

Description	Max score	Total score	Query cover	E value	Ident	Accession
Bacillus circulans strain NBRC 13626 16S ribosomal RNA gene, partial sequence	2248	2248	97%	0.0	94%	<a href="#">NR_112632.1</a>
Bacillus fengquiensis strain NPK15 16S ribosomal RNA, partial sequence	2246	2246	97%	0.0	94%	<a href="#">NR_133973.1</a>
Bacillus lentus strain NBRC 16444 16S ribosomal RNA gene, partial sequence	2246	2246	97%	0.0	94%	<a href="#">NR_112631.1</a>
Bacillus coahuilensis strain m4-4 16S ribosomal RNA gene, partial sequence	2244	2244	91%	0.0	96%	<a href="#">NR_115934.1</a>
Bacillus kribbensis strain BT080 16S ribosomal RNA gene, partial sequence	2244	2244	98%	0.0	94%	<a href="#">NR_043682.1</a>
Bacillus coahuilensis strain m4-4 16S ribosomal RNA gene, partial sequence	2242	2242	91%	0.0	96%	<a href="#">NR_115933.1</a>
Bacillus taiwanensis strain FJAT-14571 16S ribosomal RNA, partial sequence	2241	2241	95%	0.0	95%	<a href="#">NR_136461.1</a>

## Alignments

Bacillus cereus ATCC 14579 16S ribosomal RNA (rRNA) gene, complete sequence

Sequence ID: **NR\_074540.1** Length: 1512 Number of Matches: 1

Range 1: 1 to 1512

Score	Expect	Identities	Gaps	Strand	Frame
2793 bits(1512)	0.0()	1512/1512(100%)	0/1512(0%)	Plus/Plus	

Features:

Query 1	TTATTGGAGAGTTT	GATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCAA	60
Sbjct 1	TTATTGGAGAGTTT	GATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCAA	60
Query 61	GTCGAGCGAATGGATTAAAGAGCTTGCTCTTATGAAGTTAGCGGCGGACGGGTGAGTAACA	120	
Sbjct 61	GTCGAGCGAATGGATTAAAGAGCTTGCTCTTATGAAGTTAGCGGCGGACGGGTGAGTAACA	120	
Query 121	CGTGGGTAACCTGCCATAAAGACTGGGATAAATCCGGGAAACCGGGGCTAATACCGGATA	180	
Sbjct 121	CGTGGGTAACCTGCCATAAAGACTGGGATAAATCCGGGAAACCGGGGCTAATACCGGATA	180	
Query 181	ACATTTTGAACCGCATGGTTCGAAATTGAAAGGCGGCTTCGGCTGTCACTTATGGATGGA	240	
Sbjct 181	ACATTTTGAACCGCATGGTTCGAAATTGAAAGGCGGCTTCGGCTGTCACTTATGGATGGA	240	
Query 241	CCCCGCTCGCATTAGCTAGTTGGTGAAGTAAACGGCTCACCAAGGCAACGATGCGTAGCCG	300	
Sbjct 241	CCCCGCTCGCATTAGCTAGTTGGTGAAGTAAACGGCTCACCAAGGCAACGATGCGTAGCCG	300	
Query 301	ACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGC	360	
Sbjct 301	ACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGC	360	
Query 361	AGCAGTAGGGAACTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCCGTGAGTGAT	420	
Sbjct 361	AGCAGTAGGGAACTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCCGTGAGTGAT	420	
Query 421	GAAGGCTTTCGGGTCGTAATAACTCTGTTGTTAGGGAAGAACAAGTCTAGTTGAATAAGC	480	
Sbjct 421	GAAGGCTTTCGGGTCGTAATAACTCTGTTGTTAGGGAAGAACAAGTCTAGTTGAATAAGC	480	
Query 481	TGGCACCTTGACGGTACCTAACAGAAAGCCACGGCTAACCTACGTGCCAGCAGCCGCGGT	540	
Sbjct 481	TGGCACCTTGACGGTACCTAACAGAAAGCCACGGCTAACCTACGTGCCAGCAGCCGCGGT	540	
Query 541	AATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCAGGTGGTTT	600	
Sbjct 541	AATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCAGGTGGTTT	600	
Query 601	CTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGGAGAC	660	
Sbjct 601	CTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGGAGAC	660	
Query 661	TTGAGTGCAGAAGAGGAAAGTGGAAATCCATGTGTAGCGGTGAAATGCGTAGAGATATGG	720	
Sbjct 661	TTGAGTGCAGAAGAGGAAAGTGGAAATCCATGTGTAGCGGTGAAATGCGTAGAGATATGG	720	
Query 721	AGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACCTGACACTGAGGCGCGAAAGCG	780	
Sbjct 721	AGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACCTGACACTGAGGCGCGAAAGCG	780	

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Query 781 TGGGGAGCAAACAGGATTAGATACCTGGTAGTCCACGCCGTA AACGATGAGTGCTAAGT 840
Sbjct 781 TGGGGAGCAAACAGGATTAGATACCTGGTAGTCCACGCCGTA AACGATGAGTGCTAAGT 840
Query 841 GTTAGAGGGTTTCCGCCCTTTAGTGCTGAAGTTAACGCATTAAGCACTCCGCCTGGGGAG 900
Sbjct 841 GTTAGAGGGTTTCCGCCCTTTAGTGCTGAAGTTAACGCATTAAGCACTCCGCCTGGGGAG 900
Query 901 TACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCAT 960
Sbjct 901 TACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCAT 960
Query 961 GTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCTTGACATCCTCTGAAAACCC 1020
Sbjct 961 GTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCTTGACATCCTCTGAAAACCC 1020
Query 1021 TAGAGATAGGGCTTCTCCTTCGGGAGCAGAGTGACAGGTGGTGCATGGTTGTCGTCAGCT 1080
Sbjct 1021 TAGAGATAGGGCTTCTCCTTCGGGAGCAGAGTGACAGGTGGTGCATGGTTGTCGTCAGCT 1080
Query 1081 CGTGTGTCGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTGATCTTAGTTGCCA 1140
Sbjct 1081 CGTGTGTCGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTGATCTTAGTTGCCA 1140
Query 1141 TCATTAAGTTGGGCACTCTAAGGTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGA 1200
Sbjct 1141 TCATTAAGTTGGGCACTCTAAGGTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGA 1200
Query 1201 CGTCAAATCATCATGCCCTTATGACCTGGGCTACACACGTGCTACAATGGACGGTACAA 1260
Sbjct 1201 CGTCAAATCATCATGCCCTTATGACCTGGGCTACACACGTGCTACAATGGACGGTACAA 1260
Query 1261 AGAGCTGCAAGACCGGAGGTGGAGCTAATCTCATAAAACCGTCTCAGTTCGGATTGTA 1320
Sbjct 1261 AGAGCTGCAAGACCGGAGGTGGAGCTAATCTCATAAAACCGTCTCAGTTCGGATTGTA 1320
Query 1321 GGCTGCAACTCGCCTACATGAAGCTGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGG 1380
Sbjct 1321 GGCTGCAACTCGCCTACATGAAGCTGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGG 1380
Query 1381 TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAAACACC 1440
Sbjct 1381 TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAAACACC 1440
Query 1441 GAAGTCGGTGGGGTAACCTTTTTGGAGCCAGCCGCTAAGGTGGGACAGATGATTGGGGT 1500
Sbjct 1441 GAAGTCGGTGGGGTAACCTTTTTGGAGCCAGCCGCTAAGGTGGGACAGATGATTGGGGT 1500
Query 1501 GAAGTCGTAACA 1512
Sbjct 1501 GAAGTCGTAACA 1512
    
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Bacillus cereus strain CCM 2010 16S ribosomal RNA gene, complete sequence

Sequence ID: **NR\_115714.1** Length: 1535 Number of Matches: 1

Range 1: 1 to 1505

Score	Expect	Identities	Gaps	Strand	Frame
2780 bits(1505)	0.0()	1505/1505(100%)	0/1505(0%)	Plus/Plus	

Features:

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Query 8 AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGC 67
Sbjct 1 AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGC 60
Query 68 GAATGGATTAAGAGCTTGCTCTTATGAAGTTAGCGGCGGACGGGTGAGTAACACGTGGGT 127
Sbjct 61 GAATGGATTAAGAGCTTGCTCTTATGAAGTTAGCGGCGGACGGGTGAGTAACACGTGGGT 120
Query 128 AACCTGCCATAAAGACTGGGATAAATCCGGGAAACCGGGGCTAATACCGGATAACATTTT 187
Sbjct 121 AACCTGCCATAAAGACTGGGATAAATCCGGGAAACCGGGGCTAATACCGGATAACATTTT 180
Query 188 GAACCGCATGGTTCGAAATGAAAGGCGGCTTCGGCTGTCACTTATGGATGGACCCGCGT 247
Sbjct 181 GAACCGCATGGTTCGAAATGAAAGGCGGCTTCGGCTGTCACTTATGGATGGACCCGCGT 240
Query 248 CGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCAACGATGCGTAGCCGACCTGAG 307
Sbjct 241 CGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCAACGATGCGTAGCCGACCTGAG 300
Query 308 AGGGTGATCGGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTA 367
Sbjct 301 AGGGTGATCGGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTA 360
Query 368 GGGAACTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCTGAGTGATGAAGGCT 427
Sbjct 361 GGGAACTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCTGAGTGATGAAGGCT 420
Query 428 TTCGGGTCGTA AAACTCTGTTGTTAGGGAAGAACAAGTGC TAGTTGAATAAGCTGGCACC 487
Sbjct 421 TTCGGGTCGTA AAACTCTGTTGTTAGGGAAGAACAAGTGC TAGTTGAATAAGCTGGCACC 480
    
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