

<https://blast.ncbi.nlm.nih.gov/Blast.cgi>

NNNNNNNNACGNNANNNNNNNNNCGNCNNNNCTNCNACATGCAAGTCGAACGATGANCC
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TNNCNCANGCANGCNCCT

Query: None Query ID: lcl|Query_6788295 Length: 1119

>Streptomyces tubercidicus strain DSM 40261 16S ribosomal RNA, partial sequence

Sequence ID: NR_025623.1 Length: 1498

Range 1: 22 to 933

Score	Expert Identities	Gaps	Strand
1474 bits(798)	0.0 873/922(95%)	11/922(1%)	Plus/Plus
Query 38	ACATGCAAGTCGAACGATGANCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAA		97
Sbjct 22	ACATGCAAGTCGAACGATGAACCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAA		81
Query 98	CACGTGGGCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATACCGGA		157
Sbjct 82	CACGTGGGCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATACCGGA		141
Query 158	TACGACTACCGACCGCATGGTCTGGTGGTGGAAAGCTCCGGCGNGAAGGATGAGCCCGC		217
Sbjct 142	TACGACTACCGACCGCATGGTCTGGTGGTGGAAAGCTCCGGCGGTGAAGGATGAGCCCGC		201
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Sbjct 202	GGCCTATCAGCTTGTGNTGGGGTGATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTG		261
Query 278	AGAGGGCGACCGGCCACGCTGGGACTGAGACNCGCCAGACTCCTACGGGAGGCAGCAG		337
Sbjct 262	AGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAG		321
Query 338	TGGGGAATATTGCACNATGGGCGAAAGCCTGATGCAGCGACNCCGCGTGAGGGATGACGG	397	
Sbjct 322	TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGGGATGACGG	381	
Query 398	CCTTCGGGTTGTAAACCTCTTTCAGCAGGGAANAAGCGAGAGTGACGGTACCTGCAGAAG	457	
Sbjct 382	CCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAGAGTGACGGTACCTGCAGAAG	441	
Query 458	AAGCGCCGGGTAACCTACGTGCCAGCAGCCGCGTAATACGTAGGGCGCAAGCGTTGTCCG	517	
Sbjct 442	AAGCGCCGGGTAACCTACGTGCCAGCAGCCGCGTAATACGTAGGGCGCAAGCGTTGTCCG	501	
Query 518	GAATTATTGGGCGTAAAGAGCTCGTAGGCGNGGCTTGTACGTCGGATGTGAAAGCCCGG	577	
Sbjct 502	GAATTATTGGGCGTAAAGAGCTCGTAGGC--GGCTTGTACGTCGGATGTGAAAGCCCGG	559	
Query 578	GGCTTAACCCCGGGTCTGCATTTCGATACGGGCGAGCTAGAGTTCGGNAGGGGAGATCGGA	637	
Sbjct 560	GGCTTAACCCCGGGTCTGCATTTCGATACGGGCGAGCTAGAGTTCGGTAGGGGAGATCGGA	619	
Query 638	ATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAAGAGGAACACCGGTGGCGAAGGCGGA	697	
Sbjct 620	ATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGA	679	
Query 698	TCTCTGGGCCGATACTGACGCTGANGAGCGAANGCGTGGGGAGCGAACAGGATTANATAC	757	
Sbjct 680	TCTCTGGGCCGATACTGACGCTGAGGAGCGAANGCGTGGGGAGCGAACAGGATTAGATAC	739	

