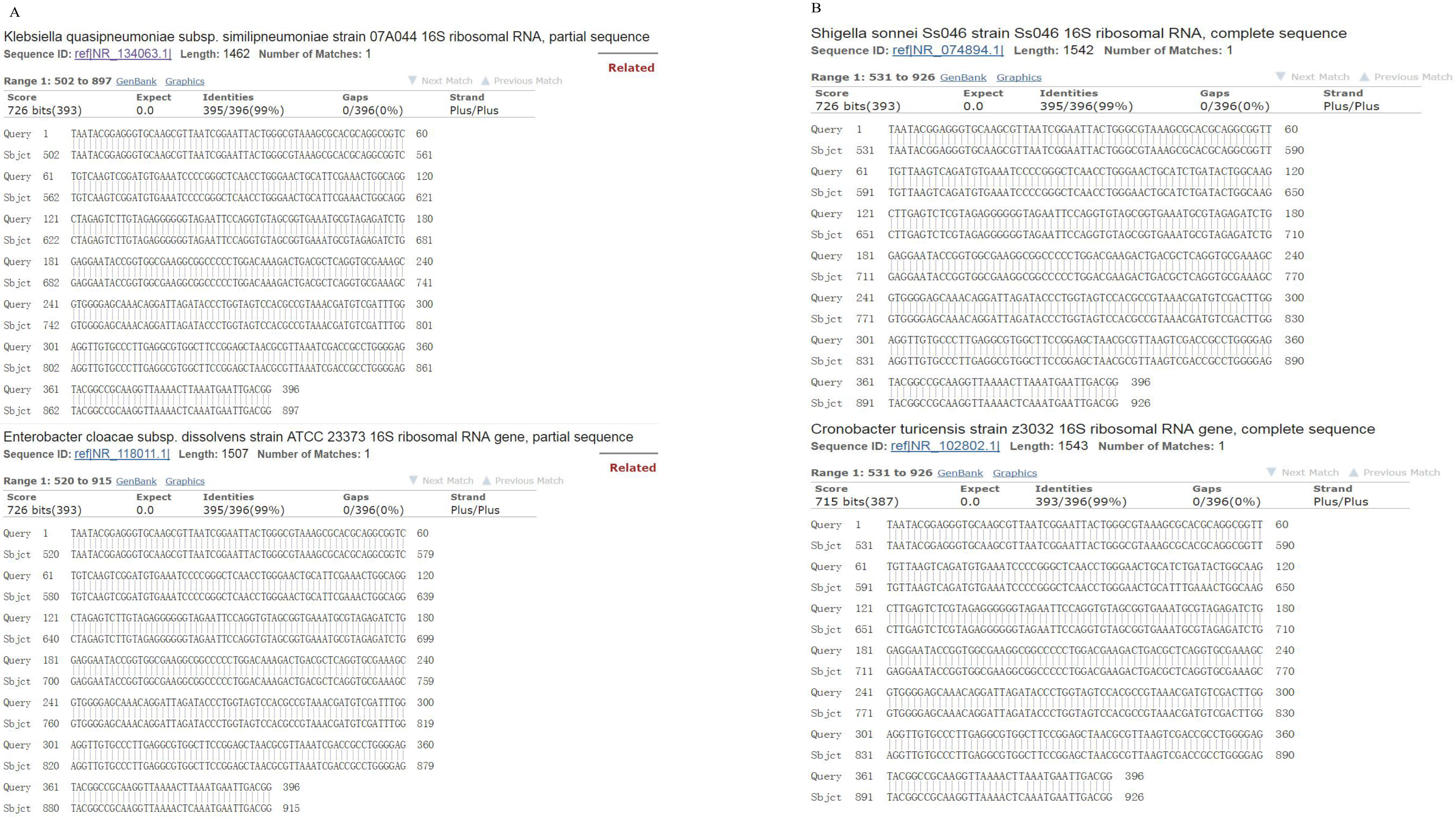

A

Klebsiella quasipneumoniae subsp. similipneumoniae strain 07A044 16S ribosomal RNA, partial sequence

Sequence ID: ref|NR_134063.1| **Length:** 1462 **Number of Matches:** 1

Range 1: 502 to 897 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
726 bits(393)	0.0	395/396(99%)	0/396(0%)	Plus/Plus

```
Query  1    TAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502  TAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTC  561

Query  61   TGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  562  TGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGG  621

Query  121  CTAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  622  CTAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTG  681

Query  181  GAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  682  GAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGC  741

Query  241  GTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGATTTGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742  GTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGATTTGG  801

Query  301  AGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAATCGACCGCCTGGGGAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  802  AGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAATCGACCGCCTGGGGAG  861

Query  361  TACGGCCGCAAGGTTAAAACTTAAATGAATTGACGG  396
            |||||||||||||||||||| |||||||||||||||
Sbjct  862  TACGGCCGCAAGGTTAAAACTCAAATGAATTGACGG  897
```

Enterobacter cloacae subsp. dissolvens strain ATCC 23373 16S ribosomal RNA gene, partial sequence

Sequence ID: ref|NR_118011.1| **Length:** 1507 **Number of Matches:** 1

Range 1: 520 to 915 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
726 bits(393)	0.0	395/396(99%)	0/396(0%)	Plus/Plus

```
Query  1    TAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  520  TAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTC  579

Query  61   TGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  580  TGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGG  639

Query  121  CTAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  640  CTAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTG  699

Query  181  GAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  700  GAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGC  759

Query  241  GTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGATTTGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  760  GTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGATTTGG  819

Query  301  AGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAATCGACCGCCTGGGGAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  820  AGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAATCGACCGCCTGGGGAG  879

Query  361  TACGGCCGCAAGGTTAAAACTTAAATGAATTGACGG  396
            |||||||||||||||||||| |||||||||||||||
Sbjct  880  TACGGCCGCAAGGTTAAAACTCAAATGAATTGACGG  915
```

B

Shigella sonnei Ss046 strain Ss046 16S ribosomal RNA, complete sequence

Sequence ID: ref|NR_074894.1| **Length:** 1542 **Number of Matches:** 1

Range 1: 531 to 926 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
726 bits(393)	0.0	395/396(99%)	0/396(0%)	Plus/Plus

```
Query  1    TAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  531  TAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTT  590

Query  61   TGTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCTGATACTGGCAAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  591  TGTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCTGATACTGGCAAG  650

Query  121  CTTGAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  651  CTTGAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTG  710

Query  181  GAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  711  GAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGC  770

Query  241  GTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  771  GTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGG  830

Query  301  AGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  831  AGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAG  890

Query  361  TACGGCCGCAAGGTTAAAACTTAAATGAATTGACGG  396
            |||||||||||||||||||| |||||||||||||||
Sbjct  891  TACGGCCGCAAGGTTAAAACTCAAATGAATTGACGG  926
```

Cronobacter turicensis strain z3032 16S ribosomal RNA gene, complete sequence

Sequence ID: ref|NR_102802.1| **Length:** 1543 **Number of Matches:** 1

Range 1: 531 to 926 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
715 bits(387)	0.0	393/396(99%)	0/396(0%)	Plus/Plus

```
Query  1    TAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  531  TAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTT  590

Query  61   TGTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCTGATACTGGCAAG  120
            |||||||||||||||||||||||||||||||||||||||||||||| ||| |||||||||
Sbjct  591  TGTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTTGAAACTGGCAAG  650

Query  121  CTTGAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  651  CTTGAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTG  710

Query  181  GAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  711  GAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGC  770

Query  241  GTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  771  GTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGG  830

Query  301  AGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  831  AGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAG  890

Query  361  TACGGCCGCAAGGTTAAAACTTAAATGAATTGACGG  396
            |||||||||||||||||||| |||||||||||||||
Sbjct  891  TACGGCCGCAAGGTTAAAACTCAAATGAATTGACGG  926
```