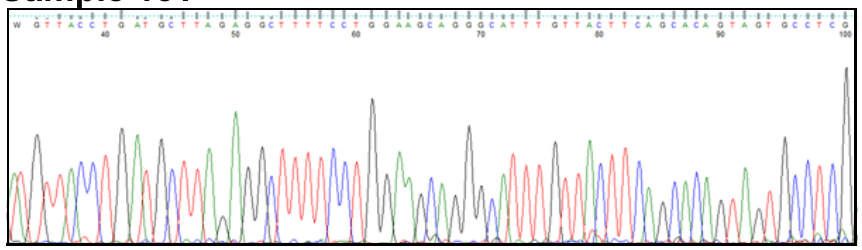
Sample 15T



Salmonella enterica subsp. enterica serovar Choleraesuis strain C500, complete genome
Sequence ID: gb|CP007639.1| Length: 4751585 Number of Matches: 6

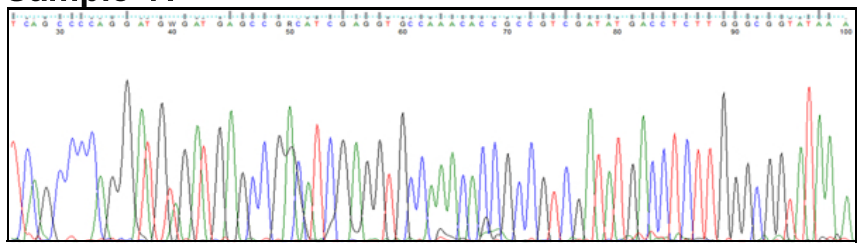
Range 1: 4093811 to 4093893 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
137 bits(74)	3e-29	79/83(95%)	0/83(0%)	Plus/Minus

```
Query  15       TTGGGACTRCTTCAGCCCCAGGATGWGATGAGCCGRCATCGAGGTGCCAAACACCGCCGT  74
                 ||||||||  ||||||||||||||||  ||||||||  ||||||||||||||||||||||
Sbjct  4093893  TTGGGACTACTTCAGCCCCAGGATGTGATGAGCCGACATCGAGGTGCCAAACACCGCCGT  4093834

Query  75       CGATATGACCTCTTGGGCGGTAT  97
                 ||||||||  ||||||||||||||
Sbjct  4093833  CGATATGAACTCTTGGGCGGTAT  4093811
```

Sample 4T



Salmonella enterica subsp. enterica serovar Pullorum str. ATCC 9120, complete genome
Sequence ID: gb|CP012347.1| Length: 4694842 Number of Matches: 7

Range 1: 465209 to 465297 GenBank Graphics ▼ Next Match ▲ Previous Match

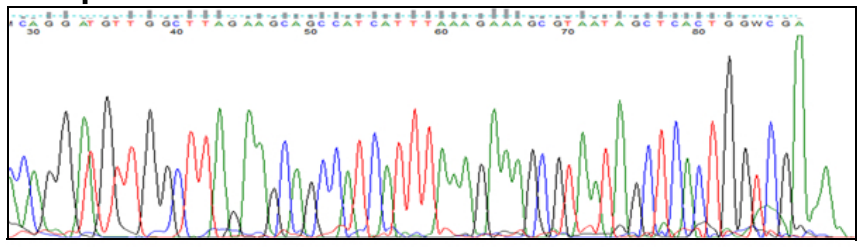
Score	Expect	Identities	Gaps	Strand
128 bits(69)	2e-26	82/89(92%)	3/89(3%)	Plus/Minus

Features: rRNA-23S ribosomal RNA

```
Query  15       TCGG-TTGGGGT-MGATTT-RWGTTACCTGATGCTTAGAGGCTTTTCCTGGAAGCAGGGC  71
                 ||||  |||||||  |||||   ||||||||||||||||||||||||||||||||||||
Sbjct  465297   TCGGTTTGGGGTACGATTTGATGTTACCTGATGCTTAGAGGCTTTTCCTGGAAGCAGGGC  465238

Query  72       ATTTGTTACTTCAGCACAGTAGTGCCTCG  100
                 ||||||||||||||| ||||||||||||
Sbjct  465237   ATTTGTTACTTCAGCACCGTAGTGCCTCG  465209
```

Sample 9T



Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000189, complete genome
Sequence ID: gb|CP006053.1| Length: 4730612 Number of Matches: 7

Range 1: 524605 to 524686 GenBank Graphics ▼ Next Match ▲ Previous Match

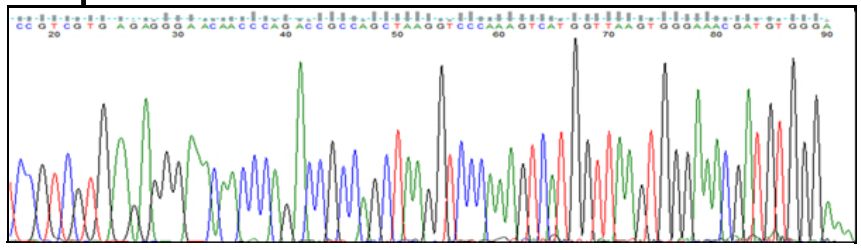
Score	Expect	Identities	Gaps	Strand
126 bits(68)	4e-26	76/82(93%)	1/82(1%)	Plus/Plus

Features: rRNA-23S ribosomal RNA

```
Query  7        CGATGWGRG-AGGCAYAGACAGMCAGGATGTTGGCTTAGAAGCAGCCATCATTTAAAGAA  65
                 |||||  | |||||| ||||||  ||||||||||||||||||||||||||||||||||||
Sbjct  524605   CGATGTGGGAAGGCACAGACAGCCAGGATGTTGGCTTAGAAGCAGCCATCATTTAAAGAA  524664

Query  66       AGCGTAATAGCTCACTGGWCGA  87
                 ||||||||||||||||| |||
Sbjct  524665   AGCGTAATAGCTCACTGGTCGA  524686
```

Sample 1T



Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601 complete genome, strain AKU_12601
Sequence ID: emb|FM200053.1| Length: 4581797 Number of Matches: 7

Range 1: 3371134 to 3371222 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
139 bits(75)	6e-30	85/89(96%)	4/89(4%)	Plus/Minus

Features: rRNA-23S ribosomal RNA

```
Query  6        CGA-TGCT-ACGTCCGTCGTGA-GAGGG-AACAACCCAGACCGCCAGCTAAGGTCCCAAA  61
                 ||| |||| ||||||||||||| ||||| ||||||||||||||||||||||||||||||
Sbjct  3371222  CGAGTGCTAACGTCCGTCGTGAAGAGGGAAACAACCCAGACCGCCAGCTAAGGTCCCAAA  3371163

Query  62       GTCATGGTTAAGTGGGAAACGATGTGGGA  90
                 |||||||||||||||||||||||||||||
Sbjct  3371162  GTCATGGTTAAGTGGGAAACGATGTGGGA  3371134
```