

APPENDICES

Appendix 1

Alignment nucleotide sequence from all samples after BLAST program in NCBI data.

Uncultured bacterium partial 16S rRNA gene, clone To13				
Sequence ID: FN567982.1 Length: 794 Number of Matches: 1				
Range 1: 349 to 414 GenBank Graphics Next Match Previous Match				
Score	Expect	Identities	Gaps	Strand
102 bits(55)	4e-18	64/68(94%)	2/68(2%)	Plus/Plus
Query 8	GGGCGCAAGGCCTGAATGCAGCCATGCCGCGTGTATGAAGAAGGCTTTCGGATCGTAAAG	67		
Sbjct 349	GGGCGCAA-GCCTG-ATGCAGCCATGCCGCGTGTATGAAGAAGGCTTTCGGTCTGAAG	406		

Porphyromonas gingivalis ATCC 33277 16S ribosomal RNA, partial sequence				
Sequence ID: NR_074234.1 Length: 1475 Number of Matches: 1				
Range 1: 381 to 791 GenBank Graphics Next Match Previous Match				
Score	Expect	Identities	Gaps	Strand
671 bits(363)	0.0	397/413(96%)	4/413(0%)	Plus/Plus
Query 2	GGGCGAAGA-CCTGAA-CAGCCAAGTCGCGTGAAGGAAGACTGTCCTAAGGATTGTAAC	59		
Sbjct 381	GGGCG-AGAGCCTGAACCAGCCAAGTCGCGTGAAGGAAGACTGTCCTAAGGATTGTAAC	439		
Query 60	TTCTTTTATACGGGAATAACGGCGATACGAGTATGCATTGAATGTACCGTAAGCAATAA	119		
Sbjct 440	TTCTTTTATACGGGAATAACGGCGATACGAGTATGCATTGAATGTACCGTAAGCAATAA	499		
Query 120	GCATCGGCTAACTCCGTGCCAGCAGCCGCGTAATACGAGGATGCGACCGTATCCGGA	179		
Sbjct 500	GCATCGGCTAACTCCGTGCCAGCAGCCGCGTAATACGAGGATGCGACCGTATCCGGA	559		
Query 180	TTTATTGGGTTTCAAGGGTGCCTACGTTGTTCCGTAATCAGCGGTAAACCTGAGCGCT	239		
Sbjct 560	TTTATTGGGTTTAAAGGGTGCCTACGTTGTTCCGTAATCAGCGGTAAACCTGAGCGCT	619		
Query 240	CAACGTTCTGCTGCGTTGAAACTGCGGGCTTGATTCAGCGGCGGCAGGCGGAATTC	299		
Sbjct 620	CAACGTTGAGCCTGCGTTGAAACTGCGGGCTTGATTCAGCGGCGGCAGGCGGAATTC	679		
Query 300	TGGGTGAGCGGTGATATCATATATCAGGAACTCCGATTGCGAAGGCAGCTTGC	359		
Sbjct 680	TGGGTGAGCGGTGATATCATATATCAGGAACTCCGATTGCGAAGGCAGCTTGC	739		
Query 360	CATACTGTGACTGACACTGAAGCACGAACGCGTGGGTATCAAACTGATTAG	412		
Sbjct 740	CATACTGCGACTGACACTGAAGCACGAAGCGTGGGTATCAAACTGATTAG	791		

Sample 1

Streptococcus mutans strain NPL952 16S ribosomal RNA gene, partial sequence

Sequence ID: [MK908372.1](#) Length: 417 Number of Matches: 1

Range 1: 4 to 62 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
110 bits(59)	3e-20	59/59(100%)	0/59(0%)	Plus/Plus
Query 15	GAGTCTGACCGAGCAGCGCGGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG	73		
Sbjct 4	GAGTCTGACCGAGCAGCGCGGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG	62		

Sample 2

Streptococcus mutans strain KCOM 1075 16S ribosomal RNA gene, partial sequence

Sequence ID: [MT233343.1](#) Length: 1530 Number of Matches: 1

Range 1: 392 to 447 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
104 bits(56)	2e-18	56/56(100%)	0/56(0%)	Plus/Plus
Query 20	TCTGACCGAGCAGCGCGGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG	75		
Sbjct 392	TCTGACCGAGCAGCGCGGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG	447		

Sample 3

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Streptococcus gordonii strain POPI_666 16S ribosomal RNA gene, partial sequence

Sequence ID: MT436688.1 Length: 396 Number of Matches: 1

Range 1: 1 to 53

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Score	Expect	Identities	Gaps	Strand
99.0 bits(53)	1e-16	53/53(100%)	0/53(0%)	Plus/Plus
Query 16	CTGACGACACCGCCGCTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG	68		
Sbjct 1	CTGACGACACCGCCGCTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG	53		

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Streptococcus mutans strain POPI_553 16S ribosomal RNA gene, partial sequence

Sequence ID: [MT436632.1](#) Length: 396 Number of Matches: 1

Range 1: 1 to 53

GenBank

Graphics

Next Match

Previous Match

Score	Expect	Identities	Gaps	Strand
99.0 bits(53)	1e-16	53/53(100%)	0/53(0%)	Plus/Plus
Query 16	CTGACGACACCGCCGCTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG	68		
Sbjct 1	CTGACGACACCGCCGCTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG	53		

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Streptococcus oralis strain POPI_384 16S ribosomal RNA gene, partial sequence

Sequence ID: [MT436586.1](#) Length: 396 Number of Matches: 1

Range 1: 1 to 53

GenBank

Graphics

Next Match

Previous Match

Score	Expect	Identities	Gaps	Strand
99.0 bits(53)	1e-16	53/53(100%)	0/53(0%)	Plus/Plus
Query 16	CTGACGACACCGCCGCTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG	68		
Sbjct 1	CTGACGACACCGCCGCTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG	53		

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Streptococcus sanguinis strain POPI_145 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT436525.1](#) Length: 396 Number of Matches: 1

Range 1: 1 to 53 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
99.0 bits(53)	1e-16	53/53(100%)	0/53(0%)	Plus/Plus

Query 16 CTGACGAGCAGCGCGGTGAGTGAGAAGTTTTTCGGATCGTAAAGCTCTGTTG 68
Sbjct 1 CTGACGAGCAGCGCGGTGAGTGAGAAGTTTTTCGGATCGTAAAGCTCTGTTG 53

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Streptococcus mutans strain NPL952 16S ribosomal RNA gene, partial sequence
Sequence ID: [MK908372.1](#) Length: 417 Number of Matches: 1

Range 1: 1 to 62 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
100 bits(54)	6e-18	61/64(95%)	2/64(3%)	Plus/Plus

Query 13 GGAGCAGTCTGACCGAGCAGCGCGGTGAGTGAGAAGTTTTTCGGATCGTACAGCTCT 72
Sbjct 1 GGAG-AGTCTGACCGAGCAGCGCGGTGAGTGAGAAGTTTTTCGGAT-CGTAAAGCTCT 58
Query 73 GTTG 76
Sbjct 59 GTTG 62

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Streptococcus agalactiae strain StrepA 16S ribosomal RNA gene, partial sequence
Sequence ID: [MH359095.1](#) Length: 1473 Number of Matches: 1

Range 1: 312 to 369 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
97.1 bits(52)	8e-17	57/59(97%)	1/59(1%)	Plus/Plus

Query 18 AGTCTGACCGAGCAGCGCGGTGAGTGAGAAGTTTTTCGGATCGTACAGCTCTGTTG 76
Sbjct 312 AGTCTGACCGAGCAGCGCGGTGAGTGAGAAGTTTTTCGGAT-CGTAAAGCTCTGTTG 369

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Streptococcus downei strain ChDC YD3 16S ribosomal RNA gene, partial sequence
Sequence ID: [AY942563.1](#) Length: 1521 Number of Matches: 1

Range 1: 390 to 447 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
97.1 bits(52)	8e-17	57/59(97%)	1/59(1%)	Plus/Plus

Query 18 AGTCTGACCGAGCAGCGCGGTGAGTGAGAAGTTTTTCGGATCGTACAGCTCTGTTG 76
Sbjct 390 AGTCTGACCGAGCAGCGCGGTGAGTGAGAAGTTTTTCGGAT-CGTAAAGCTCTGTTG 447

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Streptococcus lutetiensis strain LC1 16S ribosomal RNA gene, partial sequence
Sequence ID: [KT628400.1](#) Length: 552 Number of Matches: 1

Range 1: 4 to 72 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
95.3 bits(61)	3e-16	64/70(91%)	2/70(2%)	Plus/Plus

Query 8 GCAT-GGGGACAGTCTGACCGAGCAGCGCGGTGAGTGAGAAGTTTTTCGGATCGGTAC 66
Sbjct 4 GCATGGGGACACCTGACCGAGCAGCGCGGTGAGTGAGAAGTTTTTCGAT-CGTAA 62
Query 67 AGCTCTGTTG 76
Sbjct 63 AGCTCTGTTG 72

Sample 4

Klebsiella sp. strain C-3 16S ribosomal RNA gene, partial sequence

Sequence ID: [MT605302.1](#) Length: 1476 Number of Matches: 1

Range 1: 334 to 765 [GenBank](#) [Graphics](#)

[Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
791 bits(428)	0.0	431/432(99%)	1/432(0%)	Plus/Minus
Query 8	CGCTTTCGC - CCTGAGCGTCAGTCTTTGTCCAGGGGGCGCCTTCGCCACCGGTATTCTCT	66		
Sbjct 765	CGCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCGCCTTCGCCACCGGTATTCTCT	706		
Query 67	CCAGATCTCTACGCATTTACCCGCTACACCTGGAATTCACCCCTCTACAAGACTCTA	126		
Sbjct 705	CCAGATCTCTACGCATTTACCCGCTACACCTGGAATTCACCCCTCTACAAGACTCTA	646		
Query 127	GCCTGCCAGTTTCGAATGCAAGTCCAGGTTGAGCCCGGGGATTCACATCCGACTTGAC	186		
Sbjct 645	GCCTGCCAGTTTCGAATGCAAGTCCAGGTTGAGCCCGGGGATTCACATCCGACTTGAC	586		
Query 187	AGACCGCTCGCTGCGCTTTACGCCAGTAATTCGATTAAACGTTGACCTCCGTATT	246		
Sbjct 585	AGACCGCTCGCTGCGCTTTACGCCAGTAATTCGATTAAACGTTGACCTCCGTATT	526		
Query 247	ACCGCGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCGCGGTAACGTCATCGACAA	306		
Sbjct 525	ACCGCGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCGCGGTAACGTCATCGACAA	466		
Query 307	GGTTATTAACCTTATCGCTTCTCCCGCTGAAAGTGCTTTACAACCGAAGGCTTCT	366		
Sbjct 465	GGTTATTAACCTTATCGCTTCTCCCGCTGAAAGTGCTTTACAACCGAAGGCTTCT	406		
Query 367	TCATACACGGGATGGCTGCATCAGGCTTGCGCCATTGTGCAATATTCCTCACTGCTG	426		
Sbjct 405	TCATACACGGGATGGCTGCATCAGGCTTGCGCCATTGTGCAATATTCCTCACTGCTG	346		
Query 427	CCTCCCGTAGGA	438		
Sbjct 345	CCTCCCGTAGGA	334		

Sample 5

Descriptions	Graphic Summary	Alignments	Taxonomy
Alignment view Pairwise ☐ ClustalW Restore defaults Download			
4 sequences selected			
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Klebsiella pneumoniae strain NOS_08 16S ribosomal RNA gene, partial sequence Sequence ID: MF652091.1 Length: 871 Number of Matches: 1			
Range 1: 333 to 764 GenBank Graphics			
Score	Expect	Identities	Gaps
792 bits(423)	0.0	429/432(99%)	0/432(0%)
Query 4	CGCTTTCGCCACTGACGTGCTTTGTCCAGGGGGCGCCTTCGCCACCGGTATTCTCT	66	
Sbjct 764	CGCTTTCGCCACCTGAGCGTCAGTCTTTGTCCAGGGGGCGCCTTCGCCACCGGTATTCTCT	705	
Query 64	CCAGATCTCTACGCATTTACCCGCTACACCTGGAATTCACCCCTCTACAAGACTCTA	123	
Sbjct 704	CCAGATCTCTACGCATTTACCCGCTACACCTGGAATTCACCCCTCTACAAGACTCTA	645	
Query 124	GCCTGCCAGTTTCGAATGCAAGTCCAGGTTGAGCCCGGGGATTCACATCCGACTTGAC	183	
Sbjct 644	GCCTGCCAGTTTCGAATGCAAGTCCAGGTTGAGCCCGGGGATTCACATCCGACTTGAC	585	
Query 184	AGACCGCTCGCTGCGCTTTACGCCAGTAATTCGATTAAACGTTGACCTCCGTATT	243	
Sbjct 584	AGACCGCTCGCTGCGCTTTACGCCAGTAATTCGATTAAACGTTGACCTCCGTATT	525	
Query 244	ACCGCGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCGCGGTAACGTCATCGACAA	303	
Sbjct 524	ACCGCGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCGCGGTAACGTCATCGACAA	465	
Query 304	GGTTATTAACCTTATCGCTTCTCCCGCTGAAAGTGCTTTACAACCGAAGGCTTCT	363	
Sbjct 464	GGTTATTAACCTTATCGCTTCTCCCGCTGAAAGTGCTTTACAACCGAAGGCTTCT	405	
Query 364	TCATACACGGGATGGCTGCATCAGGCTTGCGCCATTGTGCAATATTCCTCACTGCTG	423	
Sbjct 404	TCATACACGGGATGGCTGCATCAGGCTTGCGCCATTGTGCAATATTCCTCACTGCTG	345	
Query 424	CCTCCCGTAGGA	435	
Sbjct 344	CCTCCCGTAGGA	333	

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Klebsiella pneumoniae strain F501-6-2 16S ribosomal RNA gene, partial sequence
Sequence ID: [MK457128.1](#) Length: 791 Number of Matches: 1

Range 1: 232 to 663 [GenBank](#) [Graphics](#) ▾ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
782 bits(423)	0.0	429/432(99%)	0/432(0%)	Plus/Minus
Query 4	CGCTTTGCGCACTGAACGTCA	CGCTTTGCGCACTGAACGTCA		63
Sbjct 663	CGCTTTGCGCACTGAACGTCA	CGCTTTGCGCACTGAACGTCA		684
Query 64	CCAGATCTCTACGATTTTCA	CCAGATCTCTACGATTTTCA		123
Sbjct 683	CCAGATCTCTACGATTTTCA	CCAGATCTCTACGATTTTCA		544
Query 124	GCCTGCGAGTTTGAATGCA	GCCTGCGAGTTTGAATGCA		183
Sbjct 543	GCCTGCGAGTTTGAATGCA	GCCTGCGAGTTTGAATGCA		484
Query 184	AGACCGCTGCGTGCCTTTA	AGACCGCTGCGTGCCTTTA		243
Sbjct 483	AGACCGCTGCGTGCCTTTA	AGACCGCTGCGTGCCTTTA		424
Query 244	ACCGCGGCTGCGACGAGTT	ACCGCGGCTGCGACGAGTT		303
Sbjct 423	ACCGCGGCTGCGACGAGTT	ACCGCGGCTGCGACGAGTT		364
Query 384	GGTTATTAACTTAAACGCT	GGTTATTAACTTAAACGCT		363
Sbjct 363	GGTTATTAACTTAAACGCT	GGTTATTAACTTAAACGCT		384
Query 364	TCACACACGGGATGGCTGC	TCACACACGGGATGGCTGC		423
Sbjct 383	TCACACACGGGATGGCTGC	TCACACACGGGATGGCTGC		244
Query 424	CCTCCCGTAGGA	CCTCCCGTAGGA		435
Sbjct 243	CCTCCCGTAGGA	CCTCCCGTAGGA		232

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Klebsiella pneumoniae strain P4549 16S ribosomal RNA gene, partial sequence
Sequence ID: [KT248958.1](#) Length: 1259 Number of Matches: 1

Range 1: 278 to 709 [GenBank](#) [Graphics](#) ▾ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
782 bits(423)	0.0	429/432(99%)	0/432(0%)	Plus/Minus
Query 4	CGCTTTGCGCACTGAACGTCA	CGCTTTGCGCACTGAACGTCA		63
Sbjct 789	CGCTTTGCGCACTGAACGTCA	CGCTTTGCGCACTGAACGTCA		658
Query 64	CCAGATCTCTACGATTTTCA	CCAGATCTCTACGATTTTCA		123
Sbjct 649	CCAGATCTCTACGATTTTCA	CCAGATCTCTACGATTTTCA		589
Query 124	GCCTGCGAGTTTGAATGCA	GCCTGCGAGTTTGAATGCA		183
Sbjct 589	GCCTGCGAGTTTGAATGCA	GCCTGCGAGTTTGAATGCA		530
Query 184	AGACCGCTGCGTGCCTTTA	AGACCGCTGCGTGCCTTTA		243
Sbjct 529	AGACCGCTGCGTGCCTTTA	AGACCGCTGCGTGCCTTTA		479
Query 244	ACCGCGGCTGCGACGAGTT	ACCGCGGCTGCGACGAGTT		303
Sbjct 469	ACCGCGGCTGCGACGAGTT	ACCGCGGCTGCGACGAGTT		418
Query 384	GGTTATTAACTTAAACGCT	GGTTATTAACTTAAACGCT		363
Sbjct 409	GGTTATTAACTTAAACGCT	GGTTATTAACTTAAACGCT		350
Query 364	TCACACACGGGATGGCTGC	TCACACACGGGATGGCTGC		423
Sbjct 349	TCACACACGGGATGGCTGC	TCACACACGGGATGGCTGC		290
Query 424	CCTCCCGTAGGA	CCTCCCGTAGGA		435
Sbjct 289	CCTCCCGTAGGA	CCTCCCGTAGGA		278

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Klebsiella pneumoniae strain P4574 16S ribosomal RNA gene, partial sequence
Sequence ID: [KT215415.1](#) Length: 1399 Number of Matches: 1

Range 1: 288 to 719 [GenBank](#) [Graphics](#) ▾ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
782 bits(423)	0.0	429/432(99%)	0/432(0%)	Plus/Minus
Query 4	CGCTTTGCGCACTGAACGTCA	CGCTTTGCGCACTGAACGTCA		63
Sbjct 719	CGCTTTGCGCACTGAACGTCA	CGCTTTGCGCACTGAACGTCA		658
Query 64	CCAGATCTCTACGATTTTCA	CCAGATCTCTACGATTTTCA		123
Sbjct 659	CCAGATCTCTACGATTTTCA	CCAGATCTCTACGATTTTCA		608
Query 124	GCCTGCGAGTTTGAATGCA	GCCTGCGAGTTTGAATGCA		183
Sbjct 599	GCCTGCGAGTTTGAATGCA	GCCTGCGAGTTTGAATGCA		548
Query 184	AGACCGCTGCGTGCCTTTA	AGACCGCTGCGTGCCTTTA		243
Sbjct 639	AGACCGCTGCGTGCCTTTA	AGACCGCTGCGTGCCTTTA		488
Query 244	ACCGCGGCTGCGACGAGTT	ACCGCGGCTGCGACGAGTT		303
Sbjct 493	ACCGCGGCTGCGACGAGTT	ACCGCGGCTGCGACGAGTT		428
Query 384	GGTTATTAACTTAAACGCT	GGTTATTAACTTAAACGCT		363
Sbjct 419	GGTTATTAACTTAAACGCT	GGTTATTAACTTAAACGCT		368
Query 364	TCACACACGGGATGGCTGC	TCACACACGGGATGGCTGC		423
Sbjct 359	TCACACACGGGATGGCTGC	TCACACACGGGATGGCTGC		388
Query 424	CCTCCCGTAGGA	CCTCCCGTAGGA		435
Sbjct 299	CCTCCCGTAGGA	CCTCCCGTAGGA		288

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Enterobacter sp. strain EF2 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT613374.1](#) Length: 1433 Number of Matches: 1

Range 1: 297 to 728 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
793 bits(429)	0.0	432/433(99%)	1/433(0%)	Plus/Minus

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Query 7  CGCTTTGCGCCACTGAGCGTCAGTCTTTGTCCAGGGGGCGCCTTGCCACCGGATATCC 66
Sbjct 728 CGCTTTGCG-CACCTGAGCGTCAGTCTTTGTCCAGGGGGCGCCTTGCCACCGGATATCC 678

Query 67  TCCAGATCTCTACGCATTTACCGGTACACCTGGAAATCTACCCCCCTCTACAAGACTCC 126
Sbjct 669 TCCAGATCTCTACGCATTTACCGGTACACCTGGAAATCTACCCCCCTCTACAAGACTCC 610

Query 127  AGCCTGCCAGTTTCGAATGCAGTTCCAGGTTGAGCCCGGGGATTTACATCCGACTTGA 186
Sbjct 609 AGCCTGCCAGTTTCGAATGCAGTTCCAGGTTGAGCCCGGGGATTTACATCCGACTTGA 590

Query 187  CAGACCGCCTGCGTGCCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT 246
Sbjct 549 CAGACCGCCTGCGTGCCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT 490

Query 247  TACCGCGCTGCTGGCAGGAGTTAGCCGGTCTTCTCTGCGGGTAACGTCAATTGCTG 386
Sbjct 489 TACCGCGCTGCTGGCAGGAGTTAGCCGGTCTTCTCTGCGGGTAACGTCAATTGCTG 430

Query 397  TGGTATTAAACCAACACCTTCTCCCCGCTGAAAGTACTTTACAACCGAAGGCTTC 366
Sbjct 429 TGGTATTAAACCAACACCTTCTCCCCGCTGAAAGTACTTTACAACCGAAGGCTTC 378

Query 367  TTCATACACGGGATGGCTGCATCAGGCTTGCGCCCATTTGTGCAATATCCCCACTGCT 426
Sbjct 369 TTCATACACGGGATGGCTGCATCAGGCTTGCGCCCATTTGTGCAATATCCCCACTGCT 310

Query 427  GCCTCCCGTAGGA 439
Sbjct 309 GCCTCCCGTAGGA 297

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Enterobacter cloacae strain HS-6 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT520149.1](#) Length: 1406 Number of Matches: 1

Range 1: 282 to 713 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
793 bits(429)	0.0	432/433(99%)	1/433(0%)	Plus/Minus

```

Query 7  CGCTTTGCGCCACTGAGCGTCAGTCTTTGTCCAGGGGGCGCCTTGCCACCGGATATCC 66
Sbjct 713 CGCTTTGCG-CACCTGAGCGTCAGTCTTTGTCCAGGGGGCGCCTTGCCACCGGATATCC 655

Query 67  TCCAGATCTCTACGCATTTACCGGTACACCTGGAAATCTACCCCCCTCTACAAGACTCC 126
Sbjct 654 TCCAGATCTCTACGCATTTACCGGTACACCTGGAAATCTACCCCCCTCTACAAGACTCC 595

Query 127  AGCCTGCCAGTTTCGAATGCAGTTCCAGGTTGAGCCCGGGGATTTACATCCGACTTGA 186
Sbjct 594 AGCCTGCCAGTTTCGAATGCAGTTCCAGGTTGAGCCCGGGGATTTACATCCGACTTGA 535

Query 187  CAGACCGCCTGCGTGCCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT 246
Sbjct 534 CAGACCGCCTGCGTGCCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT 475

Query 247  TACCGCGCTGCTGGCAGGAGTTAGCCGGTCTTCTCTGCGGGTAACGTCAATTGCTG 386
Sbjct 474 TACCGCGCTGCTGGCAGGAGTTAGCCGGTCTTCTCTGCGGGTAACGTCAATTGCTG 415

Query 397  TGGTATTAAACCAACACCTTCTCCCCGCTGAAAGTACTTTACAACCGAAGGCTTC 366
Sbjct 414 TGGTATTAAACCAACACCTTCTCCCCGCTGAAAGTACTTTACAACCGAAGGCTTC 353

Query 367  TTCATACACGGGATGGCTGCATCAGGCTTGCGCCCATTTGTGCAATATCCCCACTGCT 426
Sbjct 354 TTCATACACGGGATGGCTGCATCAGGCTTGCGCCCATTTGTGCAATATCCCCACTGCT 295

Query 427  GCCTCCCGTAGGA 439
Sbjct 294 GCCTCCCGTAGGA 282

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Klebsiella pneumoniae strain SILX19 16S ribosomal RNA gene, partial sequence
Sequence ID: [MK789854.1](#) Length: 1411 Number of Matches: 1

Range 1: 277 to 708 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
793 bits(429)	0.0	432/433(99%)	1/433(0%)	Plus/Minus

```

Query 7  CGCTTTGCGCCACTGAGCGTCAGTCTTTGTCCAGGGGGCGCCTTGCCACCGGATATCC 66
Sbjct 728 CGCTTTGCG-CACCTGAGCGTCAGTCTTTGTCCAGGGGGCGCCTTGCCACCGGATATCC 650

Query 67  TCCAGATCTCTACGCATTTACCGGTACACCTGGAAATCTACCCCCCTCTACAAGACTCC 126
Sbjct 649 TCCAGATCTCTACGCATTTACCGGTACACCTGGAAATCTACCCCCCTCTACAAGACTCC 590

Query 127  AGCCTGCCAGTTTCGAATGCAGTTCCAGGTTGAGCCCGGGGATTTACATCCGACTTGA 186
Sbjct 589 AGCCTGCCAGTTTCGAATGCAGTTCCAGGTTGAGCCCGGGGATTTACATCCGACTTGA 530

Query 187  CAGACCGCCTGCGTGCCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT 246
Sbjct 529 CAGACCGCCTGCGTGCCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT 470

Query 247  TACCGCGCTGCTGGCAGGAGTTAGCCGGTCTTCTCTGCGGGTAACGTCAATTGCTG 386
Sbjct 469 TACCGCGCTGCTGGCAGGAGTTAGCCGGTCTTCTCTGCGGGTAACGTCAATTGCTG 410

Query 397  TGGTATTAAACCAACACCTTCTCCCCGCTGAAAGTACTTTACAACCGAAGGCTTC 366
Sbjct 409 TGGTATTAAACCAACACCTTCTCCCCGCTGAAAGTACTTTACAACCGAAGGCTTC 350

Query 367  TTCATACACGGGATGGCTGCATCAGGCTTGCGCCCATTTGTGCAATATCCCCACTGCT 426
Sbjct 349 TTCATACACGGGATGGCTGCATCAGGCTTGCGCCCATTTGTGCAATATCCCCACTGCT 290

Query 427  GCCTCCCGTAGGA 439
Sbjct 289 GCCTCCCGTAGGA 277

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Salmonella enterica subsp. enterica strain SURX10 16S ribosomal RNA gene, partial sequence
Sequence ID: [MK780660.1](#) Length: 1458 Number of Matches: 1

Range 1: 330 to 761 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
793 bits(429)	0.0	432/433(99%)	1/433(0%)	Plus/Minus
Query 7	CGCTTTGCGACCTGAGCTCAGTCTTTGTCCAGGGGGCGCCCTTCGCCACCGGATTCC	66		
Sbjct 761	CGCTTTGCGACCTGAGCTCAGTCTTTGTCCAGGGGGCGCCCTTCGCCACCGGATTCC	703		
Query 67	TCCAGATCTCTACGCAATTTACCGCTACACCTGGAATTTACCCCTCTACAAGACTCC	126		
Sbjct 702	TCCAGATCTCTACGCAATTTACCGCTACACCTGGAATTTACCCCTCTACAAGACTCC	643		
Query 127	AGCCTGCCAGTTTGAATGCAAGTTCCAGGTTGAGCCGGGGATTTCACATCCGACTGA	186		
Sbjct 642	AGCCTGCCAGTTTGAATGCAAGTTCCAGGTTGAGCCGGGGATTTCACATCCGACTGA	583		
Query 187	CAGACCGCTGCTGCGCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT	246		
Sbjct 582	CAGACCGCTGCTGCGCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT	523		
Query 247	TACCGGGGCTGGACAGGAGTTAGCCGGTCTTCTTCGGGGTAACGTAATTCGCTG	306		
Sbjct 522	TACCGGGGCTGGACAGGAGTTAGCCGGTCTTCTTCGGGGTAACGTAATTCGCTG	463		
Query 307	TGGTATTAAACCAACACCTTCTCCCGCTGAAAGTACTTTACAACCGAAGGCTTC	366		
Sbjct 462	TGGTATTAAACCAACACCTTCTCCCGCTGAAAGTACTTTACAACCGAAGGCTTC	403		
Query 367	TTCATACACGGGATGGCTGCATCAGGCTTGCCGCCATTGTGCAATATTCCTCACTGC	426		
Sbjct 402	TTCATACACGGGATGGCTGCATCAGGCTTGCCGCCATTGTGCAATATTCCTCACTGC	343		
Query 427	GCCTCCCGTAGGA	439		
Sbjct 342	GCCTCCCGTAGGA	330		

Descriptions Graphic Summary Alignments Taxonomy

Alignment view Pairwise CDS feature Restore defaults Download

6 sequences selected

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Enterobacter ludwigii strain Bac155 16S ribosomal RNA gene, partial sequence
Sequence ID: [KX641539.1](#) Length: 1132 Number of Matches: 1

Range 1: 23 to 455 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
784 bits(424)	0.0	431/434(99%)	1/434(0%)	Plus/Minus
Query 7	CGCTTTGCGACCTGAGCTCAGTCTTTGTCCAGGGGGCGCCCTTCGCCACCGGATTCC	66		
Sbjct 455	CGCTTTGCGACCTGAGCTCAGTCTTTGTCCAGGGGGCGCCCTTCGCCACCGGATTCC	597		
Query 67	TCCAGATCTCTACGCAATTTACCGCTACACCTGGAATTTACCCCTCTACAAGACTCC	126		
Sbjct 396	TCCAGATCTCTACGCAATTTACCGCTACACCTGGAATTTACCCCTCTACAAGACTCC	337		
Query 127	AGCCTGCCAGTTTGAATGCAAGTTCCAGGTTGAGCCGGGGATTTCACATCCGACTGA	186		
Sbjct 336	AGCCTGCCAGTTTGAATGCAAGTTCCAGGTTGAGCCGGGGATTTCACATCCGACTGA	277		
Query 187	CAGACCGCTGCTGCGCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT	246		
Sbjct 276	CAGACCGCTGCTGCGCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT	217		
Query 247	TACCGGGGCTGGACAGGAGTTAGCCGGTCTTCTTCGGGGTAACGTAATTCGCTG	306		
Sbjct 216	TACCGGGGCTGGACAGGAGTTAGCCGGTCTTCTTCGGGGTAACGTAATTCGCTG	157		
Query 307	TGGTATTAAACCAACACCTTCTCCCGCTGAAAGTACTTTACAACCGAAGGCTTC	366		
Sbjct 156	TGGTATTAAACCAACACCTTCTCCCGCTGAAAGTACTTTACAACCGAAGGCTTC	97		
Query 367	TTCATACACGGGATGGCTGCATCAGGCTTGCCGCCATTGTGCAATATTCCTCACTGC	426		
Sbjct 96	TTCATACACGGGATGGCTGCATCAGGCTTGCCGCCATTGTGCAATATTCCTCACTGC	37		
Query 427	GCCTCCCGTAGGA	439		
Sbjct 36	GCCTCCCGTAGGA	23		

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Enterobacter mori strain AS5 16S ribosomal RNA gene, partial sequence
Sequence ID: [M1613379.1](#) Length: 1427 Number of Matches: 1

Range 1: 390 to 721 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
782 bits(423)	0.0	430/433(99%)	1/433(0%)	Plus/Minus
Query 7	CGCTTTGCGACCTGAGCTCAGTCTTTGTCCAGGGGGCGCCCTTCGCCACCGGATTCC	66		
Sbjct 721	CGCTTTGCGACCTGAGCTCAGTCTTTGTCCAGGGGGCGCCCTTCGCCACCGGATTCC	663		
Query 67	TCCAGATCTCTACGCAATTTACCGCTACACCTGGAATTTACCCCTCTACAAGACTCC	126		
Sbjct 609	TCCAGATCTCTACGCAATTTACCGCTACACCTGGAATTTACCCCTCTACAAGACTCC	603		
Query 127	AGCCTGCCAGTTTGAATGCAAGTTCCAGGTTGAGCCGGGGATTTCACATCCGACTGA	186		
Sbjct 602	AGCCTGCCAGTTTGAATGCAAGTTCCAGGTTGAGCCGGGGATTTCACATCCGACTGA	543		
Query 187	CAGACCGCTGCTGCGCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT	246		
Sbjct 542	CAGACCGCTGCTGCGCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT	483		
Query 247	TACCGGGGCTGGACAGGAGTTAGCCGGTCTTCTTCGGGGTAACGTAATTCGCTG	306		
Sbjct 482	TACCGGGGCTGGACAGGAGTTAGCCGGTCTTCTTCGGGGTAACGTAATTCGCTG	423		
Query 307	TGGTATTAAACCAACACCTTCTCCCGCTGAAAGTACTTTACAACCGAAGGCTTC	366		
Sbjct 422	TGGTATTAAACCAACACCTTCTCCCGCTGAAAGTACTTTACAACCGAAGGCTTC	363		
Query 367	TTCATACACGGGATGGCTGCATCAGGCTTGCCGCCATTGTGCAATATTCCTCACTGC	426		
Sbjct 362	TTCATACACGGGATGGCTGCATCAGGCTTGCCGCCATTGTGCAATATTCCTCACTGC	303		
Query 427	GCCTCCCGTAGGA	439		
Sbjct 302	GCCTCCCGTAGGA	290		

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Enterobacter rogenkampii strain ED5 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT613373.1](#) Length: 1447 Number of Matches: 1

Range 1: 313 to 744 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
782 bits(423)	0.0	430/433(99%)	1/433(0%)	Plus/Minus
Query 7	CGCTTTGACACTGAAGCGTCAGTCTTTGTCCAGGGGGCGCCCTTCGCCACCGGATTCC	66		
Sbjct 744	CGCTTTGACACTGA-GCGTCAGTCTTTGTCCAGGGGGCGCCCTTCGCCACCGGATTCC	686		
Query 67	TCCAGATCTCTACGATTTACCGGTACACCTGGAAATCTACCCCTCTACAAGACTCC	126		
Sbjct 685	TCCAGATCTCTACGATTTACCGGTACACCTGGAAATCTACCCCTCTACAAGACTCT	626		
Query 127	AGCCTGCCAGTTTGAATGCAGTTCACCGGTGAGCCCGGGGATTTCACATCCGACTTGA	186		
Sbjct 625	AGCCTGCCAGTTTGAATGCAGTTCACCGGTGAGCCCGGGGATTTCACATCCGACTTGA	566		
Query 187	CAGACCGCTGCGTGCCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT	246		
Sbjct 565	CAGACCGCTGCGTGCCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT	506		
Query 247	TACCGCGGCTGCTGGCAGGAGTTAGCCGGTCTTCTTTCGCGGTAAAGTCAATCGCTG	306		
Sbjct 505	TACCGCGGCTGCTGGCAGGAGTTAGCCGGTCTTCTTTCGCGGTAAAGTCAATCGCTG	446		
Query 307	AGGTTATTAACTCAACGCCTTCTCCCGCTGAAAGTACTTTACAACCGAAGGCTTC	366		
Sbjct 445	AGGTTATTAACTCAACGCCTTCTCCCGCTGAAAGTACTTTACAACCGAAGGCTTC	386		
Query 367	TTATACACGGGATGGCTGATCAGGCTTGCGCCATTGTGCAATATTCCTCCACTGCT	426		
Sbjct 385	TTATACACGGGATGGCTGATCAGGCTTGCGCCATTGTGCAATATTCCTCCACTGCT	326		
Query 427	GCCTCCCGTAGGA 439			
Sbjct 325	GCCTCCCGTAGGA 313			

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Enterobacter cloacae strain AH1 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT613363.1](#) Length: 1436 Number of Matches: 1

Range 1: 303 to 734 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
782 bits(423)	0.0	430/433(99%)	1/433(0%)	Plus/Minus
Query 7	CGCTTTGACACTGAAGCGTCAGTCTTTGTCCAGGGGGCGCCCTTCGCCACCGGATTCC	66		
Sbjct 734	CGCTTTGACACTGA-GCGTCAGTCTTTGTCCAGGGGGCGCCCTTCGCCACCGGATTCC	676		
Query 67	TCCAGATCTCTACGATTTACCGGTACACCTGGAAATCTACCCCTCTACAAGACTCC	126		
Sbjct 675	TCCAGATCTCTACGATTTACCGGTACACCTGGAAATCTACCCCTCTACAAGACTCT	616		
Query 127	AGCCTGCCAGTTTGAATGCAGTTCACCGGTGAGCCCGGGGATTTCACATCCGACTTGA	186		
Sbjct 615	AGCCTGCCAGTTTGAATGCAGTTCACCGGTGAGCCCGGGGATTTCACATCCGACTTGA	596		
Query 187	CAGACCGCTGCGTGCCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT	246		
Sbjct 555	CAGACCGCTGCGTGCCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT	496		
Query 247	TACCGCGGCTGCTGGCAGGAGTTAGCCGGTCTTCTTTCGCGGTAAAGTCAATCGCTG	306		
Sbjct 495	TACCGCGGCTGCTGGCAGGAGTTAGCCGGTCTTCTTTCGCGGTAAAGTCAATCGCTG	436		
Query 307	AGGTTATTAACTCAACGCCTTCTCCCGCTGAAAGTACTTTACAACCGAAGGCTTC	366		
Sbjct 435	AGGTTATTAACTCAACGCCTTCTCCCGCTGAAAGTACTTTACAACCGAAGGCTTC	376		
Query 367	TTATACACGGGATGGCTGATCAGGCTTGCGCCATTGTGCAATATTCCTCCACTGCT	426		
Sbjct 375	TTATACACGGGATGGCTGATCAGGCTTGCGCCATTGTGCAATATTCCTCCACTGCT	316		
Query 427	GCCTCCCGTAGGA 439			
Sbjct 315	GCCTCCCGTAGGA 303			

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Enterobacter tabaci strain BCB11 16S ribosomal RNA gene, partial sequence
Sequence ID: [MK715464.1](#) Length: 1108 Number of Matches: 1

Range 1: 209 to 640 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
782 bits(423)	0.0	430/433(99%)	1/433(0%)	Plus/Minus
Query 7	CGCTTTGACACTGAAGCGTCAGTCTTTGTCCAGGGGGCGCCCTTCGCCACCGGATTCC	66		
Sbjct 640	CGCTTTGACACTGA-GCGTCAGTCTTTGTCCAGGGGGCGCCCTTCGCCACCGGATTCC	592		
Query 67	TCCAGATCTCTACGATTTACCGGTACACCTGGAAATCTACCCCTCTACAAGACTCC	126		
Sbjct 581	TCCAGATCTCTACGATTTACCGGTACACCTGGAAATCTACCCCTCTACAAGACTCT	522		
Query 127	AGCCTGCCAGTTTGAATGCAGTTCACCGGTGAGCCCGGGGATTTCACATCCGACTTGA	186		
Sbjct 521	AGCCTGCCAGTTTGAATGCAGTTCACCGGTGAGCCCGGGGATTTCACATCCGACTTGA	462		
Query 187	CAGACCGCTGCGTGCCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT	246		
Sbjct 461	CAGACCGCTGCGTGCCTTTACGCCAGTAATTCGATTAAACGCTTGACACCTCCGAT	402		
Query 247	TACCGCGGCTGCTGGCAGGAGTTAGCCGGTCTTCTTTCGCGGTAAAGTCAATCGCTG	306		
Sbjct 401	TACCGCGGCTGCTGGCAGGAGTTAGCCGGTCTTCTTTCGCGGTAAAGTCAATCGCTG	342		
Query 307	AGGTTATTAACTCAACGCCTTCTCCCGCTGAAAGTACTTTACAACCGAAGGCTTC	366		
Sbjct 341	AGGTTATTAACTCAACGCCTTCTCCCGCTGAAAGTACTTTACAACCGAAGGCTTC	282		
Query 367	TTATACACGGGATGGCTGATCAGGCTTGCGCCATTGTGCAATATTCCTCCACTGCT	426		
Sbjct 281	TTATACACGGGATGGCTGATCAGGCTTGCGCCATTGTGCAATATTCCTCCACTGCT	222		
Query 427	GCCTCCCGTAGGA 439			
Sbjct 221	GCCTCCCGTAGGA 209			

Download	GenBank	Graphics	Next	Previous	Descriptions
Klebsiella pneumoniae subsp. pneumoniae strain 47 16S ribosomal RNA gene, partial sequence					
Sequence ID: MT180487.1 Length: 1376 Number of Matches: 1					
Range 1: 312 to 743 GenBank Graphics Next Match Previous Match					
Score	Expect	Identities	Gaps	Strand	
782 bits(423)	0.0	430/433(99%)	1/433(0%)	Plus/Minus	
Query	7	CGCTTCGACCTGAAGCGTCAGTCTTTGTCCAGGGGGCGCCTTCGCCACCGGATTCC	66		
Sbjct	743	CGCTTCGACCTGA-GCGTCAGTCTTTGTCCAGGGGGCGCCTTCGCCACCGGATTCC	685		
Query	67	TCCAGATCTCTACGCATTTCACCGCTACACCTGGAAATTCACCCCTCTACAAGACTCC	126		
Sbjct	684	TCCAGATCTCTACGCATTTCACCGCTACACCTGGAAATTCACCCCTCTACAAGACTCT	625		
Query	127	AGCCTGCGAGTTTGAATGCAATGCCAGTTCCAGGTTGAGCCGGGGATTTCACATCCGACTGA	186		
Sbjct	624	AGCCTGCGAGTTTGAATGCAATGCCAGTTCCAGGTTGAGCCGGGGATTTCACATCCGACTGA	565		
Query	187	CAGACGGCTGCGTGGCTTTACGCCAGTAATTCGATTAAAGCTTGACCTCCGAT	246		
Sbjct	564	CAGACGGCTGCGTGGCTTTACGCCAGTAATTCGATTAAAGCTTGACCTCCGAT	505		
Query	247	TACCGCGCTGCTGGCAGGATTAGCGGTCTTCTTCTGCGGGTAACTCAATCGCTG	306		
Sbjct	504	TACCGCGCTGCTGGCAGGATTAGCGGTCTTCTTCTGCGGGTAACTCAATCGCTG	445		
Query	307	AGGTTATTAACTCAACGCTTCTCCCGCTGAAAGTCTTTACAACCGAAGGCTTC	366		
Sbjct	444	AGGTTATTAACTCAACGCTTCTCCCGCTGAAAGTCTTTACAACCGAAGGCTTC	385		
Query	367	TTTACACCGCGCATGGCTGATCAGGCTTGCGCCATTGTCAATATCCCACTGCT	426		
Sbjct	384	TTTACACCGCGCATGGCTGATCAGGCTTGCGCCATTGTCAATATCCCACTGCT	325		
Query	427	GCCTCCCGTAGGA	439		
Sbjct	324	GCCTCCCGTAGGA	312		

Sample 6

Descriptions	Graphic Summary	Alignments	Taxonomy
Alignment view Pairwise ☐ CDS feature Restore defaults Download			
5 sequences selected			
Download	GenBank	Graphics	Next Previous Descriptions
Streptococcus mutans strain YAA 13 16S ribosomal RNA gene, partial sequence			
Sequence ID: MT605307.1 Length: 1078 Number of Matches: 1			
Range 1: 390 to 447 GenBank Graphics Next Match Previous Match			
Score	Expect	Identities	Gaps
108 bits(58)	4e-20	58/58(100%)	0/58(0%)
Query	16	AGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTCGGATCGTAAGCTCTGTTG	73
Sbjct	390	AGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTCGGATCGTAAGCTCTGTTG	447

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Streptococcus mutans strain YAA 12 16S ribosomal RNA gene, partial sequence			
Sequence ID: MT605306.1 Length: 1155 Number of Matches: 1			
Range 1: 389 to 446 GenBank Graphics Next Match Previous Match			
Score	Expect	Identities	Gaps
108 bits(58)	4e-20	58/58(100%)	0/58(0%)
Query	16	AGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTCGGATCGTAAGCTCTGTTG	73
Sbjct	389	AGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTCGGATCGTAAGCTCTGTTG	446
Download	GenBank	Graphics	Next Previous Descriptions
Streptococcus mutans strain KCOM 1075 16S ribosomal RNA gene, partial sequence			
Sequence ID: MT233343.1 Length: 1530 Number of Matches: 1			
Range 1: 390 to 447 GenBank Graphics Next Match Previous Match			
Score	Expect	Identities	Gaps
108 bits(58)	4e-20	58/58(100%)	0/58(0%)
Query	16	AGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTCGGATCGTAAGCTCTGTTG	73
Sbjct	390	AGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTCGGATCGTAAGCTCTGTTG	447

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Streptococcus mutans strain NPL952 16S ribosomal RNA gene, partial sequence
Sequence ID: [MK908372.1](#) Length: 417 Number of Matches: 1

Range 1: 5 to 62 [GenBank](#) [Graphics](#) ▾ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
108 bits(58)	4e-20	58/58(100%)	0/58(0%)	Plus/Plus

Query 16 AGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCTCTGTTG 73
Sbjct 5 AGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCTCTGTTG 62

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Streptococcus agalactiae strain StrepA 16S ribosomal RNA gene, partial sequence
Sequence ID: [MH359095.1](#) Length: 1473 Number of Matches: 1

Range 1: 312 to 369 [GenBank](#) [Graphics](#) ▾ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
108 bits(58)	4e-20	58/58(100%)	0/58(0%)	Plus/Plus

Query 16 AGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCTCTGTTG 73
Sbjct 312 AGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCTCTGTTG 369

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise ▾ ☐ CDS feature [Restore defaults](#) Download ▾

2 sequences selected ⓘ

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Streptococcus mutans strain NPL952 16S ribosomal RNA gene, partial sequence
Sequence ID: [MK908372.1](#) Length: 417 Number of Matches: 1

Range 1: 4 to 62 [GenBank](#) [Graphics](#) ▾ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
110 bits(59)	1e-20	59/59(100%)	0/59(0%)	Plus/Plus

Query 16 GAGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCTCTGTTG 74
Sbjct 4 GAGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCTCTGTTG 62

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Streptococcus agalactiae strain StrepA 16S ribosomal RNA gene, partial sequence
Sequence ID: [MH359095.1](#) Length: 1473 Number of Matches: 1

Range 1: 308 to 369 [GenBank](#) [Graphics](#) ▾ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
110 bits(59)	1e-20	61/62(98%)	0/52(0%)	Plus/Plus

Query 13 CGGAGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCTCTGTTG 72
Sbjct 308 CGAAGTCTGACCGAGCACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCTCTGTTG 367
Query 73 TG 74
Sbjct 368 TG 369

Sample 7

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise ☐ CDS feature [Restore defaults](#)

1 sequences selected

[Download](#) [GenBank](#) [Graphics](#)

Streptococcus salivarius strain PR23a 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT579923.1](#) Length: 870 Number of Matches: 1

Range 1: 303 to 736 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

	Score	Expect	Identities	Gaps	Strand
	785 bits(425)	0.0	432/435(99%)	2/435(0%)	Plus/Minus
Query 7	CCA-GCTTACGAGCTCAGCGTCAGTTACAGACCAGAGAGCCGCTTTCGCCACCGGTGTTG				65
Sbjct 736	CCAGCCTTTCGAGCTCAGCGTCAGTTACAGACCAGAGAGCCGCTTTCGCCACCGGTGTTG				677
Query 66	CTCCATATATCTACGCATTTCACCGCTACACATGGAATTCACCTCTCCCTTCTGCACTG				125
Sbjct 676	CTCCATATATCTACGCATTTCACCGCTACACATGGAATTCACCTCTCCCTTCTGCACTG				617
Query 126	AAGTTTGACAGTTTCCAAAGCGAAGTATGTTGAGCCACAGCCTTTAACTTCAGACTTAT				185
Sbjct 616	AAGTTTGACAGTTTCCAAAGCGAAGTATGTTGAGCCACAGCCTTTAACTTCAGACTTAT				557
Query 186	CAAACCGCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTAT				245
Sbjct 556	CAAACCGCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTAT				497
Query 246	TACCGCGGCTGCTGGCAGTAGTTAGCCGTCCTTTCTGTTAAGCTACCGTCACAGTGTG				305
Sbjct 496	TACCGCGGCTGCTGGCAGTAGTTAGCCGTCCTTTCTGTTAAGCTACCGTCACAGTGTG				437
Query 306	AACTTTCCACTCTCACACTCGTTCTTGACTTACACAGAGCTTTACGATCCGAAAACCTT				365
Sbjct 436	AACTTTCCACTCTCACACTCGTTCTTGACTTACACAGAGCTTTACGATCCGAAAACCTT				379
Query 366	CTTCACTCACGCGGCGTTGCTCGGTCAAGGTTGCCCATTCGCCGAAGATTCCTACTGC				425
Sbjct 376	CTTCACTCACGCGGCGTTGCTCGGTCAAGGTTGCCCATTCGCCGAAGATTCCTACTGC				317
Query 426	TGCTCTCCCGTAGGA 440				
Sbjct 316	TGCTCTCCCGTAGGA 303				

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise ☐ CDS feature [Restore defaults](#)

1 sequences selected

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Streptococcus anginosus strain KCOM 2722 (= ChDC KB64) 16S ribosomal RNA gene, partial sequence.
Sequence ID: [MW404400.1](#) Length: 1477 Number of Matches: 1

Range 1: 227 to 756 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

	Score	Expect	Identities	Gaps	Strand
	789 bits(427)	0.0	430/431(99%)	1/431(0%)	Plus/Minus
Query 9	GCTTTCGAGCTCAGCGTCAGTTACAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCTCC				68
Sbjct 756	GCTTTCGAGCTCAGCGTCAGTTACAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCTCC				697
Query 69	ATATATCTAGCATTTACCGCTACACATGGAATTCACCTCTCCCTTCTGCACTCAAGT				128
Sbjct 696	ATATATCTAGCATTTACCGCTACACATGGAATTCACCTCTCCCTTCTGCACTCAAGT				637
Query 129	TAAACAGTTTCCAAAGCTTACAATGTTGAGCCACTGCTTTCACTTCAGACTTTTCTAA				188
Sbjct 636	TAAACAGTTTCCAAAGCTTACAATGTTGAGCCACTGCTTTCACTTCAGACTTTTCTAA				577
Query 189	CGGCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTACC				248
Sbjct 576	CGGCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTACC				517
Query 249	CGGCTGCTGGCAGTAGTTAGCCGTCCTTTCTGTTAAGTACCGTCACAGTATGAAT				308
Sbjct 516	CGGCTGCTGGCAGTAGTTAGCCGTCCTTTCTGTTAAGTACCGTCACAGTATGAAT				457
Query 309	TTCCATTCTCACACTCGTTCTTCTTAAACAACAGAGCTTACGATCCGAAAACCTTCTTC				368
Sbjct 456	TTCCATTCTCACACTCGTTCTTCTTAAACAACAGAGCTTACGATCCGAAAACCTTCTTC				397
Query 369	ACTCACGCGGCTTGCTCGGTCAAGGTTCCCCCATTCGCCGAAGATTCCTACTGCTGCC				428
Sbjct 396	ACTCACGCGGCTTGCTCGGTCAAGGTTCCCCCATTCGCCGAAGATTCCTACTGCTGCC				337
Query 429	TCCCCGTAGGA 439				
Sbjct 336	TCCC-GTAGGA 327				

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise ☐ CDS feature ? Re

1 sequences selected ?

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Streptococcus anginosus partial 16S rRNA gene, isolate 75N_2366
Sequence ID: [LT676952.1](#) Length: 773 Number of Matches: 1

Range 1: 327 to 752 [GenBank](#) [Graphics](#) [Next Match](#) ▲

Score	Expect	Identities	Gaps	Strand
776 bits(420)	0.0	425/427(99%)	2/427(0%)	Plus/Minus
Query 12	CGAG-CTCAGCGTCAGTGACAGACCAGAGAGCCGCTTTTCGCCACCGGTCTCTCCCATAT	70		
Sbjct 752	CGAGCCTCAGCGTCAGTGACAGACCAGAGAGCCGCTTTTCGCCACCGGTCTCTCCCATAT	693		
Query 71	ATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTTCTGCACTCAAGTTAAA	130		
Sbjct 692	ATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTTCTGCACTCAAGTTAAA	633		
Query 131	CAGTTTCAAAGCCTACAATGGTTGAGCCACTGCCTTTCACTTCAGACTTTCTAAGCCGC	190		
Sbjct 632	CAGTTTCAAAGCCTACAATGGTTGAGCCACTGCCTTTCACTTCAGACTTTCTAAGCCGC	578		
Query 191	CTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTACCGCGG	250		
Sbjct 572	CTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTACCGCGG	513		
Query 251	CTGCTGGCACGTAGTTAGCCGTCCTTTCTGTTAAGTACGTCAATATGAAGTTTCC	310		
Sbjct 512	CTGCTGGCACGTAGTTAGCCGTCCTTTCTGTTAAGTACGTCAATATGAAGTTTCC	453		
Query 311	ATTCTCACACTCGTTCTTCTTAAACAACAGAGCTTTACGATCCGAAACCTTCTTCACTC	370		
Sbjct 452	ATTCTCACACTCGTTCTTCTTAAACAACAGAGCTTTACGATCCGAAACCTTCTTCACTC	393		
Query 371	ACGCGGCGTTGCTCGGTCAAGGTTCCGCCATTGCGGAAGATTCCCTACTGCTGCCTCCC	430		
Sbjct 392	ACGCGGCGTTGCTCGGTCAAGGTTCCGCCATTGCGGAAGATTCCCTACTGCTGCCTCCC	333		
Query 431	CGTAGGA 437			
Sbjct 332	-GTAGGA 327			

Sample 8

Streptococcus mutans strain KCOM 1075 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT233343.1](#) Length: 1530 Number of Matches: 1

Range 1: 390 to 447 [GenBank](#) [Graphics](#) ▼ [Next Match](#) ▲ [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
108 bits(58)	1e-19	58/58(100%)	0/58(0%)	Plus/Plus
Query 15	AGTCGATCGAGACGCGCGCTGATGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG	72		
Sbjct 390	AGTCGATCGAGACGCGCGCTGATGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG	447		

Sample 9

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise ☐ CDS feature [Restore defaults](#)

4 sequences selected [?](#)

[Download](#) [GenBank](#) [Graphics](#)

Streptococcus oralis strain 69 16S ribosomal RNA gene, partial sequence
Sequence ID: [MH997774.1](#) Length: 894 Number of Matches: 1

Range 1: 323 to 391 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
108 bits(58)	8e-20	68/72(94%)	3/72(4%)	Plus/Plus

Query 3 AAAGGAAGGAAGTCTGAACCGAAGCCAACGCCGCTGAGTGAAGAAGGTTTCGGATCGT 62
Sbjct 323 AATGGACGGAAGTCTGA-CCG-AG-CAACGCCGCTGAGTGAAGAAGGTTTCGGATCGT 379

Query 63 AAAGCTCTGTTG 74
Sbjct 380 AAAGCTCTGTTG 391

Streptococcus mitis clone BJ038 16S ribosomal RNA gene, partial sequence
Sequence ID: [GU422219.1](#) Length: 441 Number of Matches: 1

Range 1: 342 to 411 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
104 bits(56)	1e-18	67/72(93%)	2/72(2%)	Plus/Plus

Query 3 AAAGGAAGGAAGTCTGAACCGAAGCCAACGCCGCTGAGTGAAGAAGGTTTCGGATCGT 62
Sbjct 342 AATGGACGGAAGTCTGAACCGA-G-CAACGCCGCTGAGTGAAGAAGGTTTCGGATCGT 399

Query 63 AAAGCTCTGTTG 74
Sbjct 400 AAAGCTCTGTTG 411

[Download](#) [GenBank](#) [Graphics](#)

Streptococcus cristatus clone CMC470 16S ribosomal RNA gene, partial sequence
Sequence ID: [GU416365.1](#) Length: 456 Number of Matches: 1

Range 1: 352 to 421 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
104 bits(56)	1e-18	67/72(93%)	2/72(2%)	Plus/Plus

Query 3 AAAGGAAGGAAGTCTGAACCGAAGCCAACGCCGCTGAGTGAAGAAGGTTTCGGATCGT 62
Sbjct 352 AATGGACGGAAGTCTGA-CCG-AGCCTACGCCGCTGAGTGAAGAAGGTTTCGGATCGT 409

Query 63 AAAGCTCTGTTG 74
Sbjct 410 AAAGCTCTGTTG 421

Streptococcus pneumoniae strain Nghean-Sp936-15A 16S ribosomal RNA gene, partial sequence
Sequence ID: [MZ007499.1](#) Length: 1419 Number of Matches: 1

Range 1: 322 to 390 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
102 bits(55)	4e-18	67/72(93%)	3/72(4%)	Plus/Plus

Query 3 AAAGGAAGGAAGTCTGAACCGAAGCCAACGCCGCTGAGTGAAGAAGGTTTCGGATCGT 62
Sbjct 322 AATGGACGGAAGTCTGA-CCG-AG-CAACGCCGCTGAGTGAAGAAGGTTTCGGATCGT 378

Query 63 AAAGCTCTGTTG 74
Sbjct 379 AAAGCTCTGTTG 390

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise ☐ CDS feature [Restore defaults](#)

4 sequences selected

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Streptococcus infantis strain 1795 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT626073.1](#) Length: 1418 Number of Matches: 1

Range 1: 310 to 741 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
798 bits(432)	0.0	432/432(100%)	0/432(0%)	Plus/Minus
Query 8	CGCTTTCGAGCCTCAGCGTCAGTTACAAGCCAGAGAGCCGCTTCGCCACCGGTGTTCT	67		
Sbjct 741	CGCTTTCGAGCCTCAGCGTCAGTTACAAGCCAGAGAGCCGCTTCGCCACCGGTGTTCT	682		
Query 68	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	127		
Sbjct 681	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	622		
Query 128	GTTAAACAGTTTCCAAAGCGTACTATGGTTAAGCCACAGCCTTTAACTTCAGACTTATCT	187		
Sbjct 621	GTTAAACAGTTTCCAAAGCGTACTATGGTTAAGCCACAGCCTTTAACTTCAGACTTATCT	562		
Query 188	AACGCGCTGCGCTCGCTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	247		
Sbjct 561	AACGCGCTGCGCTCGCTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	502		
Query 248	CCGCGGCTGCTGGCAGTGTAGCCGTCCTTTCTGGTAAGATACCGTCACAGTGTGAA	307		
Sbjct 501	CCGCGGCTGCTGGCAGTGTAGCCGTCCTTTCTGGTAAGATACCGTCACAGTGTGAA	442		
Query 308	CTTTCCACTCTCACACTCGTTCTTCTTCAACAGAGCTTTACGATCCGAAACCTTCT	367		
Sbjct 441	CTTTCCACTCTCACACTCGTTCTTCTTCAACAGAGCTTTACGATCCGAAACCTTCT	382		
Query 368	TCACTCACGCGGCTTGTCTGGTCAGACTTCGGTCCATTGCCGAAGATTCCCTACTGCTG	427		
Sbjct 381	TCACTCACGCGGCTTGTCTGGTCAGACTTCGGTCCATTGCCGAAGATTCCCTACTGCTG	502		
Query 428	CCTCCCGTAGGA	439		
Sbjct 321	CCTCCCGTAGGA	310		

Streptococcus pseudopneumoniae strain 3203 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT613549.1](#) Length: 1435 Number of Matches: 1

Range 1: 297 to 728 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
798 bits(432)	0.0	432/432(100%)	0/432(0%)	Plus/Minus
Query 8	CGCTTTCGAGCCTCAGCGTCAGTTACAAGCCAGAGAGCCGCTTCGCCACCGGTGTTCT	67		
Sbjct 728	CGCTTTCGAGCCTCAGCGTCAGTTACAAGCCAGAGAGCCGCTTCGCCACCGGTGTTCT	669		
Query 68	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	127		
Sbjct 668	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	609		
Query 128	GTTAAACAGTTTCCAAAGCGTACTATGGTTAAGCCACAGCCTTTAACTTCAGACTTATCT	187		
Sbjct 608	GTTAAACAGTTTCCAAAGCGTACTATGGTTAAGCCACAGCCTTTAACTTCAGACTTATCT	549		
Query 188	AACGCGCTGCGCTCGCTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	247		
Sbjct 548	AACGCGCTGCGCTCGCTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	489		
Query 248	CCGCGGCTGCTGGCAGTGTAGCCGTCCTTTCTGGTAAGATACCGTCACAGTGTGAA	307		
Sbjct 488	CCGCGGCTGCTGGCAGTGTAGCCGTCCTTTCTGGTAAGATACCGTCACAGTGTGAA	429		
Query 308	CTTTCCACTCTCACACTCGTTCTTCTTCAACAGAGCTTTACGATCCGAAACCTTCT	367		
Sbjct 428	CTTTCCACTCTCACACTCGTTCTTCTTCAACAGAGCTTTACGATCCGAAACCTTCT	369		
Query 368	TCACTCACGCGGCTTGTCTGGTCAGACTTCGGTCCATTGCCGAAGATTCCCTACTGCTG	427		
Sbjct 368	TCACTCACGCGGCTTGTCTGGTCAGACTTCGGTCCATTGCCGAAGATTCCCTACTGCTG	309		
Query 428	CCTCCCGTAGGA	439		
Sbjct 308	CCTCCCGTAGGA	297		

Streptococcus oralis subsp. tigurinus strain 2620 16S ribosomal RNA gene, partial sequenceSequence ID: [MT611642.1](#) Length: 1457 Number of Matches: 1Range 1: 312 to 743 [GenBank](#) [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
798 bits(432)	0.0	432/432(100%)	0/432(0%)	Plus/Minus
Query 8	CGCTTTGAGCCTCAGCGTCAGTTACAAGCCAGAGAGCCGCTTTCGCCACCGGTGTTCT	67		
Sbjct 743	CGCTTTGAGCCTCAGCGTCAGTTACAAGCCAGAGAGCCGCTTTCGCCACCGGTGTTCT	684		
Query 68	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	127		
Sbjct 683	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	624		
Query 128	GTTAAACAGTTTCCAAGCGTACTATGGTTAAGCCACAGCCTTTAACTTCAGACTTATCT	187		
Sbjct 623	GTTAAACAGTTTCCAAGCGTACTATGGTTAAGCCACAGCCTTTAACTTCAGACTTATCT	564		
Query 188	AACCGCCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	247		
Sbjct 563	AACCGCCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	584		
Query 248	CCGCGGCTGCTGGCAGTAGTTAGCGTCCCTTTCTGGTAAGATACCGTCACAGTGTGAA	307		
Sbjct 503	CCGCGGCTGCTGGCAGTAGTTAGCGTCCCTTTCTGGTAAGATACCGTCACAGTGTGAA	444		
Query 308	CTTTCACCTCTCACACTCGTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCT	367		
Sbjct 443	CTTTCACCTCTCACACTCGTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCT	384		
Query 368	TCACTCACGCGGCGTTGCTCGGTACAGCTTCGGTCCATTGCCGAAGATTCCCTACTGCTG	427		
Sbjct 383	TCACTCACGCGGCGTTGCTCGGTACAGCTTCGGTCCATTGCCGAAGATTCCCTACTGCTG	324		
Query 428	CCTCCCGTAGGA	439		
Sbjct 323	CCTCCCGTAGGA	312		

Streptococcus mitis strain 582 16S ribosomal RNA gene, partial sequenceSequence ID: [MT573139.1](#) Length: 1413 Number of Matches: 1Range 1: 287 to 718 [GenBank](#) [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
798 bits(432)	0.0	432/432(100%)	0/432(0%)	Plus/Minus
Query 8	CGCTTTGAGCCTCAGCGTCAGTTACAAGCCAGAGAGCCGCTTTCGCCACCGGTGTTCT	67		
Sbjct 718	CGCTTTGAGCCTCAGCGTCAGTTACAAGCCAGAGAGCCGCTTTCGCCACCGGTGTTCT	659		
Query 68	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	127		
Sbjct 658	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	599		
Query 128	GTTAAACAGTTTCCAAGCGTACTATGGTTAAGCCACAGCCTTTAACTTCAGACTTATCT	187		
Sbjct 598	GTTAAACAGTTTCCAAGCGTACTATGGTTAAGCCACAGCCTTTAACTTCAGACTTATCT	539		
Query 188	AACCGCCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	247		
Sbjct 538	AACCGCCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	479		
Query 248	CCGCGGCTGCTGGCAGTAGTTAGCGTCCCTTTCTGGTAAGATACCGTCACAGTGTGAA	307		
Sbjct 478	CCGCGGCTGCTGGCAGTAGTTAGCGTCCCTTTCTGGTAAGATACCGTCACAGTGTGAA	419		
Query 308	CTTTCACCTCTCACACTCGTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCT	367		
Sbjct 418	CTTTCACCTCTCACACTCGTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCT	359		
Query 368	TCACTCACGCGGCGTTGCTCGGTACAGCTTCGGTCCATTGCCGAAGATTCCCTACTGCTG	427		
Sbjct 358	TCACTCACGCGGCGTTGCTCGGTACAGCTTCGGTCCATTGCCGAAGATTCCCTACTGCTG	299		
Query 428	CCTCCCGTAGGA	439		
Sbjct 298	CCTCCCGTAGGA	287		

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise ☐ CDS feature [Restore default](#)

4 sequences selected

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Streptococcus infantis strain 1795 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT626073.1](#) Length: 1418 Number of Matches: 1

Range 1: 500 to 777 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
514 bits(278)	1e-141	278/278(100%)	0/278(0%)	Plus/Plus
Query 7	GGTAATACGTAGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGG	66		
Sbjct 500	GGTAATACGTAGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGG	559		
Query 67	TTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTA	126		
Sbjct 560	TTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTA	619		
Query 127	ACTTGAGTGCAAGAGGGGAGAGTGGAAATCCATGTGTAGCGGTGAAATGCGTAGATATAT	186		
Sbjct 620	ACTTGAGTGCAAGAGGGGAGAGTGGAAATCCATGTGTAGCGGTGAAATGCGTAGATATAT	679		
Query 187	GGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACGTACGCTGAGGCTCGAAAG	246		
Sbjct 680	GGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACGTACGCTGAGGCTCGAAAG	739		
Query 247	CGTGGGGAGCAACAGGATTAGATACCCCTGGTAGTCCA	284		
Sbjct 740	CGTGGGGAGCAACAGGATTAGATACCCCTGGTAGTCCA	777		

Streptococcus pseudopneumoniae strain 3203 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT613549.1](#) Length: 1435 Number of Matches: 1

Range 1: 487 to 764 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
514 bits(278)	1e-141	278/278(100%)	0/278(0%)	Plus/Plus
Query 7	GGTAATACGTAGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGG	66		
Sbjct 487	GGTAATACGTAGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGG	546		
Query 67	TTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTA	126		
Sbjct 547	TTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTA	606		
Query 127	ACTTGAGTGCAAGAGGGGAGAGTGGAAATCCATGTGTAGCGGTGAAATGCGTAGATATAT	186		
Sbjct 607	ACTTGAGTGCAAGAGGGGAGAGTGGAAATCCATGTGTAGCGGTGAAATGCGTAGATATAT	666		
Query 187	GGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACGTACGCTGAGGCTCGAAAG	246		
Sbjct 667	GGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACGTACGCTGAGGCTCGAAAG	726		
Query 247	CGTGGGGAGCAACAGGATTAGATACCCCTGGTAGTCCA	284		
Sbjct 727	CGTGGGGAGCAACAGGATTAGATACCCCTGGTAGTCCA	764		

Streptococcus oralis subsp. tigurinus strain 2620 16S ribosomal RNA gene, partial sequenceSequence ID: [MT611642.1](#) Length: 1457 Number of Matches: 1Range 1: 502 to 779 [GenBank](#) [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
514 bits(278)	1e-141	278/278(100%)	0/278(0%)	Plus/Plus
Query 7	GGTAATACGTAGGTC	CGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGG	66	
Sbjct 502	GGTAATACGTAGGTC	CGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGG	561	
Query 67	TTAGATAAGTCTGAAGT	TAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTA	126	
Sbjct 562	TTAGATAAGTCTGAAGT	TAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTA	621	
Query 127	ACTTGAGTGCAAGAGGGG	GAGTGAATTCCATGTGTAGCGGTGAAATGCGTAGATATAT	186	
Sbjct 622	ACTTGAGTGCAAGAGGGG	GAGTGAATTCCATGTGTAGCGGTGAAATGCGTAGATATAT	681	
Query 187	GGAGGAACACCGGTGGC	GAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAG	246	
Sbjct 682	GGAGGAACACCGGTGGC	GAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAG	741	
Query 247	CGTGGGGAGCAAAACAGG	ATTAGATACCCTGGTAGTCCA	284	
Sbjct 742	CGTGGGGAGCAAAACAGG	ATTAGATACCCTGGTAGTCCA	779	

Streptococcus mitis strain 582 16S ribosomal RNA gene, partial sequenceSequence ID: [MT573139.1](#) Length: 1413 Number of Matches: 1Range 1: 477 to 754 [GenBank](#) [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
514 bits(278)	1e-141	278/278(100%)	0/278(0%)	Plus/Plus
Query 7	GGTAATACGTAGGTC	CGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGG	66	
Sbjct 477	GGTAATACGTAGGTC	CGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGG	536	
Query 67	TTAGATAAGTCTGAAGT	TAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTA	126	
Sbjct 537	TTAGATAAGTCTGAAGT	TAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTA	596	
Query 127	ACTTGAGTGCAAGAGGGG	GAGTGAATTCCATGTGTAGCGGTGAAATGCGTAGATATAT	186	
Sbjct 597	ACTTGAGTGCAAGAGGGG	GAGTGAATTCCATGTGTAGCGGTGAAATGCGTAGATATAT	656	
Query 187	GGAGGAACACCGGTGGC	GAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAG	246	
Sbjct 657	GGAGGAACACCGGTGGC	GAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAG	716	
Query 247	CGTGGGGAGCAAAACAGG	ATTAGATACCCTGGTAGTCCA	284	
Sbjct 717	CGTGGGGAGCAAAACAGG	ATTAGATACCCTGGTAGTCCA	754	

Descriptions [Graphic Summary](#) **Alignments** [Taxonomy](#)Alignment view [Pairwise](#)☐ CDS feature[Restore defaults](#)

6 sequences selected

[Download](#) [GenBank](#) [Graphics](#)**Streptococcus pneumoniae strain Nghean-Sp936-15A 16S ribosomal RNA gene, partial sequence**Sequence ID: [MZ007499.1](#) Length: 1419 Number of Matches: 1Range 1: 326 to 390 [GenBank](#) [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand	
110 bits(59)	1e-20	64/66(97%)	2/66(3%)	Plus/Plus	
Query 1	GACGGAA-TCTGAACCGAGCAACGC	CGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCT	59		
Sbjct 326	GACGGAAAGTCTG-ACC	GAGCAACGC	CGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCT	384	
Query 60	CTGTTG	65			
Sbjct 385	CTGTTG	390			

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise ☐ CDS feature [Restore defaults](#)

7 sequences selected

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Streptococcus pneumoniae strain Nghean-Sp911-23F 16S ribosomal RNA gene, partial sequence
Sequence ID: [MZ007497.1](#) Length: 1415 Number of Matches: 1

Range 1: 336 to 387 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
97.1 bits(52)	6e-17	52/52(100%)	0/52(0%)	Plus/Plus

Query 1 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 52
Sbjct 336 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 387

[Download](#) [GenBank](#) [Graphics](#)

Streptococcus sp. strain L0023-03 16S ribosomal RNA gene, partial sequence
Sequence ID: [MW866505.1](#) Length: 1545 Number of Matches: 1

Range 1: 393 to 444 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
97.1 bits(52)	6e-17	52/52(100%)	0/52(0%)	Plus/Plus

Query 1 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 52
Sbjct 393 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 444

Streptococcus gordonii strain KCOM 3746 (=ChDC P030-Aa1) 16S ribosomal RNA gene, partial sequence
Sequence ID: [MW581916.1](#) Length: 1479 Number of Matches: 1

Range 1: 377 to 428 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
97.1 bits(52)	6e-17	52/52(100%)	0/52(0%)	Plus/Plus

Query 1 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 52
Sbjct 377 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 428

[Download](#) [GenBank](#) [Graphics](#) [Next](#)

Streptococcus intermedius strain KCOM 3731 (= JS595) 16S ribosomal RNA gene, partial sequence
Sequence ID: [MW581895.1](#) Length: 1478 Number of Matches: 1

Range 1: 377 to 428 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
97.1 bits(52)	6e-17	52/52(100%)	0/52(0%)	Plus/Plus

Query 1 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 52
Sbjct 377 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 428

Streptococcus mutans strain SCF35 16S ribosomal RNA gene, partial sequence
Sequence ID: [MW560204.1](#) Length: 1593 Number of Matches: 1

Range 1: 384 to 435 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
97.1 bits(52)	6e-17	52/52(100%)	0/52(0%)	Plus/Plus

Query 1 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 52
Sbjct 384 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 435

Streptococcus sanguinis strain KCOM 3727 (= JS591) 16S ribosomal RNA gene, partial sequence
Sequence ID: [MW581858.1](#) Length: 1469 Number of Matches: 1

Range 1: 369 to 420 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
97.1 bits(52)	6e-17	52/52(100%)	0/52(0%)	Plus/Plus

Query 1 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 52
Sbjct 369 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 420

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Streptococcus salivarius strain SCF59 16S ribosomal RNA gene, partial sequence
Sequence ID: [MW560212.1](#) Length: 1489 Number of Matches: 1

Range 1: 379 to 430 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
97.1 bits(52)	6e-17	52/52(100%)	0/52(0%)	Plus/Plus

Query 1 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 52
Sbjct 379 CCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTG 430

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view ☐ CDS feature [Restore default](#)

5 sequences selected

[Download](#) [GenBank](#) [Graphics](#)

Streptococcus infantis strain 1795 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT626073.1](#) Length: 1418 Number of Matches: 1

Range 1: 310 to 740 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
791 bits(428)	0.0	431/432(99%)	1/432(0%)	Plus/Minus

Query 7 GCTTTGAGCCTCAGCGTCAGTTACAAGACCAAGAGCCGCTTCGCCACCGGTGTTCTCT 66
Sbjct 740 GCTTTGAGCCTCAGCGTCAGTTACAAG-CCAGAGAGCCGCTTCGCCACCGGTGTTCTCT 682

Query 67 CCATATATCTACGCATTTACCGCTACATGGAATTCCTCTCCCCCTCTTGCACTCAA 126
Sbjct 681 CCATATATCTACGCATTTACCGCTACATGGAATTCCTCTCCCCCTCTTGCACTCAA 622

Query 127 GTTAAACAGTTTCAAAGCGTACTATGGTTAAGCACAGCCTTAACTTCAGACTTATCT 186
Sbjct 621 GTTAAACAGTTTCAAAGCGTACTATGGTTAAGCACAGCCTTAACTTCAGACTTATCT 562

Query 187 AACCGCCTGCGCTCGCTTACGCCCAATAATCCGGACAACGCTCGGGACCTACGTATTA 246
Sbjct 561 AACCGCCTGCGCTCGCTTACGCCCAATAATCCGGACAACGCTCGGGACCTACGTATTA 502

Query 247 CCGGGGCTGCTGGCAGTAGTTAGCCGTCCTTTCTGGTAAGATACCGTCACAGTGTGAA 306
Sbjct 501 CCGGGGCTGCTGGCAGTAGTTAGCCGTCCTTTCTGGTAAGATACCGTCACAGTGTGAA 442

Query 307 CTTTCCACTCTCACACTGCTTCTTCTTACAACAGAGCTTTACGATCCGAAAACCTTCT 366
Sbjct 441 CTTTCCACTCTCACACTGCTTCTTCTTACAACAGAGCTTTACGATCCGAAAACCTTCT 382

Query 367 TCACTCACGCGGCTTGCTCGGTACAGCTTCGTCATTGCCGAAGATTCCCTACTGCTG 426
Sbjct 381 TCACTCACGCGGCTTGCTCGGTACAGCTTCGTCATTGCCGAAGATTCCCTACTGCTG 322

Query 427 CCTCCCGTAGGA 438
Sbjct 321 CCTCCCGTAGGA 310

Streptococcus pseudopneumoniae strain 3203 16S ribosomal RNA gene, partial sequence

Sequence ID: [MT613549.1](#) Length: 1435 Number of Matches: 1

Range 1: 297 to 727 [GenBank](#) [Graphics](#)

[Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
791 bits(428)	0.0	431/432(99%)	1/432(0%)	Plus/Minus
Query 7	GCTTTCGAGCCTCAGCGTCAGTTACAAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCTCT	66		
Sbjct 727	GCTTTCGAGCCTCAGCGTCAGTTACAAG-CCAGAGAGCCGCTTTCGCCACCGGTGTTCTCT	669		
Query 67	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	126		
Sbjct 668	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	689		
Query 127	GTTAAACAGTTTCCAAAGCGTACTATGGTTAAGCCACAGCCTTTAACTTCAGACTTATCT	186		
Sbjct 608	GTTAAACAGTTTCCAAAGCGTACTATGGTTAAGCCACAGCCTTTAACTTCAGACTTATCT	549		
Query 187	AACCGCCTGCGCTCGCTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	246		
Sbjct 548	AACCGCCTGCGCTCGCTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	489		
Query 247	CCGCGGCTGCTGGCAGTAGTTAGCCGTCCTTTCTGGTAAGATACCGTCACAGTGTGAA	306		
Sbjct 488	CCGCGGCTGCTGGCAGTAGTTAGCCGTCCTTTCTGGTAAGATACCGTCACAGTGTGAA	429		
Query 307	CTTTCACCTCTCACACTCGTTCTTCTTTACAACAGAGCTTTACGATCCGAAAACCTTCT	366		
Sbjct 428	CTTTCACCTCTCACACTCGTTCTTCTTTACAACAGAGCTTTACGATCCGAAAACCTTCT	369		
Query 367	TCACTCACGCGGCGTTGCTCGGTGAGACTTCCGTCATTGCGGAAGATTCCCTACTGCTG	426		
Sbjct 368	TCACTCACGCGGCGTTGCTCGGTGAGACTTCCGTCATTGCGGAAGATTCCCTACTGCTG	389		
Query 427	CCTCCCGTAGGA	438		
Sbjct 308	CCTCCCGTAGGA	297		

Streptococcus mitis strain 582 16S ribosomal RNA gene, partial sequence

Sequence ID: [MT573139.1](#) Length: 1413 Number of Matches: 1

Range 1: 287 to 717 [GenBank](#) [Graphics](#)

[Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
791 bits(428)	0.0	431/432(99%)	1/432(0%)	Plus/Minus
Query 7	GCTTTCGAGCCTCAGCGTCAGTTACAAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCTCT	66		
Sbjct 717	GCTTTCGAGCCTCAGCGTCAGTTACAAG-CCAGAGAGCCGCTTTCGCCACCGGTGTTCTCT	659		
Query 67	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	126		
Sbjct 658	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	599		
Query 127	GTTAAACAGTTTCCAAAGCGTACTATGGTTAAGCCACAGCCTTTAACTTCAGACTTATCT	186		
Sbjct 598	GTTAAACAGTTTCCAAAGCGTACTATGGTTAAGCCACAGCCTTTAACTTCAGACTTATCT	539		
Query 187	AACCGCCTGCGCTCGCTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	246		
Sbjct 538	AACCGCCTGCGCTCGCTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	479		
Query 247	CCGCGGCTGCTGGCAGTAGTTAGCCGTCCTTTCTGGTAAGATACCGTCACAGTGTGAA	306		
Sbjct 478	CCGCGGCTGCTGGCAGTAGTTAGCCGTCCTTTCTGGTAAGATACCGTCACAGTGTGAA	419		
Query 307	CTTTCACCTCTCACACTCGTTCTTCTTTACAACAGAGCTTTACGATCCGAAAACCTTCT	366		
Sbjct 418	CTTTCACCTCTCACACTCGTTCTTCTTTACAACAGAGCTTTACGATCCGAAAACCTTCT	359		
Query 367	TCACTCACGCGGCGTTGCTCGGTGAGACTTCCGTCATTGCGGAAGATTCCCTACTGCTG	426		
Sbjct 358	TCACTCACGCGGCGTTGCTCGGTGAGACTTCCGTCATTGCGGAAGATTCCCTACTGCTG	299		
Query 427	CCTCCCGTAGGA	438		
Sbjct 298	CCTCCCGTAGGA	287		

Streptococcus anginosus subsp. whileyi partial 16S rRNA geneSequence ID: [LR761334.1](#) Length: 1082 Number of Matches: 1Range 1: 286 to 716 [GenBank](#) [Graphics](#)[Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
791 bits(428)	0.0	431/432(99%)	1/432(0%)	Plus/Minus
Query 7	GCTTTCGAGCCTCAGCGTCAGTTACAAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCTCT	66		
Sbjct 716	GCTTTCGAGCCTCAGCGTCAGTTACAAG-CCAGAGAGCCGCTTTCGCCACCGGTGTTCTCT	658		
Query 67	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	126		
Sbjct 657	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	598		
Query 127	GTTAAACAGTTTCCAAGCGTACTATGGTTAAGCCACAGCCTTTAATTTCAGACTTATCT	186		
Sbjct 597	GTTAAACAGTTTCCAAGCGTACTATGGTTAAGCCACAGCCTTTAATTTCAGACTTATCT	538		
Query 187	AACCGCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	246		
Sbjct 537	AACCGCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	478		
Query 247	CCGCGGCTGCTGGCACGTAGTTAGCCGTCCCTTTCTGGTAAGATACCGTCACAGTGTGAA	306		
Sbjct 477	CCGCGGCTGCTGGCACGTAGTTAGCCGTCCCTTTCTGGTAAGATACCGTCACAGTGTGAA	418		
Query 307	CTTTCCACTCTCACACTCGTTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCT	366		
Sbjct 417	CTTTCCACTCTCACACTCGTTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCT	358		
Query 367	TCACTCACGCGGCGTTGCTCGGTCAGACTTCGGTCCATTGCCGAAGATTCCCTACTGCTG	426		
Sbjct 357	TCACTCACGCGGCGTTGCTCGGTCAGACTTCGGTCCATTGCCGAAGATTCCCTACTGCTG	298		
Query 427	CCTCCCGTAGGA	438		
Sbjct 297	CCTCCCGTAGGA	286		

Streptococcus oralis strain KCOM 2384 (= ChDC PY-F102) 16S ribosomal RNA gene, partial sequenceSequence ID: [MT658570.1](#) Length: 1471 Number of Matches: 1Range 1: 319 to 749 [GenBank](#) [Graphics](#)[Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
791 bits(428)	0.0	431/432(99%)	1/432(0%)	Plus/Minus
Query 7	GCTTTCGAGCCTCAGCGTCAGTTACAAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCTCT	66		
Sbjct 749	GCTTTCGAGCCTCAGCGTCAGTTACAAG-CCAGAGAGCCGCTTTCGCCACCGGTGTTCTCT	691		
Query 67	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	126		
Sbjct 690	CCATATATCTACGCATTTACCGCTACACATGGAATTCACCTCTCCCTCTTGCACTCAA	631		
Query 127	GTTAAACAGTTTCCAAGCGTACTATGGTTAAGCCACAGCCTTTAATTTCAGACTTATCT	186		
Sbjct 630	GTTAAACAGTTTCCAAGCGTACTATGGTTAAGCCACAGCCTTTAATTTCAGACTTATCT	571		
Query 187	AACCGCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	246		
Sbjct 570	AACCGCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTA	511		
Query 247	CCGCGGCTGCTGGCACGTAGTTAGCCGTCCCTTTCTGGTAAGATACCGTCACAGTGTGAA	306		
Sbjct 510	CCGCGGCTGCTGGCACGTAGTTAGCCGTCCCTTTCTGGTAAGATACCGTCACAGTGTGAA	451		
Query 307	CTTTCCACTCTCACACTCGTTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCT	366		
Sbjct 450	CTTTCCACTCTCACACTCGTTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCT	391		
Query 367	TCACTCACGCGGCGTTGCTCGGTCAGACTTCGGTCCATTGCCGAAGATTCCCTACTGCTG	426		
Sbjct 390	TCACTCACGCGGCGTTGCTCGGTCAGACTTCGGTCCATTGCCGAAGATTCCCTACTGCTG	331		
Query 427	CCTCCCGTAGGA	438		
Sbjct 330	CCTCCCGTAGGA	319		

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise ☐ CDS feature [Restore defaults](#)

4 sequences selected [?](#)

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Streptococcus infantis strain 1795 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT626073.1](#) Length: 1418 Number of Matches: 1

Range 1: 500 to 777 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
508 bits(275)	7e-140	278/279(99%)	1/279(0%)	Plus/Plus
Query 5	GGTAATACGTAGGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGACCGCAGGCG	64		
Sbjct 500	GGTAATACGTA-GGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCG	558		
Query 65	GTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTT	124		
Sbjct 559	GTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTT	618		
Query 125	AAC TTGAGTGCAAGAGGGGAGAGTGGAAATCCATGTGTAGCGGTGAAATGCGTAGATATA	184		
Sbjct 619	AAC TTGAGTGCAAGAGGGGAGAGTGGAAATCCATGTGTAGCGGTGAAATGCGTAGATATA	678		
Query 185	TGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAA	244		
Sbjct 679	TGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAA	738		
Query 245	GCGTGGGGAGCAACAGGATTAGATACCCTGGTAGTCCA	283		
Sbjct 739	GCGTGGGGAGCAACAGGATTAGATACCCTGGTAGTCCA	777		

Streptococcus pseudopneumoniae strain 3203 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT613549.1](#) Length: 1435 Number of Matches: 1

Range 1: 487 to 764 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
508 bits(275)	7e-140	278/279(99%)	1/279(0%)	Plus/Plus
Query 5	GGTAATACGTAGGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGACCGCAGGCG	64		
Sbjct 487	GGTAATACGTA-GGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGACCGCAGGCG	545		
Query 65	GTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTT	124		
Sbjct 546	GTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTT	605		
Query 125	AAC TTGAGTGCAAGAGGGGAGAGTGGAAATCCATGTGTAGCGGTGAAATGCGTAGATATA	184		
Sbjct 606	AAC TTGAGTGCAAGAGGGGAGAGTGGAAATCCATGTGTAGCGGTGAAATGCGTAGATATA	665		
Query 185	TGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAA	244		
Sbjct 666	TGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAA	725		
Query 245	GCGTGGGGAGCAACAGGATTAGATACCCTGGTAGTCCA	283		
Sbjct 726	GCGTGGGGAGCAACAGGATTAGATACCCTGGTAGTCCA	764		

Streptococcus parasanguinis strain KCOM_2503 (= ChDC F238) 16S ribosomal RNA gene, partial sequence
Sequence ID: [MT678580.1](#) Length: 1470 Number of Matches: 1

Range 1: 356 to 420 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
110 bits(59)	1e-20	64/66(97%)	2/66(3%)	Plus/Plus
Query 1	GACGGAA-TCTGAACCGAGCAACGCCGCTGAGTGAAGAAGGTTTTCGGATCGTAAAGCT	59		
Sbjct 356	GACGGAAAGTCTG-ACCGAGCAACGCCGCTGAGTGAAGAAGGTTTTCGGATCGTAAAGCT	414		
Query 60	CTGTTG 65			
Sbjct 415	CTGTTG 420			

Streptococcus mitis strain 582 16S ribosomal RNA gene, partial sequenceSequence ID: [MT573139.1](#) Length: 1413 Number of Matches: 1Range 1: 477 to 754 [GenBank](#) [Graphics](#)[Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
508 bits(275)	7e-140	278/279(99%)	1/279(0%)	Plus/Plus
Query 5	GGTAATACGTAGGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCG	64		
Sbjct 477	GGTAATACGTA-GGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCG	535		
Query 65	GTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTT	124		
Sbjct 536	GTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTT	595		
Query 125	AACTTGAGTGCAAGAGGGGAGAGTGAATTCCATGTGTAGCGGTGAAATGCGTAGATATA	184		
Sbjct 596	AACTTGAGTGCAAGAGGGGAGAGTGAATTCCATGTGTAGCGGTGAAATGCGTAGATATA	655		
Query 185	TGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGAACGACGCTGAGGCTCGAAA	244		
Sbjct 656	TGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGAACGACGCTGAGGCTCGAAA	715		
Query 245	GCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAGTCCA	283		
Sbjct 716	GCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAGTCCA	754		

Streptococcus oralis strain S63 16S ribosomal RNA gene, partial sequenceSequence ID: [MT535874.1](#) Length: 1280 Number of Matches: 1Range 1: 481 to 758 [GenBank](#) [Graphics](#)[Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
508 bits(275)	7e-140	278/279(99%)	1/279(0%)	Plus/Plus
Query 5	GGTAATACGTAGGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCG	64		
Sbjct 481	GGTAATACGTA-GGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCG	539		
Query 65	GTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTT	124		
Sbjct 540	GTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTT	599		
Query 125	AACTTGAGTGCAAGAGGGGAGAGTGAATTCCATGTGTAGCGGTGAAATGCGTAGATATA	184		
Sbjct 600	AACTTGAGTGCAAGAGGGGAGAGTGAATTCCATGTGTAGCGGTGAAATGCGTAGATATA	659		
Query 185	TGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGAACGACGCTGAGGCTCGAAA	244		
Sbjct 660	TGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGAACGACGCTGAGGCTCGAAA	719		
Query 245	GCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAGTCCA	283		
Sbjct 720	GCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAGTCCA	758		

Streptococcus cristatus strain KCOM 4021 (=ChDC P050-Tf7) 16S ribosomal RNA gene, partial sequence
Sequence ID: [MW730620.1](#) Length: 1468 Number of Matches: 1

Range 1: 354 to 418 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
110 bits(59)	1e-20	64/66(97%)	2/66(3%)	Plus/Plus

```

Query 1      GACGGAA-TCTGAACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCT 59
Sbjct 354    GACGGGAAGTCTG-ACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCT 412

Query 60      CTGTTG 65
Sbjct 413    CTGTTG 418

```

[Download](#) [GenBank](#) [Graphics](#) [Next](#)

Streptococcus oralis strain SCF06 16S ribosomal RNA gene, partial sequence
Sequence ID: [MW560192.1](#) Length: 1485 Number of Matches: 1

Range 1: 362 to 426 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
110 bits(59)	1e-20	64/66(97%)	2/66(3%)	Plus/Plus

```

Query 1      GACGGAA-TCTGAACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCT 59
Sbjct 362    GACGGGAAGTCTG-ACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCT 426

Query 60      CTGTTG 65
Sbjct 421    CTGTTG 426

```

Streptococcus infantis strain KCOM 3604 (=ChDC ETd5) 16S ribosomal RNA gene, partial sequence
Sequence ID: [MW548692.1](#) Length: 1471 Number of Matches: 1

Range 1: 356 to 420 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
110 bits(59)	1e-20	64/66(97%)	2/66(3%)	Plus/Plus

```

Query 1      GACGGAA-TCTGAACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCT 59
Sbjct 356    GACGGGAAGTCTG-ACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCT 414

Query 60      CTGTTG 65
Sbjct 415    CTGTTG 420

```

[Download](#) [GenBank](#) [Graphics](#)

Streptococcus agalactiae strain AHRA S33 16S ribosomal RNA gene, partial sequence
Sequence ID: [MW092091.1](#) Length: 935 Number of Matches: 1

Range 1: 340 to 404 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
110 bits(59)	1e-20	64/66(97%)	2/66(3%)	Plus/Plus

```

Query 1      GACGGAA-TCTGAACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCT 59
Sbjct 340    GACGGGAAGTCTG-ACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAGCT 398

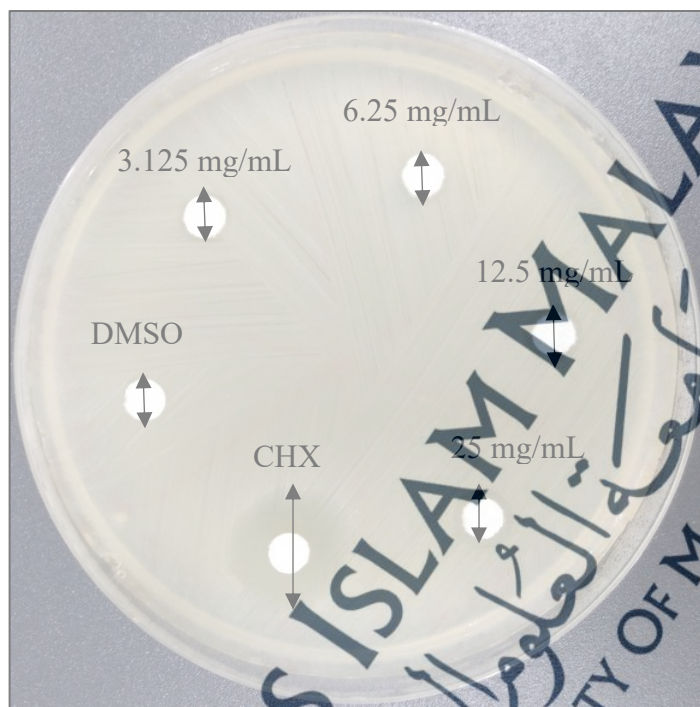
Query 60      CTGTTG 65
Sbjct 399    CTGTTG 404

```

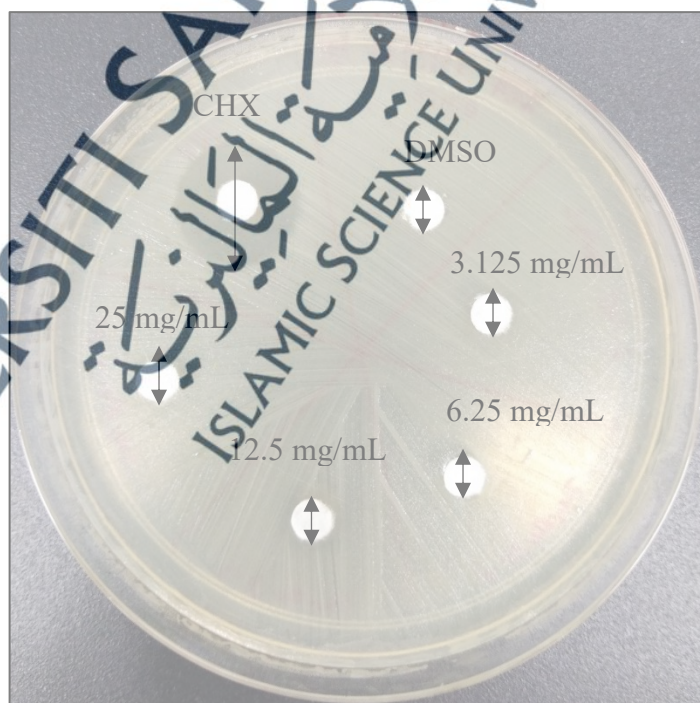
Sample 10

Appendix 2

Inhibition zone of *S. mutans* when exposed to SPSE after 24 hours.

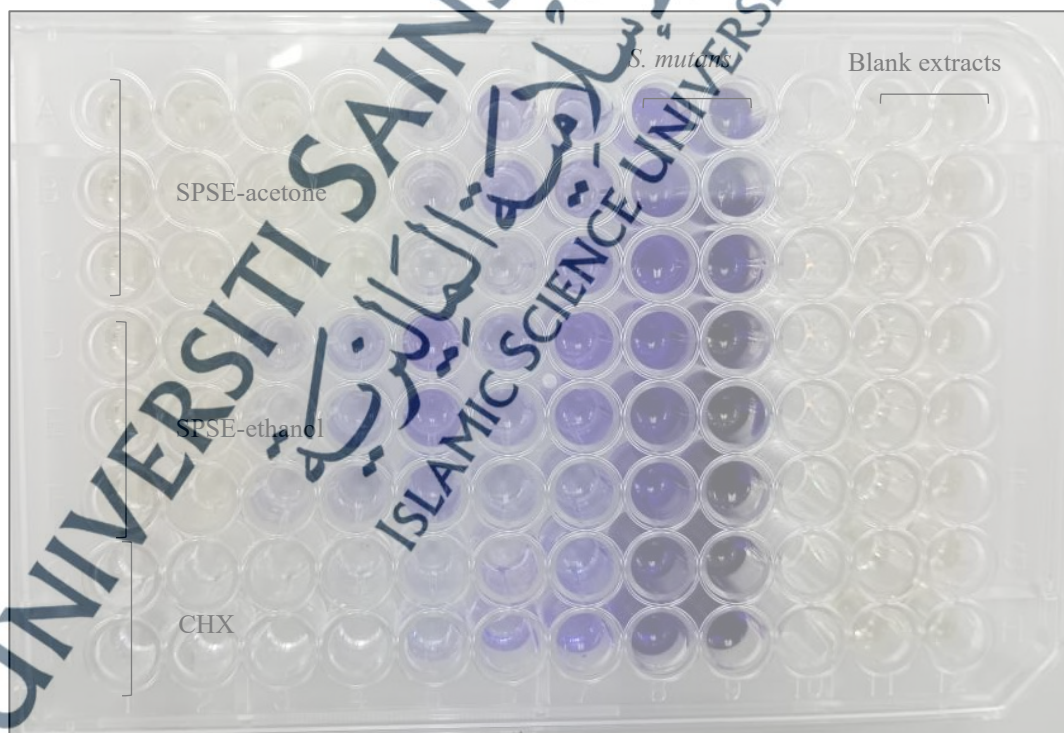
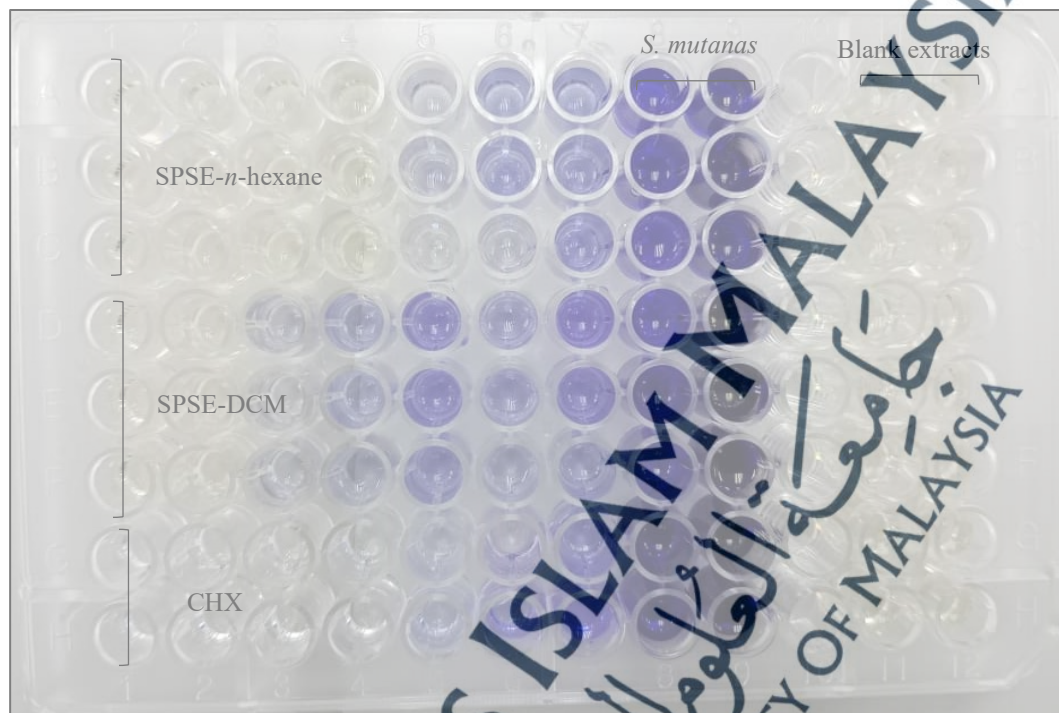


Inhibition zone of *P. gingivalis* when exposed to SPSE after 24 hours.

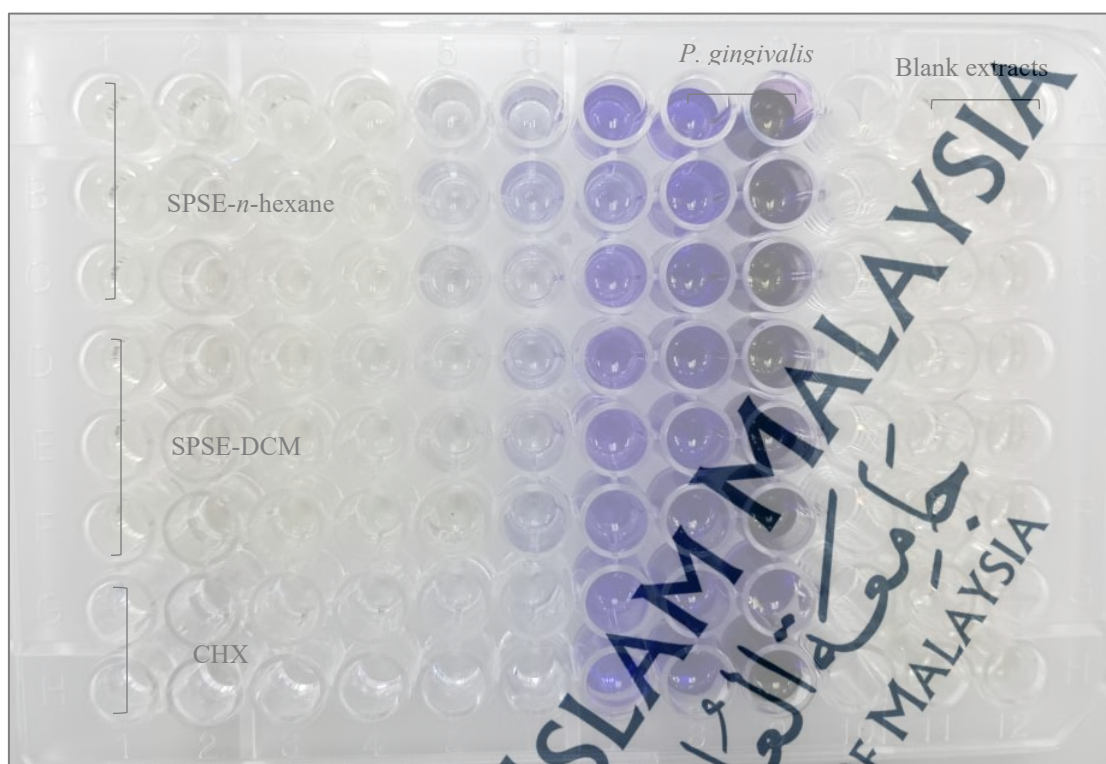


Appendix 3

Colour changes for MIC after adding MTT solutions into a 96-well plate.



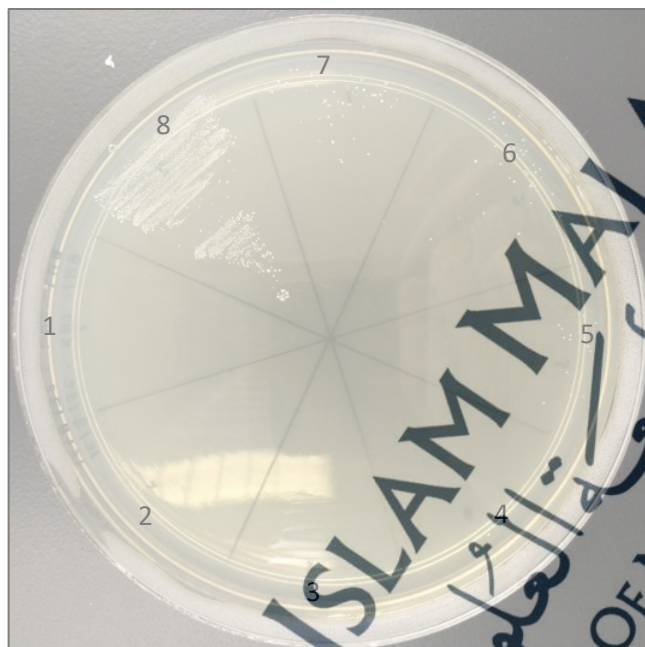
SPSE against *S. mutans*



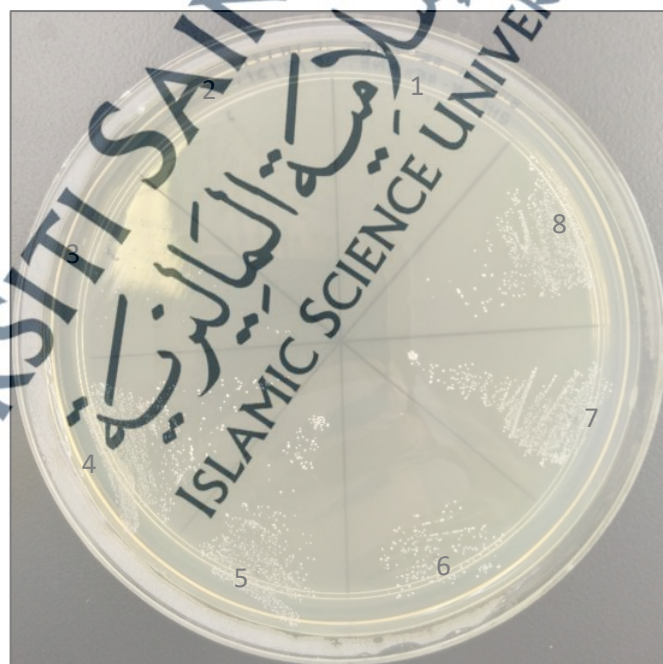
SPSE against *P. gingivalis*

Appendix 4

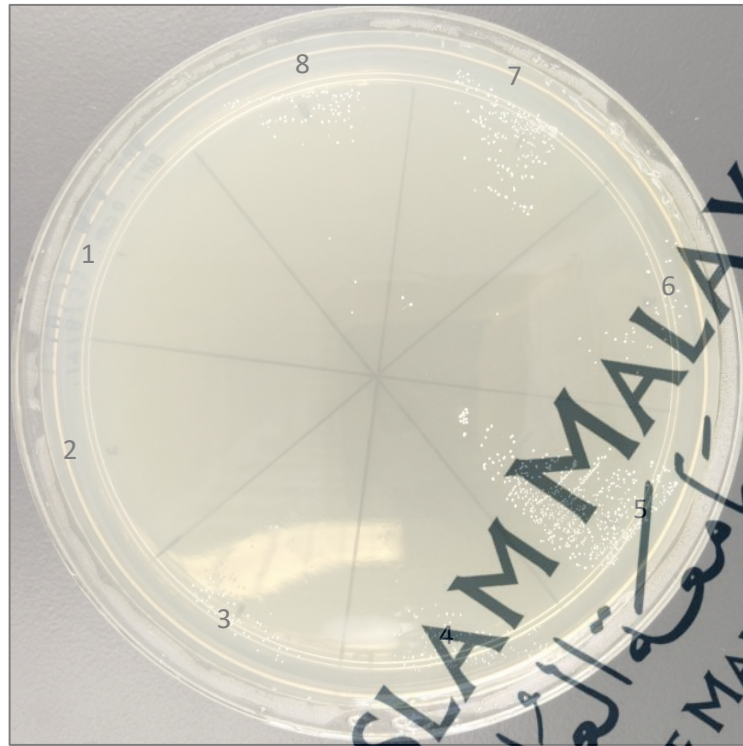
The growth colonies of *S. mutans* and *P. gingivalis* on BHI and WCA agar for MBC.



CHX against *S. mutans* after 24 hours



SPSE-*n*-hexane against *S. mutans* after 24 hours



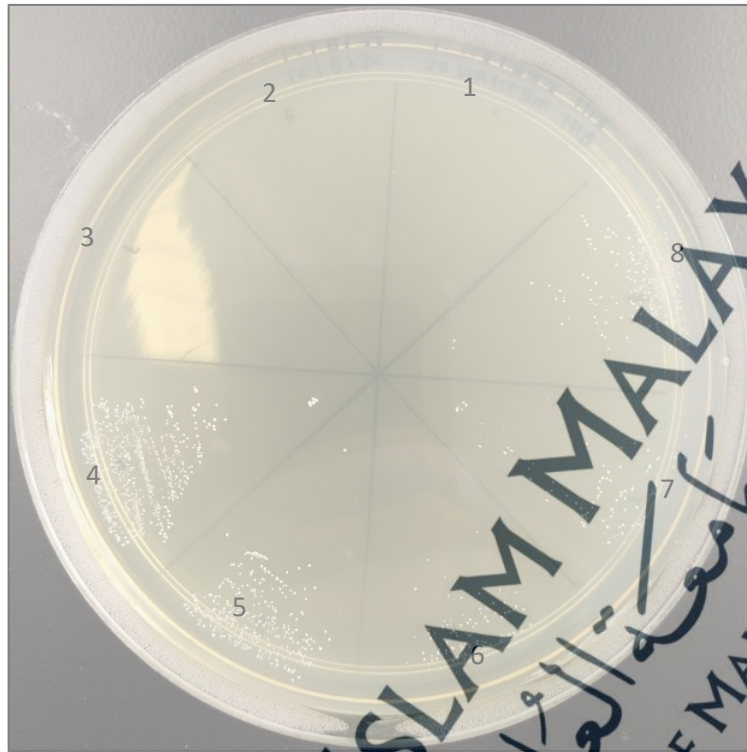
SPSE-DCM against *S. mutans* after 24 hours



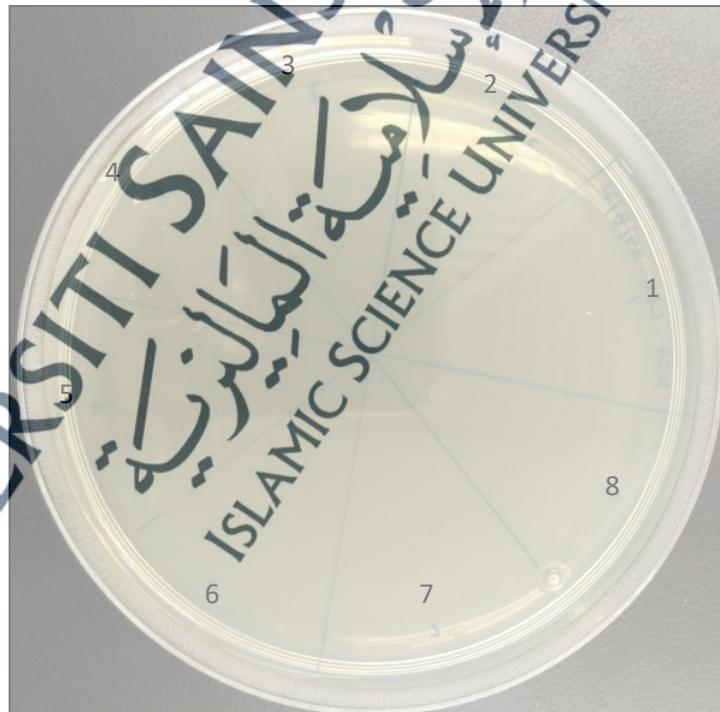
SPSE-acetone against *S. mutans* after 24 hours



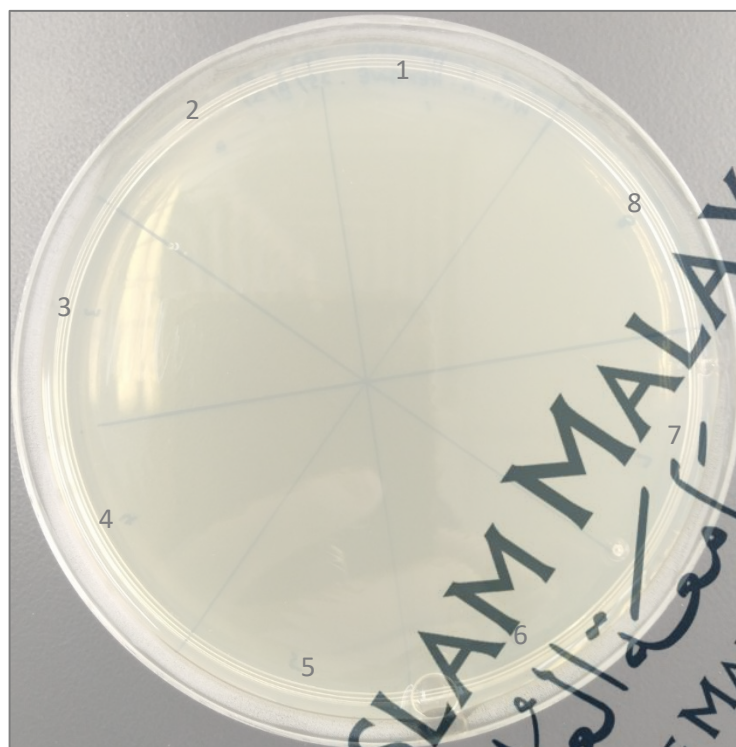
SPSE-ethanol against *S. mutans* after 24 hours



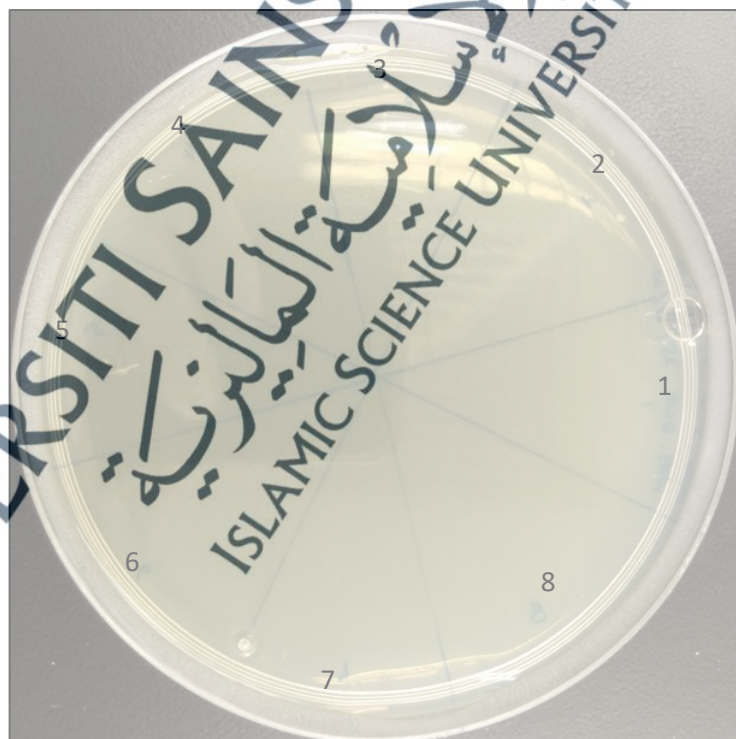
SPSE-methanol against *S. mutans* after 24 hours



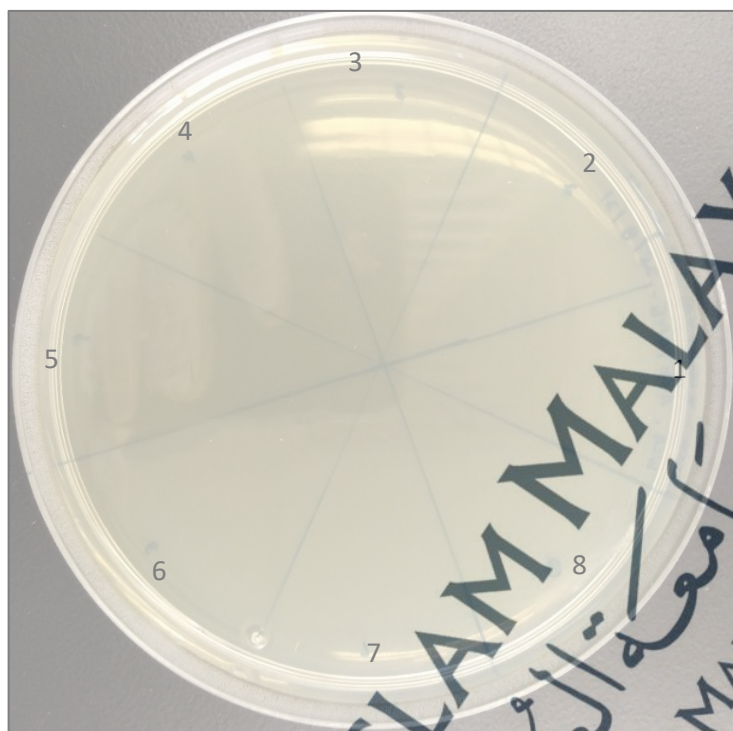
CHX against *P. gingivalis* after 24 hours



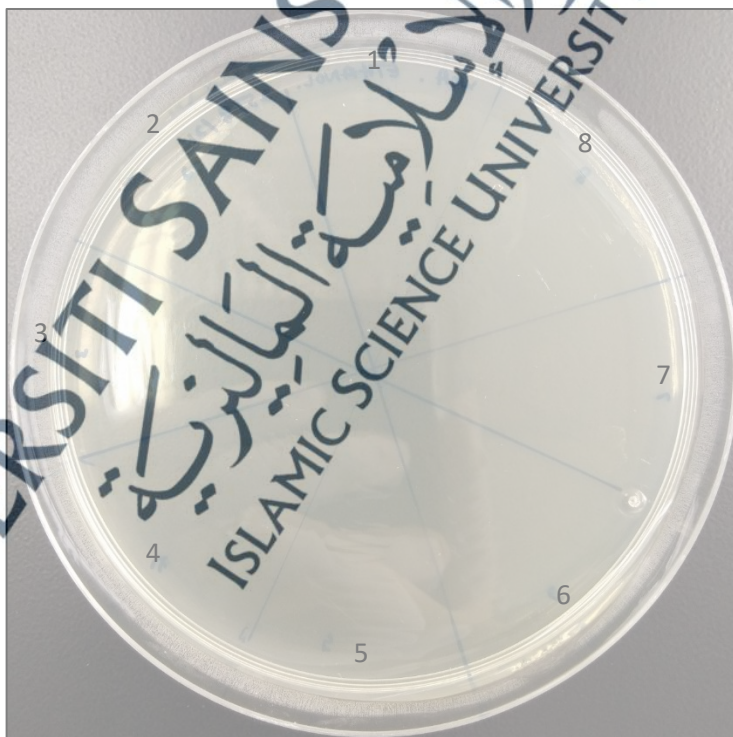
SPSE-*n*-hexane against *P. gingivalis* after 24 hours



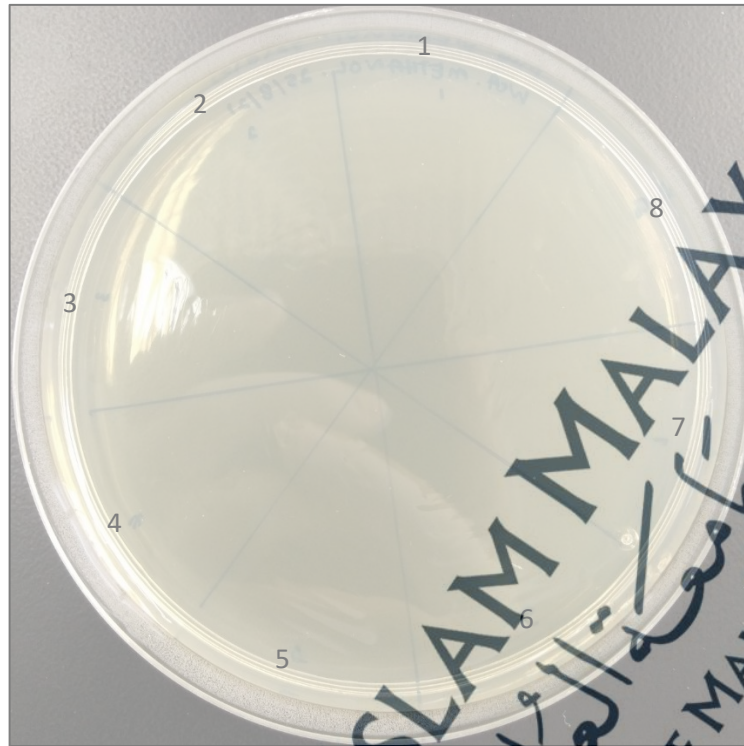
SPSE-DCM against *P. gingivalis* after 24 hours



SPSE-acetone against *P. gingivalis* after 24 hours



SPSE-ethanol against *P. gingivalis* after 24 hours



SPSE-methanol against *P. gingivalis* after 24 hours

Appendix 5

Conference.

International Conference on Drug Discovery and Translational Medicine 2021 (ICDDTM), December, 8-9, 2021 Online platform (Malaysia). Poster Presentation.

International Applied Biology Conference 2022 (IABC 2022), June, 3-5, 2022 Melaka (Malaysia). Poster Presentation.

Appendix 6

Publication.

Shahida Mohd. Said, Nur Fatimah Zaharah Salehuddin, Siti Nursyuhada Jafar, Haslinda Ramli, Tuti Ningseh Mohd. Dom & Rohazila Mohamad Hanafiah (2021). Identification of Bacteria Sample Plaque from Periodontal Disease Among Diabetic Patients, *International Journal of Research in Pharmaceutical Sciences*. Vol. 12 (1); p. 366-373. DOI: <https://doi.org/10.26452/ijrps.v12i1.4147>.

Universiti Putra Malaysia, Universiti Teknologi MARA, Universiti Sains Malaysia, UCSI University, MAHSA University, Taylor's University, University Malaya, Monash University Malaysia, Eman Biodiscoveries Sdn. Bhd., Malaysian Association for Cancer Research and GHHS Healthcare (2022). Antibacterial Activity of *Salvadora persica* Against *Porphyromonas gingivalis* And *Streptococcus mutans*, *Malaysian Journal of Medicine and Health Sciences*, Vol. 18 (1): p. 111.