Mmar\_C7|Euryarchaeota|Methanococcus maripaludis C7|1683694|1683767|Arg|GCG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCCTCATGGGGTAGGTAGGAT-ATCCTCGCGGACTGCGGATCCGTGG-----ACTC-GGGTTCAAATCCCGATGGGGGCG----  
>At1959|Tkod\_KOD1|Euryarchaeota|Thermococcus kodakaraensis KOD1|1724444|1724368|His|GTG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCCGGGGTGTGTAGCTGGTT-AGCACAGGGGACTGTGGATCCCCTA-----GCC-CCGGTTCAAATCCCGGCCCGGCCCA-  
>WENV078797|AAQL01000350|Gut microbiome of Human (healthy human stool sample 8)|10226|10138|Leu|GAG|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGCGGGGGTGGTTCAGT--GGTCAAAGGCGATAGGTTGAGGGCCTATTG-----TTCGCGGGTTCAAAGTCCCGTCTCCCGCACTTT  
>At1466|Mbar\_FUSARO\_01|Euryarchaeota|Methanosarcina barkeri str. Fusaro|92160|92076|Leu|GAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGGTTGCCAGCCAGGTCAAAGGCGCTAGGTTGAGGGCCTAGTT-----TTCGTGGGTTCAATCCCATCCCTCGCA----  
>At1467|Mbar\_FUSARO\_01|Euryarchaeota|Methanosarcina barkeri str. Fusaro|92377|92293|Leu|GAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGGTTGCCAGCCAGGTCAAAGGCGCTAGGTTGAGGGCCTAGTT-----TTCGTGGGTTCAATCCCATCCCTCGCA----  
>At1521|Mmaz\_GOE1|Euryarchaeota|Methanosarcina mazei Go1|2560706|2560790|Leu|GAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGGTTGCCAGCCAGGTCAAAGGCGCTAGGTTGAGGGCCTAGTT-----TTCGTGGGTTCAATCCCATCCCTCGCA----  
>At1502|Mmaz\_GOE1|Euryarchaeota|Methanosarcina mazei Go1|181284|181368|Leu|CAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGAGTTGCCAGCCAGGTCAAAGGCGCCAGGTTTCAGAGCCTGGTC-----TTCGTGGGTTCAATCCGCACCTCTCGCA----  
>At1284|Mmar\_JR1|Euryarchaeota|Methanoculleus marisnigri JR1|1647663|1647579|Leu|GAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGGTTGCCAAGCCAGGTCAAAGGCGCCAGGTTGAGGGCCTGGTC-----TTCGTGAGTTCAATCTCACCCCTCGCA----  
>At1107|Mmar\_C7|Euryarchaeota|Methanococcus maripaludis C7|778123|778039|Leu|GAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGGTTGCCAAGCCTGGTTAAAGGCGCTAGGTTGAGGGCCTAGTC-----TTCGAGGGTTCAATCCCTTCCTCGCA----  
>At1149|Mmar\_S2|Euryarchaeota|Methanococcus maripaludis S2|1507810|1507726|Leu|GAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGGTTGCCAAGCCTGGTTAAAGGCGCTAGGTTGAGGGCCTAGTC-----TTCGAGGGTTCAATCCCTTCCTCGCA----  
>ENV09000361|ABS01057628|Freshwater sediment metagenome lwFormaldehyde\_C1||756|840|Leu|CAG|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
-GCGAGGGTAGCCAAGCCAGGTCACGGCGCCAGGTTTCAGGGCCTGGTC-----TTCTTGGGTTCAATCCCATCCCTCGCA----  
>At2045|Tvol\_GSS1|Euryarchaeota|Thermoplasma volcanium GSS1|1089277|1089194|Leu|CAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGAGGTTGTCGAGACTGGCCAAAGGCGATGGATTTCAGGGTCCATTC-----TTCGAGGGTTCAAATCCCTCCCTCCGCA----  
>At2046|Tvol\_GSS1|Euryarchaeota|Thermoplasma volcanium GSS1|1098176|1098092|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGAGGTTGTCGAGACTGGCCAAAGGCGATGGATTTCAGGGTCCATTC-----TTCGAGGGTTCAAATCCCTCCCTCCGCA----  
>At2027|Tvol\_GSS1|Euryarchaeota|Thermoplasma volcanium GSS1|63598|63514|Leu|GAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGAGGTTGTCGAGACTGGTCAAAGGCGCCAGATTGAGGGTCTGGTT-----G-CGAGGGTTCAAATCCCTCCCTCCGCA----  
>At1435|Mbar\_FUSARO\_01|Euryarchaeota|Methanosarcina barkeri str. Fusaro|466965|467049|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGGTTGCCAGCTAGGTCAAAGGCGATGGGCTTAGGACCCATT-----TTCGTGCGTTCAATCCGCACCCCTCGCA----  
>At1452|Mbar\_FUSARO\_01|Euryarchaeota|Methanosarcina barkeri str. Fusaro|4006296|4006378|Leu|CAA|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGAGTAACCAAGC--GGTCAACGGTGGCAGACTCAAGATCTGTTC-----TTCAGGGGTTCAATCCCTTCTCCCGCA----  
>At1525|Mmaz\_GOE1|Euryarchaeota|Methanosarcina mazei Go1|3637591|3637673|Leu|CAA|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGAGTAACCAAGC--GGTCAACGGTGGCAGACTCAAGATCTGTTC-----TTCAGGGGTTCAATCCCTTCTCCCGCA----  
>At2019|Tvol\_GSS1|Euryarchaeota|Thermoplasma volcanium GSS1|1118192|1118276|Leu|TAA|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGAGGGTAACCAAGCCAGGCAACAGTGCAGGACTTAAGATCCTGTTC-----TTCGCGGGTTCAAATCCCGCCCTCGCA----  
>At1096|Mmar\_C7|Euryarchaeota|Methanococcus maripaludis C7|1156272|1156356|Leu|TAA|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGAGGGATTGCCAAGCCTGGTCAAAGGCGTGGACTTAAGATCCGATC-----TTCGAGGGTTCAAATCCCTTCCCTCCA----  
>At1127|Mmar\_S2|Euryarchaeota|Methanococcus maripaludis S2|197613|197697|Leu|TAA|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GGAGGGATTGCCAAGCCTGGTCAAAGGCGTGGACTTAAGATCCGATC-----TTCGAGGGTTCAAATCCCTTCCCTCCA----  
>At1109|Mmar\_C7|Euryarchaeota|Methanococcus maripaludis C7|893810|893726|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCAGGGGTTGTCGAGCCTGGCCAAAGATGCAGGACTTAGAATCCTGTTC-----TTCCAGGGTTCAAATCCCTGCCCTCGCA----

>At1151|Mmar\_S2|Euryarchaeota|Methanococcus maripaludis S2|1601086|1601002|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCAGGGGTTGTCGAGCCTGGCCAAAGATGCAGGACTTAGAATCCTGTC-----TTCCAGGGTTCAAATCCCTGCCCTGCA----  
>At1911|Phor\_OT3|Euryarchaeota|Pyrococcus horikoshii OT3|1448168|1448081|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGTTGCCGAGCCTGGTCAAAGGCGCGGGATTAGGGTCCCGTC-----TTCCGGGGTTCAAATCCCGCCCCGCACCA-  
>At1867|Pfur\_DSM3638|Euryarchaeota|Pyrococcus furiosus DSM 3638|1534784|1534697|Leu|CAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGTTGCCGAGCCTGGTCAAAGGCGCGGGATTAGGGTCCCGTC-----TTCCGGGGTTCAAATCCCGCCCCGCACCA-  
>At1882|Phor\_OT3|Euryarchaeota|Pyrococcus horikoshii OT3|896089|896176|Leu|CAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGTTGCCGAGCCTGGTCAAAGGCGCGGGATTAGGGTCCCGTC-----TTCCGGGGTTCAAATCCCGCCCCGCACCA-  
>At1900|Phor\_OT3|Euryarchaeota|Pyrococcus horikoshii OT3|1163638|1163551|Leu|GAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGTTGCCGAGCCTGGTCAAAGGCGCGGGATTAGGGTCCCGTC-----TTCCGGGGTTCAAATCCCGCCCCGCACCA-  
>At1811|Paby\_ORsay|Euryarchaeota|Pyrococcus abyssi|955199|955112|Leu|GAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGTTGCCGAGCCTGGTCAAAGGCGCGGGATTAGGGTCCCGTC-----TTCCGGGGTTCAAATCCCGCCCCGCACCA-  
>At1941|Tkod\_KOD1|Euryarchaeota|Thermococcus kodakaraensis KOD1|260446|260359|Leu|GAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGTTGCCGAGCCTGGTCAAAGGCGCGGGATTAGGGTCCCGTC-----TTCCGGGGTTCAAATCCCGCCCCGCACCA-  
>At1848|Pfur\_DSM3638|Euryarchaeota|Pyrococcus furiosus DSM 3638|337898|337811|Leu|CAA|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGTTGCCGAGCCTGGTCAAAGGCGGGGACTCAAGATCCCTC-----TTCCGGGGTTCAAATCCCGCCCCGCACCA-  
>At0076|Csym|Crenarchaeota|Cenarchaeum symbiosum|28673|28586|Leu|TAG|0|0|||||The tRNA gene was obtained from SPLITSdb.|GIB in DDBJ|  
-GCGGGGTTGCCGAGCCTGGTCAAAGGCGCAGGGCTTAGGACCCTGTC-----TCCGGGGTTCGAATCCCGCTCCCGCACCA-  
>ENV004173|DQ397586|Environmental sample from ENV division of INSDC||38301|38388|Leu|TAG|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
-GCGGGGTTGCCGAGCCTGGTCAAAGGCGCAGGGCTTAGGACCCTGTC-----TCCGGGGTTCGAATCCCGCTCCCGCACCA-  
>ENV004183|DQ397601|Environmental sample from ENV division of INSDC||15083|15170|Leu|TAG|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
-GCGGGGTTGCCGAGCCTGGTCAAAGGCGCAGGGCTTAGGACCCTGTC-----TCCGGGGTTCGAATCCCGCTCCCGCACCA-  
>ENV004248|DQ397872|Environmental sample from ENV division of INSDC||36187|36100|Leu|TAG|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
-GCGGGGTTGCCGAGCCTGGTCAAAGGCGCAGGGCTTAGGACCCTGTC-----TCCGGGGTTCGAATCCCGCTCCCGCACCA-  
>ENV004160|DQ397570|Environmental sample from ENV division of INSDC||15182|15093|Leu|GAG|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGCGGGTGTAGCCAGCCTGGTCAAAGGCGCTAGCTTAGGGGCTAGTC-----TTCGTGGGTTCAAATCCCATCGCCCGCACCA  
>ENV004169|DQ397579|Environmental sample from ENV division of INSDC||11120|11209|Leu|GAG|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGCGGGTGTAGCCAGCCTGGTCAAAGGCGCTAGCTTAGGGGCTAGTC-----TTCGTGGGTTCAAATCCCATCGCCCGCACCA  
>ENV004182|DQ397601|Environmental sample from ENV division of INSDC||3720|3632|Ser|GCT|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGCAGGGTACCTAGCCTGGTAGGGTGTGG--GACTGCTAATCCATG-----A-CGGGGTTCGAATCCCCCTCCCTGCGCCAT  
>ENV004196|DQ397629|Environmental sample from ENV division of INSDC||34267|34189|Phe|GAA|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGCCAGGGTAGCTCAGCCTGGGA-G-AGCACTCGGCTGAAGACCGAGCT-----GTCGCGGTTCAAATCCCGCCCTGGCACCAC  
>ENV004238|DQ397863|Environmental sample from ENV division of INSDC||7587|7509|Phe|GAA|0|0|||||ENV division in DDBJ/EMBL/GenBank|  
TGCCAGGGTAGCTCAGCCTGGGA-G-AGCACTCGGCTGAAGACCGAGCT-----GTCGCGGTTCAAATCCCGCCCTGGCACCAC  
>At1086|Mmar\_C7|Euryarchaeota|Methanococcus maripaludis C7|778253|778367|Met|CAT|778292|778331|||||The tRNA gene was obtained from SPLITSdb. tRNA-Met(elongator).|GIB in DDBJ|  
-GCCGAGGTGGCTTAGGCTGGTT-ATAGCGCTCGGCTCATAACCGAGAG-----GTCGGGGTTCAAGTCCCCCCTCGGCA----  
>At1137|Mmar\_S2|Euryarchaeota|Methanococcus maripaludis S2|1507940|1508054|Met|CAT|1507979|1508018|||||The tRNA gene was obtained from SPLITSdb. tRNA-Met(elongator).|GIB in DDBJ|  
-GCCGAGGTGGCTTAGGCTGGTT-ATAGCGCTCGGCTCATAACCGAGAG-----GTCGGGGTTCAAGTCCCCCCTCGGCA----  
>At1160|Mvan\_SB|Euryarchaeota|Methanococcus vanniellii SB|891114|891228|Met|CAT|891153|891192|||||The tRNA gene was obtained from SPLITSdb. tRNA-Met(elongator).|GIB in DDBJ|  
-GCCGAGGTGGCTTAGGCTGGTT-ATAGCGCTCGGCTCATAACCGAGAG-----GTCGGGGTTCAAGTCCCCCCTCGGCA----