

# Blast hit analysis of the 135 newly identified GOEs throughout the genomes of the *Xylella fastidiosa* strains used in this study

Update: 17 October 2007

| Query id                                                                                                                                                               | subject ids   | organism                                                        | description                                              | % identity | % positives | alignment length | Mismatches | gap opens | query start..end | subject start..end | E-value   | Bit score |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|-----------------------------------------------------------------|----------------------------------------------------------|------------|-------------|------------------|------------|-----------|------------------|--------------------|-----------|-----------|
| <b>GOE #01</b><br>SSH33_56a_GOE_01<br>SSH40_Cv21_GOE_01 (276aa)<br>SSH21_187b_GOE_01<br>SSH16_36f_GOE_01                                                               | ZP_00682678.1 | <i>Xylella fastidiosa</i> Ann-1                                 | Plasmid encoded RepA protein                             | 99.12      | 99.56       | 227              | 2          | 0         | 29..255          | 52..278            | 2.00E-129 | 462       |
|                                                                                                                                                                        | YP_361657.1   | <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> str. 85-10 | putative replication protein A                           | 75.69      | 84.40       | 218              | 52         | 1         | 39..255          | 102..319           | 3.00E-89  | 329       |
|                                                                                                                                                                        | NP_644784.1   | <i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306         | replication protein A                                    | 75.69      | 84.40       | 218              | 52         | 1         | 39..255          | 63..280            | 3.00E-89  | 329       |
| <b>GOE #02</b><br>SSH18_36f_GOE_02<br>SSH15_Cv21_GOE_02 (268aa)<br>SSH02_56a_GOE_02<br>SSH16_187b_GOE_02<br>SSH28_Fb7_GOE_02<br>SSH57_912c_GOE_02<br>SSH22_912c_GOE_02 | ZP_00682688.1 | <i>Xylella fastidiosa</i> Ann-1                                 | TrbL/VirB6 plasmid conjugal transfer protein             | 71.25      | 75.84       | 327              | 33         | 3         | 1..268           | 1..325             | 5.00E-100 | 365       |
|                                                                                                                                                                        | YP_980121.1   | <i>Verminephrobacter eiseniae</i> EF01-2                        | TrbL/VirB6 plasmid conjugal transfer protein             | 77.12      | 89.83       | 236              | 54         | 0         | 1..236           | 1..236             | 2.00E-80  | 300       |
|                                                                                                                                                                        | ZP_01506051.1 | <i>Burkholderia phymatum</i> STM815                             | TrbL/VirB6 plasmid conjugal transfer protein             | 30.36      | 50.00       | 224              | 145        | 2         | 18..241          | 26..238            | 1.00E-19  | 98.6      |
| <b>GOE #03</b><br>SSH74_912c_GOE_03<br>SSH01_56a_GOE_03 (153aa)<br>SSH23_912c_GOE_03                                                                                   | ZP_00682688.1 | <i>Xylella fastidiosa</i> Ann-1                                 | TrbL/VirB6 plasmid conjugal transfer protein             | 88.42      | 94.74       | 95               | 11         | 0         | 1..95            | 209..303           | 3.00E-37  | 156       |
|                                                                                                                                                                        | YP_980121.1   | <i>Verminephrobacter eiseniae</i> EF01-2                        | TrbL/VirB6 plasmid conjugal transfer protein             | 65.98      | 77.32       | 97               | 33         | 0         | 1..97            | 211..307           | 6.00E-25  | 115       |
| <b>GOE #04</b><br>SSH35_187b_GOE_04 (195aa)<br>SSH25_Fb7_GOE_04                                                                                                        | ZP_00682693.1 | <i>Xylella fastidiosa</i> Ann-1                                 | TRAG protein                                             | 97.84      | 99.46       | 185              | 4          | 0         | 1..185           | 1..185             | 4.00E-90  | 332       |
|                                                                                                                                                                        | YP_980116.1   | <i>Verminephrobacter eiseniae</i> EF01-2                        | TRAG family protein                                      | 84.86      | 94.05       | 185              | 28         | 0         | 1..185           | 1..185             | 2.00E-81  | 303       |
|                                                                                                                                                                        | NP_660238.1   | <i>Haemophilus influenzae</i> biotype <i>aegyptius</i>          | TraK-like protein                                        | 43.81      | 62.37       | 194              | 96         | 6         | 1..184           | 5..195             | 8.00E-30  | 132       |
| <b>GOE #05</b><br>SSH36_56a_GOE_05 (244aa)<br>SSH15_36f_GOE_05<br>SSH12_187b_GOE_05<br>SSH50_912c_GOE_05                                                               | ZP_00682686.1 | <i>Xylella fastidiosa</i> Ann-1                                 | CagE. TrbE. VirB component of type IV transporter system | 97.11      | 99.42       | 173              | 5          | 0         | 57..229          | 165..337           | 2.00E-97  | 356       |
|                                                                                                                                                                        | YP_980123.1   | <i>Verminephrobacter eiseniae</i> EF01-2                        | CagE. TrbE. VirB component of type IV transporter system | 87.86      | 95.95       | 173              | 21         | 0         | 57..229          | 142..314           | 6.00E-90  | 332       |
|                                                                                                                                                                        | ZP_01506049.1 | <i>Burkholderia phymatum</i> STM815                             | CagE. TrbE. VirB component of type IV transporter system | 35.68      | 51.54       | 227              | 124        | 7         | 24..229          | 99..324            | 2.00E-25  | 117       |
| <b>GOE #06</b><br>SSH17_Cv21_GOE_06 (467aa)<br>SSH36_187b_GOE_06<br>SSH37_56a_GOE_06                                                                                   | ZP_00682686.1 | <i>Xylella fastidiosa</i> Ann-1                                 | CagE. TrbE. VirB component of type IV transporter system | 94.36      | 96.53       | 461              | 21         | 1         | 1..461           | 58..513            | 0.0       | 893       |
|                                                                                                                                                                        | YP_980123.1   | <i>Verminephrobacter eiseniae</i> EF01-2                        | CagE. TrbE. VirB component of type IV transporter system | 83.08      | 90.24       | 461              | 73         | 1         | 1..461           | 35..490            | 0.0       | 789       |
|                                                                                                                                                                        | ZP_00682673.1 | <i>Xylella fastidiosa</i> Ann-1                                 | probable conjugal transfer protein TraL                  | 98.25      | 99.12       | 114              | 2          | 0         | 109..222         | 101..214           | 2.00E-57  | 223       |

|                                                                                                                                 |                |                                                             |                                                          |       |        |     |    |   |          |          |          |      |
|---------------------------------------------------------------------------------------------------------------------------------|----------------|-------------------------------------------------------------|----------------------------------------------------------|-------|--------|-----|----|---|----------|----------|----------|------|
| <b>GOE #07</b><br>SSH07_56a_GOE_07<br>SSH23_36f_GOE_07<br>SSH30_187b_GOE_07<br>SSH20_Fb7_GOE_07<br>SSH04_912c_GOE_07<br>(232aa) | YP_980149.1    | Verminephrobacter eiseniae EF01-2                           | transfer origin protein. TraL                            | 85.09 | 92.98  | 114 | 17 | 0 | 109..222 | 101..214 | 5.00E-50 | 199  |
|                                                                                                                                 | ZP_00682686.1  | Xylella fastidiosa Ann-1                                    | CagE. TrbE. VirB component of type IV transporter system | 88.76 | 93.26  | 89  | 10 | 0 | 1..89    | 389..477 | 8.00E-42 | 172  |
| <b>GOE #08</b><br>SSH01_187b_GOE_08<br>(233aa)<br>SSH31_Cv21_GOE_08<br>SSH10_36f_GOE_08                                         | ZP_00683687.1  | Xylella fastidiosa Ann-1                                    | phage-related integrase                                  | 93.98 | 96.39  | 166 | 10 | 0 | 1..166   | 106..271 | 6.00E-84 | 311  |
|                                                                                                                                 | ZP_00683687.1  | Xylella fastidiosa Ann-1                                    | phage-related integrase                                  | 96.30 | 98.52  | 135 | 5  | 0 | 24..158  | 81..215  | 2.00E-67 | 257  |
| <b>GOE #10</b><br>SSH04_36f_GOE_10<br>SSH28_912c_GOE_10<br>(55aa)                                                               | ZP_00682686.1  | Xylella fastidiosa Ann-1                                    | CagE. TrbE. VirB component of type IV transporter system | 94.55 | 96.36  | 55  | 3  | 0 | 1..55    | 773..827 | 9.00E-24 | 112  |
|                                                                                                                                 | YP_980123.1    | Verminephrobacter eiseniae EF01-2                           | CagE. TrbE. VirB component of type IV transporter system | 85.45 | 90.91  | 55  | 8  | 0 | 1..55    | 750..804 | 2.00E-21 | 103  |
|                                                                                                                                 | CAM06592.1     | Bartonella schoenbuchensis                                  | VirB4-homolog                                            | 30.00 | 65.00  | 40  | 28 | 0 | 3..42    | 747..786 | 2.0      | 34.7 |
| <b>GOE #11</b><br>SSH31_187b_GOE_11<br>SSH13_Fb7_GOE_11<br>(185aa)                                                              | NP_454711.1    | Salmonella enterica subsp. enterica serovar Typhi str. CT18 | putative IS element transposase                          | 82.35 | 92.44  | 119 | 21 | 0 | 13..131  | 166..284 | 5.00E-48 | 192  |
|                                                                                                                                 | YP_001463237.1 | Escherichia coli E24377A                                    | transposase. IS605 orfB family                           | 81.51 | 89.92  | 119 | 22 | 0 | 13..131  | 160..278 | 1.00E-45 | 184  |
|                                                                                                                                 | YP_310889.1    | Shigella sonnei Ss046                                       | putative virulence protein                               | 81.51 | 89.92  | 119 | 22 | 0 | 13..131  | 140..258 | 1.00E-45 | 184  |
| <b>GOE #12</b><br>SSH15_912c_GOE_12<br>SSH23_Cv21_GOE_12<br>(82aa)                                                              | YP_980133.1    | Verminephrobacter eiseniae EF01-2                           | hypothetical protein Veis_5036                           | 61.25 | 82.50  | 80  | 31 | 0 | 2..81    | 4..83    | 7.00E-17 | 89.4 |
| <b>GOE #13</b><br>SSH08_56a_GOE_13<br>SSH05_912c_GOE_13<br>SSH46_Cv21_GOE_13<br>(132aa)<br>SSH24_36f_GOE_13                     | ZP_00682673.1  | Xylella fastidiosa Ann-1                                    | probable conjugal transfer protein TraL                  | 99.24 | 100.00 | 132 | 1  | 0 | 1..132   | 119..250 | 3.00E-65 | 249  |
|                                                                                                                                 | YP_980149.1    | Verminephrobacter eiseniae EF01-2                           | transfer origin protein. TraL                            | 84.85 | 93.18  | 132 | 20 | 0 | 1..132   | 119..250 | 3.00E-56 | 219  |
|                                                                                                                                 | AAP82043.1     | Stenotrophomonas maltophilia                                | putative transfer protein                                | 52.67 | 73.28  | 131 | 61 | 1 | 1..130   | 119..249 | 2.00E-32 | 140  |
| <b>GOE #14</b><br>SSH14_56a_GOE_14<br>(265aa)<br>SSH34_Cv21_GOE_14                                                              | ZP_00682691.1  | Xylella fastidiosa Ann-1                                    | conjugation TrbI-like protein                            | 89.85 | 90.36  | 197 | 12 | 2 | 1..196   | 78..267  | 4.00E-65 | 249  |
|                                                                                                                                 | YP_980118.1    | Verminephrobacter eiseniae EF01-2                           | conjugation TrbI family protein                          | 63.55 | 69.63  | 214 | 54 | 4 | 1..196   | 78..285  | 2.00E-33 | 144  |
|                                                                                                                                 | ZP_00651851.1  | Xylella fastidiosa Dixon                                    | Phage/plasmid primase P4.C-terminal                      | 79.03 | 85.48  | 62  | 13 | 0 | 204..265 | 782..843 | 1.00E-21 | 105  |
| <b>GOE #15</b><br>SSH41_56a_GOE_15<br>(113aa)<br>SSH26_912c_GOE_15                                                              | NP_779130.1    | Xylella fastidiosa Temecula1                                | hypothetical protein PD0914                              | 69.03 | 85.84  | 113 | 35 | 0 | 1..113   | 1..113   | 1.00E-37 | 158  |
|                                                                                                                                 | YP_451171.1    | Xanthomonas oryzae pv. oryzae MAFF 311018                   | hypothetical protein XOO_2142                            | 47.71 | 66.97  | 109 | 57 | 0 | 1..109   | 1..109   | 1.00E-19 | 98.6 |
|                                                                                                                                 | YP_364185.1    | Xanthomonas campestris pv. vesicatoria str. 85-10           | hypothetical protein XCV2454                             | 47.71 | 66.97  | 109 | 57 | 0 | 1..109   | 1..109   | 1.00E-19 | 98.6 |
| <b>GOE #16</b><br>SSH28_Cv21_GOE_16                                                                                             | YP_980134.1    | Verminephrobacter eiseniae EF01-2                           | Resolvase. N-terminal domain                             | 91.24 | 94.16  | 137 | 12 | 0 | 45..181  | 65..201  | 5.00E-60 | 232  |

| (181aa)<br>SSH19_56a_GOE_16                                                                                                   | ZP_00682679.1  | Xylella fastidiosa Ann-1                              | Resolvase. N-terminal:Resolvase helix-turn-helix region | 97.81      | 97.81       | 137              | 3          | 0         | 45..181          | 64..200            | 5.00E-54 | 212       |
|-------------------------------------------------------------------------------------------------------------------------------|----------------|-------------------------------------------------------|---------------------------------------------------------|------------|-------------|------------------|------------|-----------|------------------|--------------------|----------|-----------|
|                                                                                                                               | YP_973981.1    | Polaromonas naphthalenivorans CJ2                     | Resolvase. N-terminal domain                            | 60.32      | 73.02       | 126              | 50         | 0         | 45..170          | 57..182            | 8.00E-34 | 145       |
| <b>GOE #17</b><br>SSH18_56a_GOE_17<br>SSH14_Fb7_GOE_17<br>SSH34_Fb7_GOE_17<br>SSH28_187b_GOE_17 (88aa)                        | ZP_00684052.1  | Xylella fastidiosa Ann-1                              | Transcriptional regulator AbrB                          | 100.00     | 100.00      | 88               | 0          | 0         | 1..88            | 1..88              | 1.00E-35 | 151       |
|                                                                                                                               | YP_243669.1    | Xanthomonas campestris pv. campestris str. 8004       | hypothetical protein XC_2600                            | 63.29      | 78.48       | 79               | 28         | 1         | 1..79            | 48..125            | 2.00E-19 | 97.4      |
|                                                                                                                               | NP_637001.1    | Xanthomonas campestris pv. campestris str. ATCC 33913 | hypothetical protein XCC1631                            | 63.29      | 78.48       | 79               | 28         | 1         | 1..79            | 17..94             | 2.00E-18 | 94.4      |
| <b>GOE #18</b><br>SSH20_912c_GOE_18<br>SSH09_36f_GOE_18 (210aa)<br>SSH35_Cv21_GOE_18                                          | ZP_00682693.1  | Xylella fastidiosa Ann-1                              | TRAG protein                                            | 100.00     | 100.00      | 155              | 0          | 0         | 17..171          | 424..578           | 3.00E-86 | 319       |
|                                                                                                                               | YP_980116.1    | Verminephrobacter eiseniae EF01-2                     | TRAG family protein                                     | 90.97      | 94.19       | 155              | 14         | 0         | 17..171          | 424..578           | 2.00E-78 | 293       |
|                                                                                                                               | YP_558364.1    | Burkholderia xenovorans LB400                         | Putative Type IV secretory pathway protein VirD4        | 48.18      | 67.88       | 137              | 65         | 3         | 17..150          | 322..455           | 9.00E-27 | 122       |
| <b>GOE #19</b><br>SSH19_56a_GOE_19<br>SSH20_187b_GOE_19 (136aa)                                                               | YP_001463097.1 | Escherichia coli E24377A                              | transposase. IS605 family                               | 81.48      | 91.67       | 108              | 20         | 0         | 28..135          | 30..137            | 8.00E-49 | 195       |
|                                                                                                                               | NP_311304.1    | Escherichia coli O157:H7 str. Sakai                   | putative transposase TnA                                | 80.73      | 90.83       | 109              | 21         | 0         | 27..135          | 34..142            | 1.00E-48 | 194       |
|                                                                                                                               | NP_313209.1    | Escherichia coli O157:H7 str. Sakai                   | putative transposase                                    | 81.65      | 89.91       | 109              | 20         | 0         | 27..135          | 34..142            | 2.00E-48 | 194       |
| Query id                                                                                                                      | subject ids    | organism                                              | description                                             | % identity | % positives | alignment length | Mismatches | gap opens | query start..end | subject start..end | E-value  | Bit score |
| <b>GOE #20</b><br>SSH46_187b_GOE_20 (303aa)<br>SSH43_Cv21_GOE_20<br>SSH39_56a_GOE_20<br>SSH60_912c_GOE_20<br>SSH41_Fb7_GOE_20 | ZP_00653045.1  | Xylella fastidiosa Dixon                              | helix-turn-helix motif                                  | 98.82      | 98.82       | 85               | 1          | 0         | 1..85            | 1..85              | 2.00E-35 | 150       |
|                                                                                                                               | ZP_00679904.1  | Xylella fastidiosa Ann-1                              | helix-turn-helix motif                                  | 98.77      | 98.77       | 81               | 1          | 0         | 5..85            | 1..81              | 4.00E-34 | 146       |
| <b>GOE #21</b><br>SSH55_912c_GOE_21<br>SSH26_187b_GOE_21 (68aa)                                                               | No hit         |                                                       |                                                         |            |             |                  |            |           |                  |                    |          |           |
| <b>GOE #22</b><br>SSH28_36f_GOE_22 (107aa)<br>SSH52_912c_GOE_22<br>SSH06_187b_GOE_22                                          | ZP_00652000.1  | Xylella fastidiosa Dixon                              | Adenylate kinase. subfamily                             | 95.74      | 95.74       | 47               | 2          | 0         | 1..47            | 119..165           | 3.00E-18 | 93.6      |
|                                                                                                                               | Q9PGM3         |                                                       | Adenylate kinase (ATP-AMP transphosphorylase)           | 95.74      | 95.74       | 47               | 2          | 0         | 1..47            | 119..165           | 3.00E-18 | 93.6      |
| <b>GOE #23</b><br>SSH51_912c_GOE_23<br>SSH42_187b_GOE_23 (232aa)                                                              | gZP_00682694.1 | Xylella fastidiosa Ann-1                              | hypothetical protein XfasoDRAFT_2670                    | 98.28      | 98.71       | 232              | 4          | 0         | 1..232           | 137..368           | 2.00E-95 | 350       |
|                                                                                                                               | YP_980115.1    | Verminephrobacter eiseniae EF01-2                     | hypothetical protein Veis_5018                          | 89.83      | 92.80       | 236              | 20         | 1         | 1..232           | 193..428           | 2.00E-90 | 333       |
|                                                                                                                               | YP_067827.1    | Aeromonas punctata                                    | DNA primase TraC4                                       | 35.92      | 59.86       | 142              | 90         | 1         | 1..141           | 671..812           | 2.00E-17 | 91.3      |
| <b>GOE #24</b><br>SSH18_Fb7_GOE_24<br>SSH29_912c_GOE_24                                                                       | ZP_00682687.1  | Xylella fastidiosa Ann-1                              | plasmid-related exported protein                        | 91.96      | 93.75       | 224              | 14         | 3         | 1..223           | 1..221             | 6.00E-88 | 325       |
|                                                                                                                               | YP_980122.1    | Verminephrobacter                                     | type IV secretion                                       | 69.20      | 78.12       | 224              | 65         | 3         | 1..223           | 1..221             | 5.00E-60 | 232       |

|                                                                                          |                |                                                   |                                                          |        |        |     |     |   |          |          |           |      |
|------------------------------------------------------------------------------------------|----------------|---------------------------------------------------|----------------------------------------------------------|--------|--------|-----|-----|---|----------|----------|-----------|------|
| (223aa)                                                                                  |                | eiseniae EF01-2                                   | system family protein                                    |        |        |     |     |   |          |          |           |      |
|                                                                                          | YP_001257140.1 | Brucella ovis ATCC 25840                          | P-type DNA transfer protein VirB5                        | 30.84  | 48.90  | 227 | 129 | 6 | 16..222  | 9..227   | 2.00E-15  | 84.7 |
| <b>GOE #25</b><br>SSH41_Cv21_GOE_25<br>SSH18_912c_GOE_25<br>(117aa)                      | ZP_00682678.1  | Xylella fastidiosa Ann-1                          | Plasmid encoded RepA protein                             | 100.00 | 100.00 | 88  | 0   | 0 | 30..117  | 280..367 | 8.00E-45  | 181  |
|                                                                                          | YP_361657.1    | Xanthomonas campestris pv. vesicatoria str. 85-10 | putative replication protein A                           | 79.55  | 93.18  | 88  | 18  | 0 | 30..117  | 321..408 | 5.00E-35  | 149  |
|                                                                                          | NP_644784.1    | Xanthomonas axonopodis pv. citri str. 306         | replication protein A                                    | 79.55  | 93.18  | 88  | 18  | 0 | 30..117  | 282..369 | 7.00E-35  | 149  |
| <b>GOE #26</b><br>SSH64_912c_GOE_26<br>SSH30_Cv21_GOE_26<br>SSH37_187b_GOE_26<br>(288aa) | ZP_00651189.1  | Xylella fastidiosa Dixon                          | transferase hexapeptide repeat                           | 75.00  | 82.74  | 168 | 40  | 1 | 16..181  | 5..172   | 6.00E-59  | 228  |
|                                                                                          | YP_980124.1    | Verminephrobacter eiseniae EF01-2                 | type IV secretory pathway. VirB3 family protein          | 84.15  | 92.68  | 82  | 13  | 0 | 207..288 | 46..127  | 1.00E-34  | 148  |
|                                                                                          | ZP_00652852.1  | Xylella fastidiosa Dixon                          | transferase hexapeptide repeat                           | 46.43  | 60.12  | 168 | 88  | 1 | 16..181  | 5..172   | 1.00E-24  | 115  |
|                                                                                          | NP_297776.1    | Xylella fastidiosa 9a5c                           | UDP-3-O-3-hydroxymyristoyl glucosamine N-acyltransferase | 47.31  | 60.48  | 167 | 85  | 2 | 16..179  | 11..177  | 1.00E-24  | 114  |
| <b>GOE #27</b><br>SSH47_Cv21_GOE_27<br>SSH12_912c_GOE_27<br>(108aa)                      | YP_980113.1    | Verminephrobacter eiseniae EF01-2                 | Hypothetical protein Veis_5018                           | 80.43  | 86.96  | 92  | 17  | 1 | 17..108  | 275..365 | 4.00E-29  | 129  |
| <b>GOE #28</b><br>SSH06_Cv21_GOE_28<br>SSH01_912c_GOE_28<br>(86aa)<br>SSH49_187b_GOE_28  | No hit         |                                                   |                                                          |        |        |     |     |   |          |          |           |      |
| <b>GOE #29</b><br>SSH54_912c_GOE_29<br>(87aa)<br>SSH33_36f_GOE_29                        | ZP_00651848.1  | Xylella fastidiosa Dixon                          | Helix-turn-helix motif:Peptidase S24. S26A and S26B      | 76.09  | 89.13  | 46  | 11  | 0 | 42..87   | 211..256 | 1.00E-12  | 75.1 |
|                                                                                          | ZP_00682615.1  | Xylella fastidiosa Ann-1                          | Peptidase S24. S26A and S26B                             | 76.09  | 84.78  | 46  | 11  | 0 | 42..87   | 207..252 | 1.00E-11  | 71.6 |
|                                                                                          | NP_779330.1    | Xylella fastidiosa Temecula1                      | hypothetical protein PD1124                              | 76.09  | 84.78  | 46  | 11  | 0 | 42..87   | 207..252 | 1.00E-11  | 71.6 |
| <b>GOE #30</b><br>SSH19_187b_GOE_30<br>SSH24_56a_GOE_30<br>SSH14_Cv21_GOE_30<br>(236aa)  | ZP_00682689.1  | Xylella fastidiosa Ann-1                          | VirB8                                                    | 97.03  | 97.46  | 236 | 7   | 0 | 1..236   | 1..236   | 3.00E-123 | 442  |
|                                                                                          | YP_980120.1    | Verminephrobacter eiseniae EF01-2                 | VirB8 family protein                                     | 85.33  | 91.56  | 225 | 33  | 0 | 12..236  | 14..238  | 5.00E-104 | 378  |
|                                                                                          | ABI83644.1     | Aeromonas veronii                                 | conjugal transfer protein                                | 38.67  | 56.89  | 225 | 134 | 3 | 14..236  | 24..246  | 5.00E-35  | 149  |
| <b>GOE #31</b><br>SSH18_Cv21_GOE_31<br>SSH35_912c_GOE_31<br>SSH05_56a_GOE_31<br>(289aa)  | YP_980124.1    | Verminephrobacter eiseniae EF01-2                 | type IV secretory pathway. VirB3 family protein          | 84.15  | 92.68  | 82  | 13  | 0 | 208..289 | 46..127  | 6.00E-35  | 149  |
|                                                                                          | AAX12232.1     | Xanthomonas axonopodis pv. glycines               | probable conjugal transfer protein                       | 40.91  | 58.44  | 154 | 85  | 1 | 8..161   | 48..195  | 3.00E-20  | 100  |
|                                                                                          | ZP_01506048.1  | Burkholderia phymatum STM815                      | type IV secretory pathway. VirB3-like                    | 36.50  | 54.01  | 137 | 76  | 4 | 10..136  | 8..143   | 4.00E-14  | 80.1 |
| <b>GOE #32</b><br>SSH10_Fb7_GOE_32                                                       | ZP_00682692.1  | Xylella fastidiosa Ann-1                          | type II secretion system protein E                       | 96.67  | 98.89  | 90  | 3   | 0 | 1..90    | 244..333 | 1.00E-47  | 191  |

| SSH35_56a_GOE_32<br>SSH37_36f_GOE_32<br>(274aa)<br>SSH29_187b_GOE_32<br>SSH47_912c_GOE_32<br>SSH08_Cv21_GOE_32                  | YP_980117.1   | Verminephrobacter eiseniae EF01-2 | type II secretion system protein E                       | 95.56      | 98.89       | 90               | 4          | 0         | 1..90            | 244..333           | 5.00E-47  | 189       |
|---------------------------------------------------------------------------------------------------------------------------------|---------------|-----------------------------------|----------------------------------------------------------|------------|-------------|------------------|------------|-----------|------------------|--------------------|-----------|-----------|
|                                                                                                                                 | ZP_00652971.1 | Xylella fastidiosa Dixon          | phage-related protein                                    | 68.75      | 78.12       | 128              | 40         | 0         | 101..228         | 15..142            | 1.00E-44  | 181       |
| <b>GOE #33</b><br>SSH66_912c_GOE_33<br>(136aa)<br>SSH03_36f_GOE_33                                                              | ZP_00683687.1 | Xylella fastidiosa Ann-1          | phage-related integrase                                  | 87.69      | 90.00       | 130              | 13         | 1         | 1..127           | 282..411           | 2.00E-56  | 211       |
|                                                                                                                                 | NP_297770.1   | Xylella fastidiosa 9a5c           | hypothetical protein XF0480                              | 48.91      | 64.96       | 137              | 67         | 1         | 2..135           | 245..381           | 2.00E-28  | 119       |
|                                                                                                                                 | ZP_00651193.1 | Xylella fastidiosa Dixon          | phage-related integrase                                  | 51.16      | 67.44       | 129              | 60         | 1         | 2..127           | 245..373           | 3.00E-28  | 118       |
| <b>GOE #34</b><br>SSH72_912c_GOE_34<br>(136aa)<br>SSH03_36f_GOE_34                                                              | ZP_00683687.1 | Xylella fastidiosa Ann-1          | phage-related integrase                                  | 87.69      | 90.00       | 130              | 13         | 1         | 1..127           | 282..411           | 2.00E-56  | 211       |
|                                                                                                                                 | ZP_00651193.1 | Xylella fastidiosa Dixon          | phage-related integrase                                  | 51.16      | 67.44       | 129              | 60         | 1         | 2..127           | 245..373           | 3.00E-28  | 118       |
| <b>GOE #35</b><br>SSH38_187b_GOE_35<br>SSH06_56a_GOE_35<br>SSH49_912c_GOE_35<br>(317aa)<br>SSH16_Fb7_GOE_35<br>SSH07_36f_GOE_35 | ZP_00682686.1 | Xylella fastidiosa Ann-1          | CagE. TrbE. VirB component of type IV transporter system | 88.33      | 91.83       | 257              | 29         | 1         | 54..309          | 22..278            | 5.00E-133 | 474       |
|                                                                                                                                 | YP_980123.1   | Verminephrobacter eiseniae EF     | CagE. TrbE. VirB component of type IV transporter system | 76.86      | 86.27       | 255              | 58         | 1         | 56..309          | 1..255             | 2.00E-117 | 423       |
|                                                                                                                                 | ZP_01986916.1 | TraE Vibrio harveyi HY01          | conjugal transfer protein                                | 29.77      | 53.95       | 215              | 145        | 3         | 71..284          | 14..223            | 1.00E-24  | 115       |
| <b>GOE #36</b><br>SSH68_912c_GOE_36<br>(113aa)<br>SSH10_187b_GOE_36                                                             | ZP_00682678.1 | Xylella fastidiosa Ann-1          | Plasmid encoded RepA protein                             | 73.49      | 77.11       | 83               | 15         | 2         | 1..83            | 1..76              | 2.00E-21  | 104       |
| <b>GOE #37</b><br>SSH27_187b_GOE_37<br>(95aa)                                                                                   | YP_380330.1   | Geobacter metallireducens GS-15   | CopG-like DNA-binding protein                            | 54.10      | 85.25       | 61               | 28         | 0         | 4..64            | 2..62              | 4.00E-11  | 70.1      |
|                                                                                                                                 | NP_835378.1   | Acidithiobacillus caldus          | anti-toxin-like protein                                  | 64.41      | 77.97       | 59               | 21         | 0         | 4..62            | 2..60              | 7.00E-11  | 69.3      |
|                                                                                                                                 | AAG23807.1    | Pseudomonas fluorescens           | antidote                                                 | 59.02      | 75.41       | 61               | 25         | 0         | 4..64            | 2..62              | 1.00E-10  | 68.2      |
| <b>GOE #38</b><br>SSH40_187b_GOE_38<br>SSH29_36f_GOE_38<br>(213aa)<br>SSH37_Cv21_GOE_38                                         | ZP_00682692.1 | Xylella fastidiosa Ann-1          | type II secretion system protein E                       | 96.30      | 99.07       | 108              | 4          | 0         | 1..108           | 119..226           | 4.00E-57  | 222       |
|                                                                                                                                 | YP_980117.1   | Verminephrobacter eiseniae EF01-2 | type II secretion system protein E                       | 88.89      | 95.37       | 108              | 12         | 0         | 1..108           | 119..226           | 2.00E-51  | 204       |
|                                                                                                                                 | ZP_00651174.1 | Xylella fastidiosa Dixon          | N6 adenine-specific DNA methyltransferase. D12 class     | 98.57      | 98.57       | 70               | 1          | 0         | 123..192         | 25..94             | 3.00E-36  | 153       |
| <b>GOE #39</b><br>SSH26_Fb7_GOE_39<br>(88aa)<br>SSH43_912c_GOE_39                                                               | No hit        |                                   |                                                          |            |             |                  |            |           |                  |                    |           |           |
| Query id                                                                                                                        | subject ids   | organism                          | description                                              | % identity | % positives | alignment length | Mismatches | gap opens | query start..end | subject start..end | E-value   | Bit score |
| <b>GOE #40</b><br>SSH32_56a_GOE_40<br>SSH38_Cv21_GOE_40<br>SSH09_Fb7_GOE_40<br>SSH08_187b_GOE_40<br>(335aa)                     | ZP_00682686.1 | Xylella fastidiosa Ann-1          | CagE. TrbE. VirB component of type IV transporter system | 90.14      | 95.07       | 284              | 27         | 1         | 27..309          | 502..785           | 8.00E-152 | 537       |
|                                                                                                                                 | YP_980123.1   | Verminephrobacter eiseniae EF01-2 | CagE. TrbE. VirB component of type IV transporter system | 91.01      | 94.96       | 278              | 24         | 1         | 27..303          | 479..756           | 4.00E-150 | 531       |

|                                                                                                             |               |                                                                |                                                                    |        |        |     |     |   |         |          |          |      |
|-------------------------------------------------------------------------------------------------------------|---------------|----------------------------------------------------------------|--------------------------------------------------------------------|--------|--------|-----|-----|---|---------|----------|----------|------|
| SSH21_36f_GOE_40                                                                                            | BAD83765.1    | Moraxella bovis<br>Epp63                                       | VirB4-like protein                                                 | 52.13  | 67.73  | 282 | 128 | 3 | 27..303 | 483..762 | 4.00E-80 | 299  |
| <b>GOE #41</b><br>SSH29_56a_GOE_41<br>SSH12_36f_GOE_41<br>(191aa)<br>SSH32_Cv21_GOE_41<br>SSH24_912c_GOE_41 | ZP_00682692.1 | Xylella fastidiosa<br>Ann-1                                    | type II secretion<br>system protein E                              | 97.20  | 97.20  | 107 | 3   | 0 | 1..107  | 1..107   | 4.00E-54 | 213  |
|                                                                                                             | YP_980117.1   | Verminephrobacter<br>eiseniae EF01-2                           | type II secretion<br>system protein E                              | 86.92  | 95.33  | 107 | 14  | 0 | 1..107  | 1..107   | 2.00E-48 | 193  |
|                                                                                                             | CAM06593.1    | Bartonella<br>schoenbuchensis                                  | VirB11-homolog                                                     | 37.25  | 50.98  | 102 | 60  | 1 | 12..113 | 5..102   | 2.00E-09 | 64.7 |
| <b>GOE #42</b><br>SSH25_56a_GOE_42<br>SSH13_Cv21_GOE_42<br>SSH76_912c_GOE_42<br>(159aa)                     | ZP_00682690.1 | Xylella fastidiosa<br>Ann-1                                    | Conjugal transfer<br>protein<br>TrbG/VirB9/CagX                    | 88.10  | 93.65  | 126 | 14  | 1 | 1..126  | 1..125   | 2.00E-56 | 220  |
|                                                                                                             | YP_980119.1   | Verminephrobacter<br>eiseniae EF01-2                           | Conjugal transfer<br>protein<br>TrbG/VirB9/CagX                    | 82.54  | 88.10  | 126 | 21  | 1 | 1..126  | 1..125   | 1.00E-51 | 204  |
|                                                                                                             | BAD83760.1    | Moraxella bovis<br>Epp63                                       | virB9-like protein                                                 | 41.74  | 60.00  | 115 | 63  | 2 | 16..130 | 24..134  | 7.00E-18 | 92.4 |
| <b>GOE #43</b><br>SSH13_912c_GOE_43<br>(84aa)<br>SSH28_56a_GOE_43                                           | ZP_00682701.1 | Xylella fastidiosa<br>Ann-1                                    | SpoVT/AbrB-like                                                    | 82.09  | 85.07  | 67  | 12  | 0 | 1..67   | 1..67    | 3.00E-20 | 100  |
|                                                                                                             | NP_644714.1   | Xanthomonas<br>axonopodis pv. citri<br>str. 306                | plasmid stable<br>inheritance protein I                            | 80.77  | 80.77  | 52  | 10  | 0 | 1..52   | 1..52    | 7.00E-15 | 82.4 |
|                                                                                                             | AAX12222.1    | Xanthomonas<br>axonopodis pv.<br>glycines                      | probable plasmid<br>stable inheritance<br>protein I                | 73.08  | 82.69  | 52  | 14  | 0 | 1..52   | 1..52    | 1.00E-13 | 78.6 |
| <b>GOE #44</b><br>SSH05_187b_GOE_44<br>SSH11_Cv21_GOE_44<br>SSH11_36f_GOE_44<br>(144aa)                     | ZP_00682695.1 | Xylella fastidiosa<br>Ann-1                                    | hypothetical protein<br>XfasoDRAFT_2671                            | 92.50  | 96.25  | 80  | 6   | 0 | 65..144 | 255..334 | 5.00E-32 | 139  |
|                                                                                                             | YP_980114.1   | Verminephrobacter<br>eiseniae EF01-2                           | Relaxase/mobilization<br>nuclease family protein                   | 75.00  | 81.25  | 80  | 19  | 1 | 65..144 | 299..377 | 1.00E-22 | 108  |
|                                                                                                             | ZP_00682701.1 | Xylella fastidiosa<br>Ann-1                                    | SpoVT/AbrB-like                                                    | 78.67  | 81.33  | 75  | 14  | 2 | 1..75   | 1..73    | 5.00E-22 | 106  |
| <b>GOE #45</b><br>SSH13_56a_GOE_45<br>SSH22_187b_GOE_45<br>SSH31_36f_GOE_45<br>SSH07_Fb7_GOE_45<br>(194aa)  | ZP_00682672.1 | Xylella fastidiosa<br>Ann-1                                    | hypothetical protein<br>XfasoDRAFT_2648                            | 98.15  | 99.07  | 108 | 2   | 0 | 87..194 | 11..118  | 9.00E-44 | 178  |
|                                                                                                             | NP_779052.1   | Xylella fastidiosa<br>Temecula1                                | methyltransferase. type<br>III restriction-<br>modification system | 100.00 | 100.00 | 79  | 0   | 0 | 1..79   | 260..338 | 7.00E-42 | 172  |
|                                                                                                             | NP_635609.1   | Xanthomonas<br>campestris pv.<br>campestris str.<br>ATCC 33913 | methyltransferase                                                  | 76.92  | 87.18  | 78  | 18  | 0 | 2..79   | 261..338 | 1.00E-30 | 134  |
| <b>GOE #46</b><br>SSH58_912c_GOE_46<br>(110aa)<br>SSH38_Fb7_GOE_46                                          | ZP_00681894.1 | Xylella fastidiosa<br>Ann-1                                    | BRO. N-terminal                                                    | 86.75  | 89.16  | 83  | 9   | 1 | 1..81   | 1..83    | 3.00E-35 | 150  |
|                                                                                                             | ZP_00652985.1 | Xylella fastidiosa<br>Dixon                                    | BRO. N-terminal                                                    | 84.34  | 86.75  | 83  | 11  | 1 | 1..81   | 1..83    | 3.00E-33 | 143  |
|                                                                                                             | ZP_00681895.1 | Xylella fastidiosa<br>Ann-1                                    | BRO. N-terminal                                                    | 58.23  | 65.82  | 79  | 28  | 2 | 1..78   | 1..75    | 1.00E-15 | 85.1 |
| <b>GOE #47</b><br>SSH43_187b_GOE_47<br>(145aa)<br>SSH70_912c_GOE_47                                         | ZP_00682699.1 | Xylella fastidiosa<br>Ann-1                                    | hypothetical protein<br>XfasoDRAFT_2675                            | 95.51  | 97.75  | 89  | 4   | 0 | 57..145 | 18..106  | 7.00E-32 | 139  |
|                                                                                                             | YP_980125.1   | Verminephrobacter<br>eiseniae EF01-2                           | hypothetical protein<br>Veis_5028                                  | 88.73  | 95.77  | 71  | 8   | 0 | 75..145 | 32..102  | 2.00E-24 | 114  |
|                                                                                                             | ABI83638.1    | Aeromonas veronii                                              | conjugal transfer<br>prepropilin                                   | 52.86  | 68.57  | 70  | 33  | 0 | 75..144 | 30..99   | 9.00E-10 | 65.5 |
| <b>GOE #48</b><br>SSH20_36f_GOE_48<br>(138aa)<br>SSH30_Fb7_GOE_48                                           | ZP_00682691.1 | Xylella fastidiosa<br>Ann-1                                    | conjugation TrbI-like<br>protein                                   | 92.06  | 96.83  | 63  | 5   | 0 | 1..63   | 1..63    | 6.00E-24 | 112  |
|                                                                                                             | YP_980118.1   | Verminephrobacter<br>eiseniae EF01-2                           | conjugation TrbI<br>family protein                                 | 72.06  | 83.82  | 68  | 19  | 0 | 1..68   | 1..68    | 4.00E-19 | 96.3 |

[illegible]

| SSH16_56a_GOE_57<br>SSH22_Cv21_GOE_57<br>SSH61_912c_GOE_57                                                 |               |                                                 |                                            |               |                |                     |                 |              |                     |                       |          |              |
|------------------------------------------------------------------------------------------------------------|---------------|-------------------------------------------------|--------------------------------------------|---------------|----------------|---------------------|-----------------|--------------|---------------------|-----------------------|----------|--------------|
| <b>GOE #58</b><br>SSH22_36f_GOE_58<br>(51aa)<br>SSH22_Cv21_GOE_58                                          | No hit        |                                                 |                                            |               |                |                     |                 |              |                     |                       |          |              |
| <b>GOE #59</b><br>SSH08_36f_GOE_59<br>(92aa)<br>SSH15_56a_GOE_59<br>SSH45_Cv21_GOE_59<br>SSH69_912c_GOE_59 | ZP_00682672.1 | Xylella fastidiosa<br>Ann-1                     | hypothetical protein<br>XfasoDRAFT_2648    | 97.83         | 98.91          | 92                  | 2               | 0            | 1..92               | 27..118               | 8.00E-30 | 132          |
|                                                                                                            | YP_980150.1   | Verminephrobacter<br>eiseniae EF01-2            | hypothetical protein<br>Veis_5053          | 63.04         | 76.09          | 92                  | 34              | 0            | 1..92               | 26..117               | 5.00E-18 | 92.8         |
| Query id                                                                                                   | subject ids   | organism                                        | description                                | %<br>identity | %<br>positives | alignment<br>length | Mismat-<br>ches | gap<br>opens | query<br>start..end | subject<br>start..end | E-value  | Bit<br>score |
| <b>GOE #60</b><br>SSH26_36f_GOE_60<br>(105aa)<br>SSH62_912c_GOE_60<br>SSH20_56a_GOE_60                     | ZP_00682694.1 | Xylella fastidiosa<br>Ann-1                     | hypothetical protein<br>XfasoDRAFT_2670    | 99.05         | 100.00         | 105                 | 1               | 0            | 1..105              | 264..368              | 2.00E-38 | 160          |
|                                                                                                            | YP_980115.1   | Verminephrobacter<br>eiseniae EF01-2            | hypothetical protein<br>Veis_5018          | 91.43         | 94.29          | 105                 | 9               | 0            | 1..105              | 324..428              | 1.00E-36 | 154          |
| <b>GOE #61</b><br>SSH33_187b_GOE_61<br>(66aa)<br>SSH32_36f_GOE_61                                          | ZP_00684053.1 | Xylella fastidiosa<br>Ann-1                     | conserved hypothetical<br>protein          | 98.48         | 100.00         | 66                  | 1               | 0            | 1..66               | 66..131               | 2.00E-27 | 124          |
|                                                                                                            | AAW76134.1    | Xanthomonas<br>oryzae pv. oryzae<br>KACC10331   | conserved hypothetical<br>protein          | 70.77         | 81.54          | 65                  | 19              | 0            | 2..66               | 213..277              | 9.00E-20 | 98.6         |
|                                                                                                            | YP_988599.1   | Bartonella<br>bacilliformis KC583               | hypothetical protein<br>BARBAKC583_0275    | 69.23         | 84.62          | 65                  | 20              | 0            | 2..66               | 67..131               | 1.00E-19 | 98.2         |
| <b>GOE #62</b><br>SSH25_36f_GOE_62<br>(128aa)<br>SSH06_912c_GOE_62                                         | ZP_00682696.1 | Xylella fastidiosa<br>Ann-1                     | hypothetical protein<br>XfasoDRAFT_2672    | 96.75         | 97.56          | 123                 | 4               | 0            | 1..123              | 1..123                | 2.00E-53 | 211          |
|                                                                                                            | YP_980148.1   | Verminephrobacter<br>eiseniae EF01-2            | hypothetical protein<br>Veis_5051          | 74.80         | 84.55          | 123                 | 31              | 0            | 1..123              | 1..123                | 3.00E-32 | 140          |
| <b>GOE #63</b><br>SSH05_36f_GOE_63<br>(221aa)<br>SSH39_Cv21_GOE_63                                         | ZP_00682687.1 | Xylella fastidiosa<br>Ann-1                     | plasmid-related<br>exported protein        | 95.02         | 96.83          | 221                 | 11              | 0            | 1..221              | 1..221                | 6.00E-93 | 342          |
|                                                                                                            | YP_980122.1   | Verminephrobacter<br>eiseniae EF01-2            | type IV secretion<br>system family protein | 71.49         | 81.00          | 221                 | 63              | 0            | 1..221              | 1..221                | 2.00E-65 | 250          |
|                                                                                                            | NP_444522.1   | Plasmid pIPO2T                                  | TraF protein                               | 34.74         | 53.52          | 213                 | 114             | 4            | 20..207             | 15..227               | 7.00E-20 | 99.0         |
| <b>GOE #64</b><br>SSH07_187b_GOE_64<br>(137aa)<br>SSH29_Cv21_GOE_64                                        | NP_644763.1   | Xanthomonas<br>axonopodis pv. citri<br>str. 306 | hypothetical protein<br>XACb0035           | 75.74         | 88.97          | 136                 | 32              | 1            | 1..135              | 1..136                | 1.00E-50 | 201          |
| <b>GOE #65</b><br>SSH03_187b_GOE_65<br>(129aa)<br>SSH26_56a_GOE_65                                         | ZP_00682687.1 | Xylella fastidiosa<br>Ann-1                     | plasmid-related<br>exported protein        | 96.80         | 98.40          | 125                 | 4               | 0            | 5..129              | 97..221               | 7.00E-47 | 188          |
|                                                                                                            | YP_980122.1   | Verminephrobacter<br>eiseniae EF01-2            | type IV secretion<br>system family protein | 75.20         | 84.00          | 125                 | 31              | 0            | 5..129              | 97..221               | 4.00E-37 | 156          |
| <b>GOE #66</b><br>SSH13_36f_GOE_66<br>(125aa)<br>SSH19_912c_GOE_66                                         | ZP_00682691.1 | Xylella fastidiosa<br>Ann-1                     | conjugation TrbI-like<br>protein           | 96.80         | 98.40          | 125                 | 4               | 0            | 1..125              | 308..432              | 1.00E-63 | 244          |
|                                                                                                            | YP_980118.1   | Verminephrobacter<br>eiseniae EF01-2            | conjugation TrbI family<br>protein         | 92.00         | 93.60          | 125                 | 10              | 0            | 1..125              | 326..450              | 2.00E-60 | 234          |
|                                                                                                            | NP_444528.1   | Plasmid pIPO2T                                  | TraL protein                               | 47.15         | 65.85          | 123                 | 61              | 1            | 1..123              | 262..380              | 9.00E-26 | 118          |
| <b>GOE #67</b><br>SSH09_187b_GOE_67<br>(122aa)<br>SSH67_912c_GOE_67                                        | YP_980134.1   | Verminephrobacter<br>eiseniae EF01-2            | Resolvase. N-terminal<br>domain            | 90.98         | 94.26          | 122                 | 11              | 0            | 1..122              | 80..201               | 3.00E-50 | 200          |
|                                                                                                            | ZP_00682679.1 | Xylella fastidiosa<br>Ann-1                     | Resolvase. N-<br>terminal:Resolvase        | 98.36         | 98.36          | 122                 | 2               | 0            | 1..122              | 79..200               | 3.00E-44 | 179          |

|                                                                  |                 |                                           |                                                     |       |        |     |    |   |         |          |           |      |
|------------------------------------------------------------------|-----------------|-------------------------------------------|-----------------------------------------------------|-------|--------|-----|----|---|---------|----------|-----------|------|
|                                                                  |                 |                                           | helix-turn-helix region                             |       |        |     |    |   |         |          |           |      |
|                                                                  | YP_973981.1     | Polaromonas naphthalenivorans CJ2         | Resolvase. N-terminal domain                        | 57.66 | 72.07  | 111 | 47 | 0 | 1..111  | 72..182  | 1.00E-26  | 121  |
| <b>GOE #68</b><br>SSH34_912c_GOE_68 (106aa)<br>SSH19_Cv21_GOE_68 | ZP_00682699.1   | Xylella fastidiosa Ann-1                  | hypothetical protein XfasoDRAFT_2675                | 92.45 | 95.28  | 106 | 8  | 0 | 1..106  | 1..106   | 8.00E-37  | 155  |
|                                                                  | ref YP_980125.1 | Verminephrobacter eiseniae EF01-2         | hypothetical protein Veis_5028                      | 88.73 | 95.77  | 71  | 8  | 0 | 36..106 | 32..102  | 2.00E-23  | 110  |
|                                                                  | ABI83638.1      | Aeromonas veronii                         | conjugal transfer prepropilin                       | 52.86 | 68.57  | 70  | 33 | 0 | 36..105 | 30..99   | 3.00E-09  | 63.9 |
| <b>GOE #69</b><br>SSH41_912c_GOE_69<br>SSH25_Cv21_GOE_69 (101aa) | No hit          |                                           |                                                     |       |        |     |    |   |         |          |           |      |
| <b>GOE #70</b><br>SSH02_36f_GOE_70 (86aa)<br>SSH24_Cv21_GOE_70   | ZP_00682697.1   | Xylella fastidiosa Ann-1                  | hypothetical protein XfasoDRAFT_2673                | 91.86 | 95.35  | 86  | 7  | 0 | 1..86   | 74..159  | 6.00E-32  | 139  |
|                                                                  | YP_980126.1     | Verminephrobacter eiseniae EF01-2         | hypothetical protein Veis_5029                      | 46.00 | 62.00  | 100 | 40 | 2 | 1..86   | 53..152  | 8.00E-13  | 75.9 |
| <b>GOE #71</b><br>SSH27_912c_GOE_71 (80aa)<br>SSH01_Cv21_GOE_71  | ZP_00652969.1   | Xylella fastidiosa Dixon                  | Helix-turn-helix motif:Peptidase S24. S26A and S26B | 98.75 | 100.00 | 80  | 1  | 0 | 1..80   | 145..224 | 1.00E-39  | 164  |
|                                                                  | NP_297986.1     | Xylella fastidiosa 9a5c                   | phage-related repressor protein                     | 63.75 | 75.00  | 80  | 28 | 1 | 1..80   | 143..221 | 3.00E-22  | 107  |
|                                                                  | ZP_00653051.1   | Xylella fastidiosa Dixon                  | Peptidase S24. S26A and S26B                        | 49.37 | 63.29  | 79  | 39 | 1 | 1..78   | 179..257 | 6.00E-13  | 76.3 |
| <b>GOE #72</b><br>SSH47_187b_GOE_72 (73aa)<br>SSH77_912c_GOE_72  | ZP_00682690.1   | Xylella fastidiosa Ann-1                  | Conjugal transfer protein TrbG/VirB9/CagX           | 95.89 | 98.63  | 73  | 3  | 0 | 1..73   | 187..259 | 8.00E-33  | 142  |
|                                                                  | YP_980119.1     | Verminephrobacter eiseniae EF01-2         | Conjugal transfer protein TrbG/VirB9/CagX           | 91.55 | 97.18  | 71  | 6  | 0 | 1..71   | 191..261 | 3.00E-30  | 133  |
| <b>GOE #73</b><br>SSH34_56a_GOE_73 (257aa)                       | ZP_00682693.1   | Xylella fastidiosa Ann-1                  | TRAG protein                                        | 98.35 | 99.59  | 243 | 4  | 0 | 1..243  | 1..243   | 3.00E-130 | 465  |
|                                                                  | YP_980116.1     | Verminephrobacter eiseniae EF01-2         | TRAG family protein                                 | 87.65 | 95.06  | 243 | 30 | 0 | 1..243  | 1..243   | 2.00E-120 | 433  |
|                                                                  | NP_642936.1     | Xanthomonas axonopodis pv. citri str. 306 | VirD4 protein                                       | 51.74 | 63.18  | 201 | 83 | 5 | 45..242 | 49..238  | 2.00E-44  | 180  |
| <b>GOE #74</b><br>SSH03_912C_GOE_74 (165aa)                      | AAK13432.1      | Xylella fastidiosa                        | repB/MobA-like protein                              | 95.00 | 96.00  | 100 | 5  | 0 | 37..136 | 155..254 | 6.00E-47  | 189  |
|                                                                  | NP_065281.1     | uncultured eubacterium pIE1115            | putative mobilization protein                       | 47.90 | 59.66  | 119 | 62 | 0 | 14..132 | 137..255 | 3.00E-20  | 100  |
|                                                                  | NP_862661.1     | uncultured bacterium                      | putative mobilization protein                       | 47.06 | 58.82  | 119 | 63 | 0 | 14..132 | 137..255 | 3.00E-20  | 100  |
| <b>GOE #75</b><br>SSH06_912C_GOE_75(128aa)                       | ZP_00682696.1   | Xylella fastidiosa Ann-1                  | hypothetical protein XfasoDRAFT_2672                | 96.75 | 97.56  | 123 | 4  | 0 | 1..123  | 1..123   | 2.00E-53  | 211  |
|                                                                  | YP_980148.1     | Verminephrobacter eiseniae EF01-2         | hypothetical protein Veis_5051                      | 74.80 | 84.55  | 123 | 31 | 0 | 1..123  | 1..123   | 3.00E-32  | 140  |
|                                                                  | YP_720015.1     | Trichodesmium erythraeum IMS101           | Rho termination factor-like                         | 31.51 | 46.58  | 73  | 35 | 2 | 1..73   | 31..88   | 1.1       | 35.4 |
| <b>GOE #76</b><br>SSH09_912C_GOE_76 (127aa)                      | NP_780107.1     | Xylella fastidiosa Temecula1              | fimbrial protein                                    | 60.16 | 69.92  | 123 | 44 | 2 | 1..123  | 29..146  | 1.00E-20  | 102  |
|                                                                  | ZP_00680431.1   | Xylella fastidiosa Ann-1                  | Fimbrial protein pilin                              | 61.54 | 74.36  | 117 | 38 | 3 | 1..117  | 29..138  | 1.00E-20  | 101  |

| <b>GOE #77</b><br>SSH011_912C_GOE_77<br>(113aa) | ZP_01700173.1  | Escherichia coli B                                          | transposase. IS605<br>OrfB family         | 85.57         | 92.78          | 97                  | 14              | 0            | 4..100              | 20..116               | 4.00E-41 | 169          |
|-------------------------------------------------|----------------|-------------------------------------------------------------|-------------------------------------------|---------------|----------------|---------------------|-----------------|--------------|---------------------|-----------------------|----------|--------------|
|                                                 | YP_001463237.1 | Escherichia coli<br>E24377A                                 | transposase. IS605<br>orfB family         | 84.54         | 91.75          | 97                  | 15              | 0            | 4..100              | 1..97                 | 2.00E-40 | 167          |
|                                                 | ZP_00682675.1  | Xylella fastidiosa<br>Ann-1                                 | Transposase, IS605<br>OrfB                | 58.44         | 72.73          | 77                  | 32              | 0            | 24.. 100            | 1.. 77                | 8,00E-18 | 92.4         |
| <b>GOE #78</b><br>SSH14_912C_GOE_78<br>(196aa)  | ZP_00684331.1  | Xylella fastidiosa<br>Ann-1                                 | conserved hypothetical<br>protein         | 77.97         | 86.44          | 59                  | 13              | 0            | 1..59               | 52..110               | 7.00E-22 | 105          |
|                                                 | ZP_00652856.1  | Xylella fastidiosa<br>Dixon                                 | conserved hypothetical<br>protein         | 65.52         | 72.41          | 58                  | 19              | 1            | 2..59               | 48..104               | 2.00E-14 | 81.3         |
|                                                 | NP_779334.1    | Xylella fastidiosa<br>Temecula1                             | hypothetical protein<br>PD1128            | 56.14         | 71.93          | 57                  | 25              | 0            | 2..58               | 48..104               | 3.00E-14 | 80.5         |
| <b>GOE #79</b><br>SSH15_912C_GOE_79<br>(40aa)   | No hit         |                                                             |                                           |               |                |                     |                 |              |                     |                       |          |              |
| Query id                                        | subject ids    | organism                                                    | description                               | %<br>identity | %<br>positives | alignment<br>length | Mismat-<br>ches | gap<br>opens | query<br>start..end | subject<br>start..end | E-value  | Bit<br>score |
| <b>GOE #80</b><br>SSH16_912C_GOE_80<br>(68aa)   | No hit         |                                                             |                                           |               |                |                     |                 |              |                     |                       |          |              |
| <b>GOE #81</b><br>SSH21_912C_GOE_81<br>(93aa)   | No hit         |                                                             |                                           |               |                |                     |                 |              |                     |                       |          |              |
| <b>GOE #82</b><br>SSH26_912C_GOE_82<br>(130aa)  | YP_364184.1    | Xanthomonas<br>campestris pv.<br>vesicatoria str. 85-<br>10 | filamentous phage<br>Cf1c related protein | 79.59         | 91.84          | 98                  | 20              | 0            | 1..98               | 1..98                 | 4.00E-42 | 172          |
|                                                 | YP_451170.1    | Xanthomonas<br>oryzae pv. oryzae<br>MAFF 311018             | hypothetical protein<br>XOO_2141          | 77.55         | 90.82          | 98                  | 22              | 0            | 1..98               | 1..98                 | 5.00E-41 | 169          |
|                                                 | NP_779131.1    | Xylella fastidiosa<br>Temecula1                             | hypothetical protein<br>PD0915            | 66.33         | 81.63          | 98                  | 31              | 1            | 1..96               | 12..109               | 9.00E-33 | 142          |
| <b>GOE #83</b><br>SSH30_912C_GOE_83<br>(62aa)   | AAK13433.1     | Xylella fastidiosa                                          | replication initiator-like<br>protein     | 90.32         | 95.16          | 62                  | 6               | 0            | 1..62               | 206..267              | 3.00E-23 | 110          |
|                                                 | YP_025704.1    | Pseudomonas<br>syringae pv.<br>maculicola                   | replication protein                       | 65.57         | 78.69          | 61                  | 21              | 0            | 1..61               | 223..283              | 3.00E-14 | 80.5         |
|                                                 | ABC41159.1     | Neisseria lactamica                                         | pNL18.2_p1                                | 60.00         | 73.33          | 60                  | 24              | 0            | 1..60               | 195..254              | 8.00E-13 | 75.9         |
| <b>GOE #84</b><br>SSH31_912C_GOE_84<br>(57aa)   | No hit         |                                                             |                                           |               |                |                     |                 |              |                     |                       |          |              |
| <b>GOE #85</b><br>SSH33_912C_GOE_85<br>(150aa)  | ZP_00682697.1  | Xylella fastidiosa<br>Ann-1                                 | hypothetical protein<br>XfasoDRAFT_2673   | 89.89         | 94.38          | 89                  | 9               | 0            | 62..150             | 56..144               | 4.00E-34 | 146          |
|                                                 | YP_980126.1    | Verminephrobacter<br>eiseniae EF01-2                        | hypothetical protein<br>Veis_5029         | 41.67         | 61.46          | 96                  | 42              | 2            | 69..150             | 42..137               | 7.00E-08 | 59.3         |
|                                                 | XP_001246860.1 | Coccidioides immitis<br>RS                                  | hypothetical protein<br>CIMG_00631        | 40.43         | 53.19          | 47                  | 19              | 1            | 40..77              | 18..64                | 0.65     | 36.2         |
| <b>GOE #86</b><br>SSH36_912C_GOE_86<br>(145aa)  | ZP_00682956.1  | Xylella fastidiosa<br>Ann-1                                 | conserved hypothetical<br>protein         | 94.48         | 96.55          | 145                 | 8               | 0            | 1..145              | 24..168               | 9.00E-76 | 284          |
|                                                 | NP_778539.1    | Xylella fastidiosa<br>Temecula1                             | hypothetical protein<br>PD0304            | 80.00         | 87.59          | 145                 | 28              | 1            | 1..145              | 24..167               | 8.00E-62 | 238          |
|                                                 | NP_298298.1    | Xylella fastidiosa<br>9a5c                                  | hypothetical protein<br>XF1008            | 79.31         | 86.90          | 145                 | 29              | 1            | 1..145              | 24..167               | 7.00E-61 | 235          |
| <b>GOE #87</b>                                  | NP_780283.1    | Xylella fastidiosa                                          | hypothetical protein                      | 85.27         | 90.70          | 129                 | 19              | 0            | 2..130              | 5..133                | 1.00E-54 | 214          |

|                                         |                |                                            |                                         |       |       |     |    |   |        |          |          |      |
|-----------------------------------------|----------------|--------------------------------------------|-----------------------------------------|-------|-------|-----|----|---|--------|----------|----------|------|
| SSH39_912C_GOE_87<br>(130aa)            |                | Temecula1                                  | PD2113                                  |       |       |     |    |   |        |          |          |      |
|                                         | NP_780287.1    | Xylella fastidiosa<br>Temecula1            | hypothetical protein<br>PD2117          | 86.40 | 91.20 | 125 | 17 | 0 | 6..130 | 1..125   | 1.00E-51 | 204  |
|                                         | NP_779440.1    | Xylella fastidiosa<br>Temecula1            | hypothetical protein<br>PD1239          | 80.00 | 86.15 | 130 | 26 | 0 | 1..130 | 1..130   | 2.00E-50 | 200  |
| GOE #88<br>SSH40_912C_GOE_88<br>(58aa)  | ZP_00681103.1  | Xylella fastidiosa<br>Ann-1                | conserved hypothetical<br>protein       | 84.62 | 88.46 | 52  | 8  | 0 | 1..52  | 1..52    | 2.00E-11 | 71.2 |
|                                         | NP_779332.     | Xylella fastidiosa<br>Temecula1            | hypothetical protein<br>PD1126          | 79.07 | 83.72 | 43  | 9  | 0 | 3..45  | 7..49    | 5.00E-07 | 56.6 |
| GOE #89<br>SSH53_912C_GOE_89<br>(91aa)  | No hit         |                                            |                                         |       |       |     |    |   |        |          |          |      |
| GOE #90<br>SSH65_912C_GOE_90<br>(39aa)  | No hit         |                                            |                                         |       |       |     |    |   |        |          |          |      |
| GOE #91<br>SSH71_912C_GOE91<br>(98aa)   | No hit         |                                            |                                         |       |       |     |    |   |        |          |          |      |
| GOE #92<br>SSH72_912C_GOE_92<br>(155aa) | ZP_00682629.1  | Xylella fastidiosa<br>Ann-1                | Phage integrase                         | 98.61 | 99.31 | 144 | 2  | 0 | 1..144 | 77..220  | 1.00E-82 | 307  |
|                                         | ZP_00652696.1  | Xylella fastidiosa<br>Dixon                | Phage integrase                         | 98.61 | 99.31 | 144 | 2  | 0 | 1..144 | 77..220  | 2.00E-82 | 307  |
|                                         | ZP_00683736.1  | Xylella fastidiosa<br>Ann-1                | Phage integrase                         | 98.61 | 99.31 | 144 | 2  | 0 | 1..144 | 77..220  | 2.00E-82 | 306  |
| GOE #93<br>SSH73_912C_GOE_93<br>(138aa) | NP_779954.1    | Xylella fastidiosa<br>Temecula1            | acyl-ACP-UDP-N-<br>acetylglucosamine    | 33.33 | 52.78 | 108 | 72 | 0 | 7..114 | 48..155  | 1.00E-06 | 54.7 |
| GOE #94<br>SSH75_912C_GOE_94<br>(124aa) | ZP_00682689.1  | Xylella fastidiosa<br>Ann-1                | VirB8                                   | 97.53 | 98.77 | 81  | 2  | 0 | 1..81  | 1..81    | 4.00E-35 | 149  |
|                                         | YP_980120.1    | Verminephrobacter<br>eiseniae EF01-2       | VirB8 family protein                    | 85.71 | 90.00 | 70  | 10 | 0 | 12..81 | 14..83   | 2.00E-24 | 114  |
| GOE #95<br>SSH01_Fb7_GOE_95<br>(100aa)  | ZP_00652872.1  | Xylella fastidiosa<br>Dixon                | ParB-like partition<br>protein          | 84.88 | 88.37 | 86  | 13 | 0 | 1..86  | 211..296 | 6.00E-30 | 132  |
|                                         | YP_709193.1    | IncP-1 plasmid<br>pKJK5                    | KorB protein                            | 51.09 | 63.04 | 92  | 37 | 2 | 1..86  | 211..300 | 6.00E-11 | 69.3 |
|                                         | NP_990880.1    | Achromobacter<br>denitrificans             | KorB                                    | 45.65 | 60.87 | 92  | 43 | 2 | 1..86  | 220..310 | 1.00E-08 | 61.6 |
| GOE #96<br>SSH02_Fb7_GOE_96<br>(117aa)  | ZP_00652871.1  | Xylella fastidiosa<br>Dixon                | hypothetical protein<br>XfasaDRAFT_0177 | 98.29 | 98.29 | 117 | 2  | 0 | 1..117 | 1..117   | 1.00E-52 | 207  |
|                                         | YP_112417.1    | uncultured<br>bacterium                    | KfrB protein                            | 59.83 | 71.79 | 117 | 45 | 2 | 1..117 | 1..115   | 7.00E-28 | 125  |
|                                         | YP_195664.1    | Azoarcus sp. EbN1                          | putative conjugation<br>protein TraO    | 52.99 | 74.36 | 117 | 53 | 2 | 1..117 | 1..115   | 3.00E-27 | 123  |
| GOE #97<br>SSH05_Fb7_GOE_97<br>(96aa)   | YP_001393241.1 | Yersinia<br>pseudotuberculosis<br>IP 31758 | conjugal transfer<br>protein TrbA       | 55.88 | 76.47 | 68  | 28 | 1 | 1..66  | 50..117  | 7.00E-13 | 75.9 |
|                                         | YP_195561.1    | Azoarcus sp. EbN1                          | TrbA protein of DNA<br>transfer system  | 57.35 | 72.06 | 68  | 27 | 1 | 1..66  | 50..117  | 6.00E-12 | 72.8 |
|                                         | YP_974109.1    | Acidovorax sp. JS42                        | helix-turn-helix domain<br>protein      | 62.86 | 75.71 | 70  | 24 | 1 | 1..68  | 50..119  | 8.00E-11 | 68.9 |
| GOE #98<br>SSH06_Fb7_GOE_98<br>(44aa)   | ZP_00652878.1  | Xylella fastidiosa<br>Dixon                | type II secretion<br>system protein E   | 95.00 | 95.00 | 40  | 2  | 0 | 1..40  | 2..41    | 1.00E-13 | 78.2 |
|                                         | NP_990919.1    | Achromobacter                              | TrbB                                    | 50.00 | 75.00 | 40  | 20 | 0 | 1..40  | 1..40    | 4.00E-04 | 47.0 |

|                                                 |                | denitrificans                              |                                                              |               |                |                     |                 |              |                     |                       |          |              |
|-------------------------------------------------|----------------|--------------------------------------------|--------------------------------------------------------------|---------------|----------------|---------------------|-----------------|--------------|---------------------|-----------------------|----------|--------------|
| <b>GOE #99</b><br>SSH08_Fb7_GOE_99<br>(221aa)   | ZP_00652867.1  | Xylella fastidiosa<br>Dixon                | Relaxase/mobilization<br>nuclease domain                     | 94.18         | 95.24          | 189                 | 11              | 0            | 16..204             | 454..642              | 2.00E-90 | 333          |
|                                                 | YP_001393287.1 | Yersinia<br>pseudotuberculosis<br>IP 31758 | conjugal transfer<br>protein Tral                            | 51.82         | 68.18          | 110                 | 53              | 0            | 23..132             | 462..571              | 5.00E-21 | 102          |
|                                                 | NP_990929.1    | Achromobacter<br>denitrificans             | Tral                                                         | 53.26         | 76.09          | 92                  | 43              | 0            | 26..117             | 425..516              | 2.00E-18 | 94.4         |
| Query id                                        | subject ids    | organism                                   | description                                                  | %<br>identity | %<br>positives | alignment<br>length | Mismat-<br>ches | gap<br>opens | query<br>start..end | subject<br>start..end | E-value  | Bit<br>score |
| <b>GOE #100</b><br>SSH11_Fb7_GOE_100<br>(47aa)  | ZP_00682615.1  | Xylella fastidiosa<br>Ann-1                | Peptidase S24. S26A<br>and S26B                              | 100.00        | 100.00         | 24                  | 0               | 0            | 24..47              | 229..252              | 1.00E-05 | 52.0         |
|                                                 | ZP_00683692.1  | Xylella fastidiosa<br>Ann-1                | Helix-turn-helix<br>motif:Peptidase S24.<br>S26A and S26B    | 95.83         | 100.00         | 24                  | 1               | 0            | 24..47              | 383..406              | 8.00E-05 | 48.9         |
| <b>GOE #101</b><br>SSH14_Fb7_GOE_101<br>(31aa)  | ZP_00652876.1  | Xylella fastidiosa<br>Dixon                | Plasmid encoded RepA<br>protein                              | 96.77         | 96.77          | 31                  | 1               | 0            | 1..31               | 1..31                 | 9.00E-08 | 58.9         |
| <b>GOE #102</b><br>SSH15_Fb7_GOE_102<br>(116aa) | NP_779212.1    | Xylella fastidiosa<br>Temecula1            | hypothetical protein<br>PD1000                               | 39.81         | 59.22          | 103                 | 57              | 3            | 3..103              | 39..138               | 3.00E-09 | 63.9         |
|                                                 | NP_298849.1    | Xylella fastidiosa<br>9a5c                 | hypothetical protein<br>XF1560                               | 33.60         | 54.40          | 125                 | 67              | 3            | 3..114              | 39..160               | 4.00E-09 | 63.2         |
|                                                 | YP_001084613.1 | Acinetobacter<br>baumannii ATCC<br>17978   | hypothetical protein<br>A1S_1584                             | 32.35         | 56.86          | 102                 | 60              | 2            | 23..115             | 22..123               | 5.00E-06 | 53.1         |
| <b>GOE #103</b><br>SSH17_Fb7_GOE_103<br>(200aa) | ZP_00650975.1  | Xylella fastidiosa<br>Dixon                | similar to<br>Uncharacterized<br>phage-associated<br>protein | 58.14         | 66.86          | 172                 | 66              | 1            | 1..172              | 1..166                | 8.00E-48 | 191          |
|                                                 | NP_299081.1    | Xylella fastidiosa<br>9a5c                 | hypothetical protein<br>XF1793                               | 71.43         | 80.22          | 91                  | 26              | 0            | 1..91               | 1..91                 | 3.00E-30 | 133          |
|                                                 | YP_001197194.1 | Flavobacterium<br>johnsoniae UW101         | Uncharacterized<br>phage-associated<br>protein               | 40.00         | 60.61          | 165                 | 82              | 4            | 3..167              | 2..149                | 2.00E-28 | 127          |
| <b>GOE #104</b><br>SSH19_Fb7_GOE_104<br>(61aa)  | No hit         |                                            |                                                              |               |                |                     |                 |              |                     |                       |          |              |
| <b>GOE #105</b><br>SSH23_Fb7_GOE_105<br>(106aa) | ZP_00652236.1  | Xylella fastidiosa<br>Dixon                | hypothetical protein<br>XfasaDRAFT_0897                      | 34.62         | 52.88          | 104                 | 65              | 1            | 1..101              | 8..111                | 1.00E-06 | 55.5         |
|                                                 | ZP_00684057.1  | Xylella fastidiosa<br>Ann-1                | conserved hypothetical<br>protein                            | 35.58         | 50.00          | 104                 | 64              | 1            | 1..101              | 1..104                | 1.00E-05 | 51.6         |
|                                                 | NP_299170.1    | Xylella fastidiosa<br>9a5c                 | hypothetical protein<br>XF1884                               | 37.18         | 51.28          | 78                  | 49              | 0            | 24..101             | 38..115               | 2.00E-04 | 47.8         |
| <b>GOE #106</b><br>SSH31_Fb7_GOE_106<br>(113aa) | ZP_00682687.1  | Xylella fastidiosa<br>Ann-1                | plasmid-related<br>exported protein                          | 91.84         | 94.90          | 98                  | 8               | 0            | 1..98               | 1..98                 | 6.00E-38 | 159          |
|                                                 | YP_980122.1    | Verminephrobacter<br>eiseniae EF01-2       | type IV secretion<br>system family protein                   | 66.33         | 77.55          | 98                  | 33              | 0            | 1..98               | 1..98                 | 5.00E-19 | 96.3         |
|                                                 | YP_001257140.1 | Brucella ovis ATCC<br>25840                | P-type DNA transfer<br>protein VirB5                         | 44.58         | 71.08          | 83                  | 46              | 0            | 16..98              | 9..91                 | 5.00E-14 | 79.7         |
| <b>GOE #107</b><br>SSH32_Fb7_GOE_107<br>(73aa)  | AAL25255.1     | Legionella<br>pneumophila                  | TraJ                                                         | 52.86         | 70.00          | 70                  | 33              | 0            | 1..70               | 48..117               | 4.00E-12 | 73.6         |
|                                                 | YP_001249533.1 | Legionella<br>pneumophila str.<br>Corby    | TraJ protein                                                 | 47.95         | 65.75          | 73                  | 34              | 1            | 1..73               | 48..116               | 6.00E-10 | 66.2         |

|                                                  |                |                                         |                                                             |        |        |     |    |   |         |          |          |      |
|--------------------------------------------------|----------------|-----------------------------------------|-------------------------------------------------------------|--------|--------|-----|----|---|---------|----------|----------|------|
|                                                  | YP_109861.1    | Burkholderia pseudomallei K96243        | putative plasmid conjugal transfer protein                  | 67.61  | 80.28  | 71  | 23 | 0 | 1..71   | 52..122  | 7.00E-10 | 65.9 |
| <b>GOE #108</b><br>SSH33_Fb7_GOE_108<br>(106aa)  | ZP_00652867.1  | Xylella fastidiosa Dixon                | Relaxase/mobilization nuclease domain                       | 98.81  | 98.81  | 84  | 1  | 0 | 6..89   | 46..129  | 5.00E-42 | 172  |
|                                                  | YP_001393287.1 | Yersinia pseudotuberculosis IP 31758    | conjugal transfer protein Tral                              | 60.42  | 79.17  | 96  | 32 | 2 | 4..98   | 43..133  | 1.00E-26 | 121  |
|                                                  | YP_112410.1    | uncultured bacterium                    | DNA relaxase                                                | 74.03  | 81.82  | 77  | 20 | 0 | 12..88  | 52..128  | 1.00E-26 | 121  |
| <b>GOE #109</b><br>SSH37_Fb7_GOE_109<br>(76aa)   | No hit         |                                         |                                                             |        |        |     |    |   |         |          |          |      |
| <b>GOE #110</b><br>SSH39_Fb7_GOE_110<br>(139aa)  | ZP_00682694.1  | Xylella fastidiosa Ann-1                | hypothetical protein XfasoDRAFT_2670                        | 97.41  | 99.14  | 116 | 3  | 0 | 24..139 | 253..368 | 7.00E-46 | 185  |
|                                                  | YP_980115.1    | Verminephrobacter eiseniae EF01-2       | hypothetical protein Veis_5018                              | 91.15  | 93.81  | 113 | 10 | 0 | 27..139 | 316..428 | 1.00E-41 | 171  |
| <b>GOE #111</b><br>SSH25_36f_GOE_111<br>(128aa)  | ZP_00682696.1  | Xylella fastidiosa Ann-1                | hypothetical protein XfasoDRAFT_2672                        | 96.75  | 97.56  | 123 | 4  | 0 | 1..123  | 1..123   | 2.00E-53 | 211  |
|                                                  | YP_980148.1    | Verminephrobacter eiseniae EF01-2       | hypothetical protein Veis_5051                              | 74.80  | 84.55  | 123 | 31 | 0 | 1..123  | 1..123   | 3.00E-32 | 140  |
| <b>GOE #112</b><br>SSH32_36f_GOE_112<br>(66aa)   | ZP_00684053.1  | Xylella fastidiosa Ann-1                | conserved hypothetical protein                              | 98.48  | 100.00 | 66  | 1  | 0 | 1..66   | 66..131  | 2.00E-27 | 124  |
|                                                  | AAW76134.1     | Xanthomonas oryzae pv. oryzae KACC10331 | conserved hypothetical protein                              | 70.77  | 81.54  | 65  | 19 | 0 | 2..66   | 213..277 | 9.00E-20 | 98.6 |
|                                                  | YP_988599.1    | Bartonella bacilliformis KC583          | hypothetical protein BARBAKC583_0275                        | 69.23  | 84.62  | 65  | 20 | 0 | 2..66   | 67..131  | 1.00E-19 | 98.2 |
| <b>GOE #113</b><br>SSH35_36f_GOE_113<br>(144aa)  | ZP_00652972.1  | Xylella fastidiosa Dixon                | Phage/plasmid primase P4. C-terminal                        | 64.56  | 74.68  | 79  | 23 | 2 | 71..144 | 765..843 | 4.00E-21 | 103  |
|                                                  | ZP_00651851.1  | Xylella fastidiosa Dixon                | Phage/plasmid primase P4. C-terminal                        | 65.82  | 73.42  | 79  | 22 | 2 | 71..144 | 765..843 | 6.00E-21 | 102  |
|                                                  | ZP_00679796.1  | Xylella fastidiosa Ann-1                | Phage/plasmid primase P4. C-terminal                        | 64.56  | 73.42  | 79  | 23 | 2 | 71..144 | 765..843 | 2.00E-20 | 100  |
| <b>GOE #114</b><br>SSH36_36f_GOE_114<br>(64aa)   | No hit         |                                         |                                                             |        |        |     |    |   |         |          |          |      |
| <b>GOE #115</b><br>SSH38_36f_GOE_115<br>(44aa)   | No hit         |                                         |                                                             |        |        |     |    |   |         |          |          |      |
| <b>GOE #116</b><br>SSH11_187b_GOE_116<br>(126aa) | ZP_00652969.1  | Xylella fastidiosa Dixon                | Helix-turn-helix motif:Peptidase S24. S26A and S26B         | 98.41  | 99.21  | 126 | 2  | 0 | 1..126  | 99..224  | 2.00E-66 | 254  |
|                                                  | NP_297986.1    | Xylella fastidiosa 9a5c                 | phage-related repressor protein                             | 61.90  | 77.78  | 126 | 47 | 1 | 1..126  | 97..221  | 6.00E-40 | 166  |
|                                                  | ZP_00653051.1  | Xylella fastidiosa Dixon                | Peptidase S24. S26A and S26B                                | 53.60  | 68.00  | 125 | 57 | 1 | 1..124  | 133..257 | 6.00E-30 | 132  |
| <b>GOE #117</b><br>SSH18_187b_GOE_117<br>(95aa)  | No hit         |                                         |                                                             |        |        |     |    |   |         |          |          |      |
| <b>GOE #118</b><br>SSH22_187b_GOE_118<br>(112aa) | NP_779052.1    | Xylella fastidiosa Temecula1            | methyltransferase. type III restriction-modification system | 100.00 | 100.00 | 82  | 0  | 0 | 1..82   | 260..341 | 5.00E-43 | 176  |
|                                                  | NP_635609.1    | Xanthomonas campestris pv.              | methyltransferase                                           | 76.54  | 87.65  | 81  | 19 | 0 | 2..82   | 261..341 | 2.00E-32 | 140  |

|                                                  |               | campestris str.<br>ATCC 33913                   |                                                                                  |               |                |                     |                 |              |                     |                       |           |              |
|--------------------------------------------------|---------------|-------------------------------------------------|----------------------------------------------------------------------------------|---------------|----------------|---------------------|-----------------|--------------|---------------------|-----------------------|-----------|--------------|
| <b>GOE #119</b><br>SSH32_187b_GOE_119<br>(148aa) | No hit        |                                                 |                                                                                  |               |                |                     |                 |              |                     |                       |           |              |
| Query id                                         | subject ids   | organism                                        | description                                                                      | %<br>identity | %<br>positives | alignment<br>length | Mismat-<br>ches | gap<br>opens | query<br>start..end | subject<br>start..end | E-value   | Bit<br>score |
| <b>GOE #120</b><br>SSH03_56a_GOE_120<br>(134aa)  | ZP_00681945.1 | Xylella fastidiosa<br>Ann-1                     | Peptidase S24. S26A<br>and S26B                                                  | 38.10         | 59.05          | 105                 | 57              | 4            | 1..101              | 153..253              | 3.00E-10  | 67.4         |
|                                                  | NP_459874.1   | Salmonella<br>typhimurium LT2                   | putative transcriptional<br>regulator                                            | 40.40         | 59.60          | 99                  | 56              | 3            | 2..99               | 102..198              | 6.00E-09  | 62.8         |
|                                                  | YP_207629.1   | Neisseria<br>gonorrhoeae FA<br>1090             | putative lambda<br>repressor protein cl.<br>putative phage<br>associated protein | 32.31         | 51.54          | 130                 | 75              | 3            | 2..131              | 112..228              | 6.00E-09  | 62.8         |
| <b>GOE #121</b><br>SSH12_56a_GOE_121<br>(67aa)   | No hit        |                                                 |                                                                                  |               |                |                     |                 |              |                     |                       |           |              |
| <b>GOE #122</b><br>SSH21_56a_GOE_122<br>(36aa)   | ZP_00682695.1 | Xylella fastidiosa<br>Ann-1                     | hypothetical protein<br>XfasoDRAFT_2671                                          | 100.00        | 100.00         | 36                  | 0               | 0            | 1..36               | 299..334              | 4.00E-08  | 60.1         |
| <b>GOE #123</b><br>SSH22_56a_GOE_123<br>(54aa)   | No hit        |                                                 |                                                                                  |               |                |                     |                 |              |                     |                       |           |              |
| <b>GOE #124</b><br>SSH27_56a_GOE_124<br>(154aa)  | ZP_00652969.1 | Xylella fastidiosa<br>Dixon                     | Helix-turn-helix<br>motif:Peptidase S24.<br>S26A and S26B                        | 98.48         | 99.24          | 132                 | 2               | 0            | 1..132              | 1..132                | 1.00E-65  | 251          |
|                                                  | NP_297986.1   | Xylella fastidiosa<br>9a5c                      | phage-related<br>repressor protein                                               | 51.18         | 71.65          | 127                 | 58              | 2            | 4..130              | 6..128                | 4.00E-27  | 123          |
|                                                  | ZP_01787679.1 | Haemophilus<br>influenzae 22.4-21               | hypothetical protein<br>CGSHI22421_00742                                         | 30.23         | 58.14          | 129                 | 88              | 2            | 1..127              | 1..129                | 5.00E-13  | 76.3         |
| <b>GOE #125</b><br>SSH34_56a_GOE_125<br>(257aa)  | ZP_00682693.1 | Xylella fastidiosa<br>Ann-1                     | TRAG protein                                                                     | 98.35         | 99.59          | 243                 | 4               | 0            | 1..243              | 1..243                | 3.00E-130 | 465          |
|                                                  | YP_980116.1   | Verminephrobacter<br>eiseniae EF01-2            | TRAG family protein                                                              | 87.65         | 95.06          | 243                 | 30              | 0            | 1..243              | 1..243                | 2.00E-120 | 433          |
|                                                  | NP_642936.1   | Xanthomonas<br>axonopodis pv. citri<br>str. 306 | VirD4 protein                                                                    | 51.74         | 63.18          | 201                 | 83              | 5            | 45..242             | 49..238               | 2.00E-44  | 180          |
| <b>GOE #126</b><br>SSH04_Cv21_GOE_126<br>(154aa) | NP_662757.1   | Chlorobium tepidum<br>TLS                       | type I restriction<br>system specificity<br>protein                              | 42.13         | 48.73          | 197                 | 53              | 4            | 3..138              | 124..320              | 1.00E-31  | 138          |
|                                                  | YP_997187.1   | Verminephrobacter<br>eiseniae EF01-2            | restriction modification<br>system DNA specificity<br>domain                     | 42.95         | 58.33          | 156                 | 61              | 2            | 11..138             | 143..298              | 7.00E-27  | 122          |
|                                                  | NP_223444.1   | Helicobacter pylori<br>J99                      | putative TYPE I<br>RESTRICTION<br>ENZYME<br>(SPECIFICITY<br>SUBUNIT)             | 39.31         | 52.60          | 173                 | 68              | 3            | 3..138              | 147..319              | 2.00E-25  | 117          |
| <b>GOE #127</b><br>SSH05_Cv21_GOE_127<br>(98aa)  | ZP_00684053.1 | Xylella fastidiosa<br>Ann-1                     | conserved hypothetical<br>protein                                                | 98.98         | 100.00         | 98                  | 1               | 0            | 1..98               | 34..131               | 3.00E-43  | 177          |
|                                                  | YP_988599.1   | Bartonella<br>bacilliformis KC583               | hypothetical protein<br>BARBAKC583_0275                                          | 62.24         | 79.59          | 98                  | 37              | 0            | 1..98               | 34..131               | 2.00E-28  | 127          |
|                                                  | YP_770534.1   | Rhizobium<br>leguminosarum bv.                  | hypothetical protein<br>pRL100255                                                | 61.22         | 79.59          | 98                  | 38              | 0            | 1..98               | 34..131               | 3.00E-26  | 120          |

|                                                  |               |                                                    |                                      |       |       |     |    |   |         |          |           |      |
|--------------------------------------------------|---------------|----------------------------------------------------|--------------------------------------|-------|-------|-----|----|---|---------|----------|-----------|------|
|                                                  |               | viciae 3841                                        |                                      |       |       |     |    |   |         |          |           |      |
| <b>GOE #128</b><br>SSH07_Cv21_GOE_128<br>(83aa)  | YP_980113.1   | Verminephrobacter eiseniae EF01-2                  | hypothetical protein Veis_5018       | 78.57 | 83.93 | 56  | 12 | 0 | 1..56   | 1..56    | 4.00E-17  | 90.1 |
| <b>GOE #129</b><br>SSH12_Cv21_GOE_129<br>(207aa) | ZP_00684136.1 | Xylella fastidiosa Ann-1                           | Phage integrase                      | 95.65 | 97.58 | 207 | 9  | 0 | 1..207  | 57..263  | 6.00E-102 | 371  |
|                                                  | ZP_00651242.1 | Xylella fastidiosa Dixon                           | Phage integrase                      | 95.65 | 97.58 | 207 | 9  | 0 | 1..207  | 70..276  | 3.00E-101 | 369  |
|                                                  | YP_284263.1   | Dechloromonas aromatica RCB                        | Phage integrase                      | 54.59 | 69.08 | 207 | 94 | 0 | 1..207  | 124..330 | 2.00E-52  | 207  |
| <b>GOE #130</b><br>SSH20_Cv21_GOE_130<br>(206aa) | YP_554949.1   | Burkholderia xenovorans LB400                      | hypothetical protein Bxe_B0347       | 30.46 | 46.36 | 151 | 94 | 6 | 9..157  | 18..159  | 5.00E-07  | 56.2 |
|                                                  | ZP_00592014.1 | Prosthecochloris aestuarii DSM 271                 | hypothetical protein PaesDRAFT_1019  | 28.19 | 42.95 | 149 | 84 | 6 | 10..155 | 10..138  | 4.00E-04  | 47.0 |
| <b>GOE #131</b><br>SSH26_Cv21_GOE_131<br>(56aa)  | NP_841356.1   | Nitrosomonas europaea ATCC 19718                   | hypothetical protein NE1307          | 85.71 | 91.07 | 56  | 8  | 0 | 1..56   | 55..110  | 1.00E-20  | 101  |
|                                                  | ZP_00682677.1 | Xylella fastidiosa Ann-1                           | conserved hypothetical protein       | 85.71 | 87.50 | 56  | 8  | 0 | 1..56   | 23..78   | 1.00E-17  | 91.7 |
|                                                  | YP_361540.1   | Xanthomonas campestris pv. vesicatoria str. 85-10  | hypothetical protein XCVc0024        | 80.36 | 85.71 | 56  | 11 | 0 | 1..56   | 53..108  | 8.00E-17  | 89.0 |
| <b>GOE #132</b><br>SSH27_Cv21_GOE_132<br>(94aa)  | NP_779332.1   | Xylella fastidiosa Temecula1                       | hypothetical protein PD1126          | 90.11 | 94.51 | 91  | 9  | 0 | 4..94   | 56..146  | 1.00E-33  | 145  |
|                                                  | ZP_00652684.1 | Xylella fastidiosa Dixon                           | conserved hypothetical protein       | 90.11 | 95.60 | 91  | 9  | 0 | 4..94   | 26..116  | 5.00E-33  | 142  |
|                                                  | ZP_00682619.1 | Xylella fastidiosa Ann-1                           | conserved hypothetical protein       | 90.11 | 94.51 | 91  | 9  | 0 | 4..94   | 37..127  | 7.00E-33  | 142  |
| <b>GOE #133</b><br>SSH33_Cv21_GOE_133<br>(149aa) | ZP_00682691.1 | Xylella fastidiosa Ann-1                           | conjugation Trbl-like protein        | 96.30 | 98.52 | 135 | 5  | 0 | 15..149 | 298..432 | 1.00E-67  | 258  |
|                                                  | YP_980118.1   | Verminephrobacter eiseniae EF01-2                  | conjugation Trbl family protein      | 91.11 | 94.07 | 135 | 12 | 0 | 15..149 | 316..450 | 1.00E-64  | 248  |
|                                                  | ABS71080.1    | Salmonella enterica subsp. enterica serovar Dublin | TrwE                                 | 48.12 | 66.17 | 133 | 65 | 2 | 15..147 | 261..389 | 7.00E-29  | 129  |
| <b>GOE #134</b><br>SSH36_Cv21_GOE_134<br>(61aa)  | No hit        |                                                    |                                      |       |       |     |    |   |         |          |           |      |
| <b>GOE #135</b><br>SSH45_Cv21_GOE_135<br>(92aa)  | ZP_00682672.1 | Xylella fastidiosa Ann-1                           | hypothetical protein XfasoDRAFT_2648 | 97.83 | 98.91 | 92  | 2  | 0 | 1..92   | 27..118  | 8.00E-30  | 132  |
|                                                  | YP_980150.1   | Verminephrobacter eiseniae EF01-2                  | hypothetical protein Veis_5053       | 63.04 | 76.09 | 92  | 34 | 0 | 1..92   | 26..117  | 5.00E-18  | 92.8 |