The sequences of the *Gilliamella*-like bacterial 16S rDNA sequences, alignments and Blastn search results

Different partial 16S *rRNA* gene sequences were obtained with a high similarity to that of *Gilliamella* sp. and shown below in fasta formats. Note: Lab1, my own lab, two sequences were obtained from fly surface and guts, respectively. Lab2, Dr. Erjun Ling's lab at our Institute. CFDRT, Core Facility of Drosophila Resource and Technology from the Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences.

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>Lab1-Surface
CTCTAGAGTATGGGGATCTGCCGAATGGAGGGGGACAACAGTTGGAAACGGCTGCTAATACCGCATAACGTC
GAGAGACCAAAGGGTGGGACCTTCGGGCCACTTGCCATTTGATGAGCCCATATGAGATTAGCTAGTTGGTGT
GGTAATGGCTCACCAAGGCGACGATCTCTAGCTGGTTTGAGAGGATGACCAGCCACACTGGGACTGAGACAC
GGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGGGGAACCCTGATGCAGCCATGCCG
CGTGTATGAAGAAGGCCTTAGGGTTGTAAAGTACTTTCGTGGAGGAGGAAGGGTTTACGTTTAATAGGCGTG
GACATTGACGTTACTCCAAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCG
AGCGTTAATCGGAATGACTGGGCGTAAAGGGCATGTAGGCGGATGATTAAGTTAGATGTGAAATCCCTGGGC
TTAACCTAGGAATTGCATTTAAAACTGGTTATCTAGAGTATTGTAGAGGAAGGTAGAATTCCATGTGTAGCG
GTGAAATGCGTAGAGATGTGGAGGAATACCGGTGGCGAAGGCGGCCTTCTGGACAGATACTGACGCTGAGAT
GCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTTGGAGTT
TGTTGCCTAGAGTGATGGGCTCCGAAGCTAACGCGATAAATCGACCGCCTGGGGAGTACGGCCGCAAGGTTA
AAACTCAAATGAATTGACGGGGGCCCGCACA
>Lab1-Guts
CTCTAGAGTATGGGGATCTGCCGAATGGAGGGGGACAACAGTTGGAAACGGCTGCTAATACCGCATAACGTC
GAGAGACCAAAGGGTGGGACCTTCGGGCCACTTGCCATTTGATGAGCCCATATGAGATTAGCTAGTTGGTGT
GGTAATGGCTCACCAAGGCGACGATCTCTAGCTGGTTTGAGAGGATGACCAGCCACACTGGGACTGAGACAC
GGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGGGGAACCCTGATGCAGCCATGCCG
CGTGTATGAAGAAGGCCTTAGGGTTGTAAAGTACTTTCGTGGAGGAGGAAGGGTTTACGTTTAATAGGCGTG
GACATTGACGTTACTCCAAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCG
AGCGTTAATCGGAATGACTGGGCGTAAAGGGCATGTAGGCGGATGATTAAGTTAGATGTGAAATCCCTGGGC
TTAACCTAGGAATTGCATTTAAAACTGGTTATCTAGAGTATTGTAGAGGAAGGTAGAATTCCATGTGTAGCG
GTGAAATGCGTAGAGATGTGGAGGAATACCGGTGGCGAAGGCGGCCTTCTGGACAGATACTGACGCTGAGAT
GCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTTTGGAGT
TTGTTGCCTAGAGTGATGGGCTCCGAAGCTAACGCGATAAATCGACCGCCTGGGGAGTACGGCCGCAAGGT
TAAAACTCAAATGAATTGACGGGGGCCCGCACA
>CFDRT
CTCTAGAGTATGGGGATCTGCCGAATGGAGGGGGACAACAGTTGGAAACGGCTGCTAATACCGCATAACGTC
GAGAGACCAAAGGGTGGGACCTTCGGGCCACTTGCCATTTGATGAGCCCATATGAGATTAGCTAGTTGGTGT
GGTAATGGCTCACCAAGGCGACGATCTCTAGCTGGTTTGAGAGGATGACCAGCCACACTGGGACTGAGACAC
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GGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGGGGAACCCTGATGCAGCCATGCCG
CGTGTATGAAGAAGGCCTTAGGGTTGTAAAGTACTTTCGTGGAGGAGGAAGGGTTTACGTTTAATAGGCGTG
GACATTGACGTTACTCCAAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCG
AGCGTTAATCGGAATGACTGGGCGTAAAGGGCATGTAGGCGGATGATTAAGTTAGATGTGAAATCCCTGGGC
TTAACCTAGGAATTGCATTTAAAACTGGTTATCTAGAGTATTGTAGAGGAAGGTAGAATTCCATGTGTAGCG
GTGAAATGCGTAGAGATGTGGAGGAATACCGGTGGCGAAGGCGGCCTTCTGGACAGATACTGACGCTGAGAT
GCGAAAGCGTGGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTTGGAGT
TTGTTGCCTAGAGTGATGGGCTCCGAAGCTAACGCGATAAATCGACCGCCTGGGGAGTACGGCCGCAAGGTT
AAAACTCAAATGAATTGACGGGGGCCCGCACA
>Lab2
CTCTAGAGTATGGGGACTGCCGAATGGAGGGGGACAACAGTTGGAAACGGCTGCTAATACCGCATAACGTCG
AGAGACCAAAGGGTGGGACCTTCGGGCCACTTGCCATTTGATGAGCCCATATGAGATTAGCTAGTTGGTGTG
GTAATGGCTCACCAAGGCGACGATCTCTAGCTGGTTTGAGAGGATGACCAGCCACACTGGGACTGAGACACG
GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGGGGAACCCTGATGCAGCCATGCCGC
GTGTATGAAGAAGGCCTTAGGGTTGTAAAGTACTTTCGTGGAGGAGGAAGGGTTTACGTTTAATAGGCGTGG
ACATTGACGTTACTCCAAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCGA
GCGTTAATCGGAATGACTGGGCGTAAAGGGCATGTAGGCGGATGATTAAGTTAGATGTGAAATCCCTGGGCT
TAACCTAGGAATTGCATTTAAAACTGGTTATCTAGAGTATTGTAGAGGAAGGTAGAATTCCATGTGTAGCGG
TGAAATGCGTAGAGATGTGGAGGAATACCGGTGGCGAAGGCGGCCTTCTGGACAGATACTGACGCTGAGATG
CGAAAGCGTGGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTTGGAGTTT
GTTGCCTAGAGTGATGGGCTCCGAAGCTAACGCGATAAATCGACCGCCTGGGGAGTACGGCCGCAAGGTTA
AAAACTCAAATGAATTGACGGGGGCCCGCACA

The results of the alignments of four obtained sequences:

Lab1-Surface	CTCTAGAGTATGGGGATCTGCCGAATGGAGGGGGACAACAGTTGGAAACGGCTGCTAATA
CFDRT	CTCTAGAGTATGGGGATCTGCCGAATGGAGGGGGACAACAGTTGGAAACGGCTGCTAATA
Lab1-Guts	CTCTAGAGTATGGGGATCTGCCGAATGGAGGGGGACAACAGTTGGAAACGGCTGCTAATA
Lab2	CTCTAGAGTATGGGGA-CTGCCGAATGGAGGGGGACAACAGTTGGAAACGGCTGCTAATA
	*************** **

Lab1-Surface	CCGCATAACGTCGAGAGACCAAAGGGTGGGACCTTCGGGCCACTTGCCATTTGATGAGCC
CFDRT	CCGCATAACGTCGAGAGACCAAAGGGTGGGACCTTCGGGCCACTTGCCATTTGATGAGCC
Lab1-Guts	CCGCATAACGTCGAGAGACCAAAGGGTGGGACCTTCGGGCCACTTGCCATTTGATGAGCC
Lab2	CCGCATAACGTCGAGAGACCAAAGGGTGGGACCTTCGGGCCACTTGCCATTTGATGAGCC
	**

Lab1-Surface	CATATGAGATTAGCTAGTTGGTGTGGTAATGGCTCACCAAGGCGACGATCTCTAGCTGGT
CFDRT	CATATGAGATTAGCTAGTTGGTGTGGTAATGGCTCACCAAGGCGACGATCTCTAGCTGGT
Lab1-Guts	CATATGAGATTAGCTAGTTGGTGTGGTAATGGCTCACCAAGGCGACGATCTCTAGCTGGT

Lab2   CATATGAGATTAGCTAGTTGGTGTGGTAATGGCTCACCAAGGCGACGATCTCTAGCTGGT

                             ****

Lab1-Surface   TTGAGAGGATGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG
CFDRT   TTGAGAGGATGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG
Lab1-Guts   TTGAGAGGATGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG
Lab2   TTGAGAGGATGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG

                             ****

Lab1-Surface   CAGTGGGGAATATTGCACAATGGGGGGAACCCTGATGCAGCCATGCCGCGTGTATGAAGA
CFDRT   CAGTGGGGAATATTGCACAATGGGGGGAACCCTGATGCAGCCATGCCGCGTGTATGAAGA
Lab1-Guts   CAGTGGGGAATATTGCACAATGGGGGGAACCCTGATGCAGCCATGCCGCGTGTATGAAGA
Lab2   CAGTGGGGAATATTGCACAATGGGGGGAACCCTGATGCAGCCATGCCGCGTGTATGAAGA

                             ****

Lab1-Surface   AGGCCTTAGGGTTGTAAAGTACTTTCGTGGAGGAGGAAGGGTTTACGTTTAATAGGCGTG
CFDRT   AGGCCTTAGGGTTGTAAAGTACTTTCGTGGAGGAGGAAGGGTTTACGTTTAATAGGCGTG
Lab1-Guts   AGGCCTTAGGGTTGTAAAGTACTTTCGTGGAGGAGGAAGGGTTTACGTTTAATAGGCGTG
Lab2   AGGCCTTAGGGTTGTAAAGTACTTTCGTGGAGGAGGAAGGGTTTACGTTTAATAGGCGTG

                             ****

Lab1-Surface   GACATTGACGTTACTCCAAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAAT
CFDRT   GACATTGACGTTACTCCAAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAAT
Lab1-Guts   GACATTGACGTTACTCCAAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAAT
Lab2   GACATTGACGTTACTCCAAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAAT

                             ****

Lab1-Surface   ACGGAGGGTGCGAGCGTTAATCGGAATGACTGGGCGTAAAGGGCATGTAGGCGGATGATT
CFDRT   ACGGAGGGTGCGAGCGTTAATCGGAATGACTGGGCGTAAAGGGCATGTAGGCGGATGATT
Lab1-Guts   ACGGAGGGTGCGAGCGTTAATCGGAATGACTGGGCGTAAAGGGCATGTAGGCGGATGATT
Lab2   ACGGAGGGTGCGAGCGTTAATCGGAATGACTGGGCGTAAAGGGCATGTAGGCGGATGATT

                             ****

Lab1-Surface   AAGTTAGATGTGAAATCCCTGGGCTTAACCTAGGAATTGCATTTAAAACTGGTTATCTAG
CFDRT   AAGTTAGATGTGAAATCCCTGGGCTTAACCTAGGAATTGCATTTAAAACTGGTTATCTAG

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Lab1-Guts       AAGTTAGATGTGAAATCCCTGGGCTTAACCTAGGAATTGCATTTAAAACTGGTTATCTAG
Lab2            AAGTTAGATGTGAAATCCCTGGGCTTAACCTAGGAATTGCATTTAAAACTGGTTATCTAG
                ************************************************************


Lab1-Surface    AGTATTGTAGAGGAAGGTAGAATTCCATGTGTAGCGGTGAAATGCGTAGAGATGTGGAGG
CFDRT           AGTATTGTAGAGGAAGGTAGAATTCCATGTGTAGCGGTGAAATGCGTAGAGATGTGGAGG
Lab1-Guts       AGTATTGTAGAGGAAGGTAGAATTCCATGTGTAGCGGTGAAATGCGTAGAGATGTGGAGG
Lab2            AGTATTGTAGAGGAAGGTAGAATTCCATGTGTAGCGGTGAAATGCGTAGAGATGTGGAGG
                ************************************************************


Lab1-Surface    AATACCGGTGGCGAAGGCGGCCTTCTGGACAGATACTGACGCTGAGATGCGAAAGCGTGG
CFDRT           AATACCGGTGGCGAAGGCGGCCTTCTGGACAGATACTGACGCTGAGATGCGAAAGCGTGG
Lab1-Guts       AATACCGGTGGCGAAGGCGGCCTTCTGGACAGATACTGACGCTGAGATGCGAAAGCGTGG
Lab2            AATACCGGTGGCGAAGGCGGCCTTCTGGACAGATACTGACGCTGAGATGCGAAAGCGTGG
                ************************************************************


Lab1-Surface    GG-AGCAAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTT-GGAG
CFDRT           GGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTT-GGAG
Lab1-Guts       GG-AGCAAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTTTGGAG
Lab2            GG-AGCAAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTT-GGAG
                ** ********************************************************* ****


Lab1-Surface    TTTGTTGCCTAGAGTGATGGGCTCCGAAGCTAACGCGATAAATCGACCGCCTGGGG-AGT
CFDRT           TTTGTTGCCTAGAGTGATGGGCTCCGAAGCTAACGCGATAAATCGACCGCCTGGGG-AGT
Lab1-Guts       TTTGTTGCCTAGAGTGATGGGCTCCGAAGCTAACGCGATAAATCGACCGCCTGGGGGAGT
Lab2            TTTGTTGCCTAGAGTGATGGGCTCCGAAGCTAACGCGATAAATCGACCGCCTGGGGGAGT
                ********************************************************* ***


Lab1-Surface    ACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACA
CFDRT           ACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACA
Lab1-Guts       ACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACA
Lab2            ACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACA
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Example results of Blastn search against the NCBI nr database:

Gilliamella apicola strain wkB30 16S ribosomal RNA gene, complete sequence
Sequence ID: JQ936676.2   Length: 1538   Number of Matches: 1
Range 1: 118 to 933 GenBank Graphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
1275 bits(690)	0.0	775/817(95%)	2/817(0%)	Plus/Plus

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Query  8    GTATGGGGATCTGCCGAATGGAGGGGGACAACAGTTGGAAACGGCTGCTAATACCGCATA   67
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  118  GTATGGGGATCTGCCGAATGGAGGGGGACAACAGTTGGAAACGACTGCTAATACCGCATA   177


Query  68   ACGTCGAGAGACCAAAGGGTGGGACCTTCGGGCCACTTGCCATTTGATGAGCCCATATGA   127
            |  || |||||||||||||  |||||||| |||||||    ||||||||||||| ||||||||
Sbjct  178  AAGTTGAGAGACCAAAGCATGGGACCTACGGGCCATGCGCCATTTGATGAACCCATATGG   237


Query  128  GATTAGCTAGTTGGTGTGGTAATGGCTCACCAAGGCGACGATCTCTAGCTGGTTTGAGAG   187
            ||||||||||||||||| ||||| ||||||||||||||||||||||||||||||| ||||||
Sbjct  238  GATTAGCTAGTTGGTGGGGTAAAGGCTCACCAAGGCGACGATCTCTAGCTGGTCTGAGAG   297


Query  188  GATGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGG   247
            |||||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||||
Sbjct  298  GATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGG   357


Query  248  GAATATTGCACAATGGGGGGAACCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTT   307
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  358  GAATATTGCACAATGGGGGGAACCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTT   417


Query  308  AGGGTTGTAAAGTACTTTCGTGGAGGAGGAAGG-GTTTACGTTTAATAGGCGTGGACATT   366
             |||||||||||||||||| || ||||||||| | | |  | |||||||  |    |||
Sbjct  418  CGGGTTGTAAAGTACTTTCGGTGATGAGGAAGGTGATGA-ATCTAATAGGTTTATTAATT   476


Query  367  GACGTTACTCCAAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAG   426
            ||||||| || | |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  477  GACGTTAATCACAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAG   536


Query  427  GGTGCGAGCGTTAATCGGAATGACTGGGCGTAAAGGGCATGTAGGCGGATGATTAAGTTA   486
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  537  GGTGCGAGCGTTAATCGGAATGACTGGGCGTAAAGGGCATGTAGGCGGATAATTAAGTTA   596
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Query  487  GATGTGAAATCCCTGGGCTTAACCTAGGAATTGCATTTAAAACTGGTTATCTAGAGTATT  546
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Sbjct  597  GGTGTGAAAGCCCTGGGCTCAACCTAGGAATTGCACTTAAAACTGGTTAACTAGAGTATT  656


Query  547  GTAGAGGAAGGTAGAATTCCATGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAATACC  606
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  657  GTAGAGGAAGGTAGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAATACC  716


Query  607  GGTGGCGAAGGCGGCCTTCTGGACAGATACTGACGCTGAGATGCGAAAGCGTGGGGAGCA  666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  717  GGTGGCGAAGGCGGCCTTCTGGACAGATACTGACGCTGAGATGCGAAAGCGTGGGGAGCA  776


Query  667  AACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTTGGAGTTTGTTGC  726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  777  AACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTTGGAGTTTGTTGC  836


Query  727  CTAGAGTGATGGGCTCCGAAGCTAACGCGATAAATCGACCGCCTGGGGAGTACGGCCGCA  786
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Sbjct  837  CTAGAGTGATGGGCTCCGAAGCTAACGCGATAAATCGACCGCCTGGGGAGTACGGCCGCA  896


Query  787  AGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACA  823
            |||||||||||||||||||||||||||||||||||||
Sbjct  897  AGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACA  933
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Orbus sasakiae strain C7 16S ribosomal RNA, partial sequence

Sequence ID: NR_109477.1 Length: 1301   Number of Matches: 1

See 1 more title(s)   See all Identical   Proteins (IPG)

Range 1: 91 to 906 GenBank Graphics   Next Match   Previous Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
1170 bits(633)	0.0	757/818(93%)	4/818(0%)	Plus/Plus

```
Query  8    GTATGGGGATCTGCCGAATGGAGGGGGACAACAGTTGGAAACGGCTGCTAATACCGCATA   67
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  91   GTATGGGGATCTGCCGAATGGAGGGGGACAACAGTTGGAAACGACTGCTAATACCGCATA   150


Query  68   ACGTCGAGAGACCAAAGGGTGGGACCTTCGGGCCACTTGCCATTTGATGAGCCCATATGA   127
            | |||| ||||||||| ||||||| |||||||||| | |||||||||| |||||||||
Sbjct  151  ATGTCGTAAGACCAAAGCGTGGGACTTTCGGGCCACGTACCATTTGATGAACCCATATGG   210


Query  128  GATTAGCTAGTTGGTGTGGTAATGGCTCACCAAGGCGACGATCTCTAGCTGGTTTGAGAG   187
            |||||||||| |||| ||||||||||||||| |||||||||||||||||||| ||||||
Sbjct  211  GATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCTCTAGCTGGTCTGAGAG   270


Query  188  GATGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGG   247
            |||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||
Sbjct  271  GATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGG   330


Query  248  GAATATTGCACAATGGGGGGAACCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTT   307
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  331  GAATATTGCACAATGGGGGAAACCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTT   390


Query  308  AGGGTTGTAAAGTACTTTCGTGGAGGAGGAAGGGTTTAC-GTT-TAATAGGCGTGGACAT   365
            ||||||||||||||||||||  |  ||||||  || |  || |  ||| |||  ||   ||
Sbjct  391  AGGGTTGTAAAGTACTTTCGGTAATGAGGAA-GG-TAACAATTCTAACAGGATTGTTAAT   448


Query  366  TGACGTTACTCCAAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGA   425
            ||||||| |    |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  449  TGACGTTAATTACAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGA   508


Query  426  GGGTGCGAGCGTTAATCGGAATGACTGGGCGTAAAGGGCATGTAGGCGGATGATTAAGTT   485
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  509  GGGTGCGAGCGTTAATCGGAATGACTGGGCGTAAAGGGCATGTAGGCGGATGATTAAGTT   568


Query  486  AGATGTGAAATCCCTGGGCTTAACCTAGGAATTGCATTTAAAACTGGTTATCTAGAGTAT   545
            || |||||||| ||| | |||  || | |||||||| |||||||||||||| | ||||||
Sbjct  569  AGGTGTGAAAGCCCCGAGCTCAACTTGGGAATTGCACTTAAAACTGGTCGTCTGGAGTAT   628
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Query  546  TGTAGAGGAAGGTAGAATTCCATGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAATAC  605
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  629  TGTAGAGGAAGGTAGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAATAC  688

Query  606  CGGTGGCGAAGGCGGCCTTCTGGACAGATACTGACGCTGAGATGCGAAAGCGTGGGGAGC  665
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  689  CGGTGGCGAAGGCGGCCTTCTGGACAGATACTGACGCTGAGATGCGAAAGCGTGGGGAGC  748

Query  666  AAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTTGGAGTTTGTTG  725
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Sbjct  749  AAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTTGGAGTTTGGAG  808

Query  726  CCTAGAGTGATGGGCTCCGAAGCTAACGCGATAAATCGACCGCCTGGGGAGTACGGCCGC  785
            |  ||      |||||||||| |||||||||   |||||||||||||||||||||||||||
Sbjct  809  GCATGACCTCTGGGCTCCGGAGCTAACGCATTAAATCGACCGCCTGGGGAGTACGGCCGC  868

Query  786  AAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACA  823
            ||||||||||||||||||||||||||||||||||||||
Sbjct  869  AAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACA  906
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