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BLAST Results

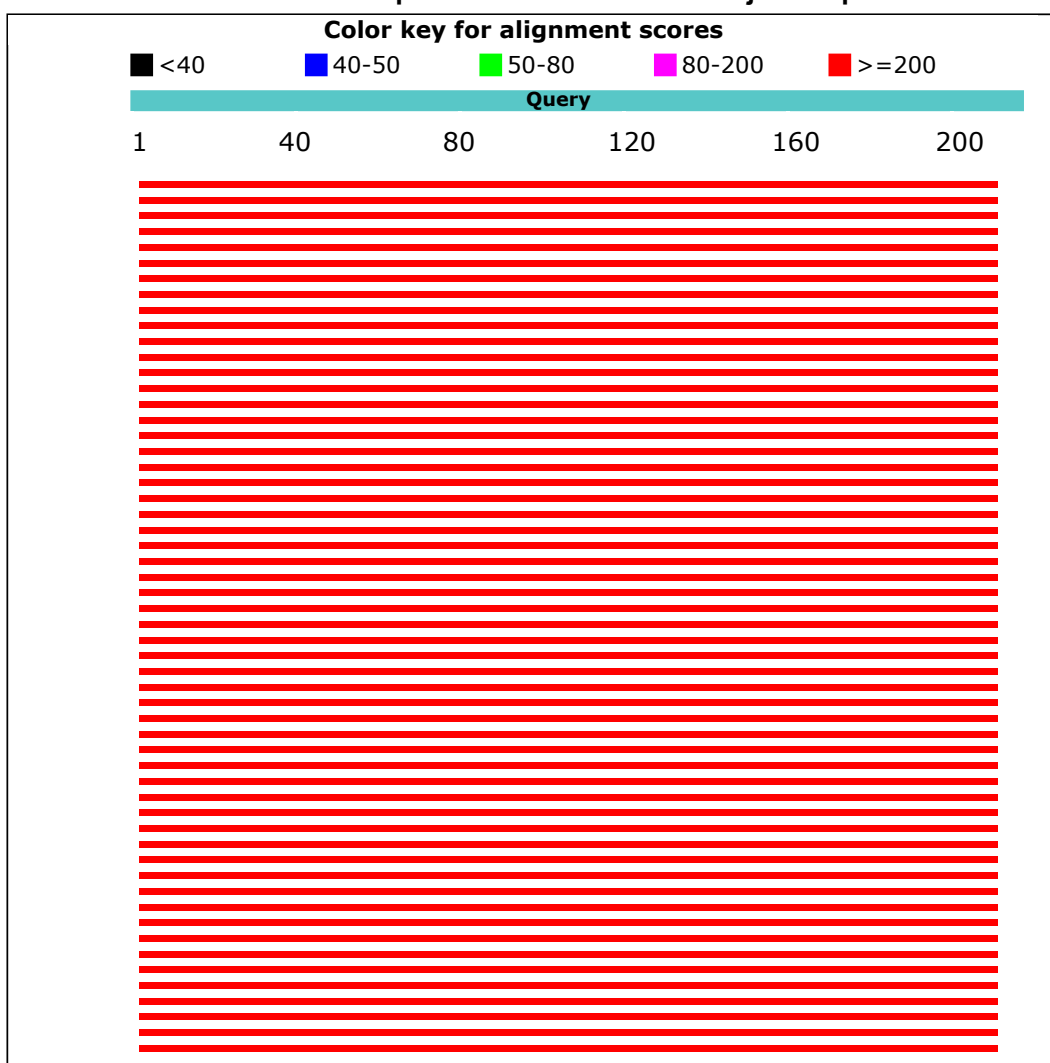
[Questions/comments](#)

Job title: Nucleotide Sequence (211 letters)

RID	Z8B5MCXU013 (Expires on 11-21 22:48 pm)	Database Name	nr
Query ID	lcl Query_215797	Description	Nucleotide collection (nt)
Description	None	Program	BLASTN 2.8.1+
Molecule type	nucleic acid		
Query Length	211		

Graphic Summary

Distribution of the top 100 Blast Hits on 100 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Bovine leukemia virus isolate S6F15, complete genome	374	374	98%	5e-100	100%	MH170028.1
Bovine leukemia virus isolate COL66 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057531.1
Bovine leukemia virus isolate COL65 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057530.1
Bovine leukemia virus isolate COL61 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057526.1
Bovine leukemia virus isolate COL60 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057525.1
Bovine leukemia virus isolate COL58 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057523.1
Bovine leukemia virus isolate COL57 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057522.1
Bovine leukemia virus isolate COL55 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057520.1
Bovine leukemia virus isolate COL51 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057516.1
Bovine leukemia virus isolate COL49 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057514.1
Bovine leukemia virus isolate COL48 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057513.1
Bovine leukemia virus isolate COL47 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057512.1
Bovine leukemia virus isolate COL40 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057505.1
Bovine leukemia virus isolate COL36 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057501.1
Bovine leukemia virus isolate COL35 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057500.1
Bovine leukemia virus isolate COL34 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057499.1
Bovine leukemia virus isolate COL33 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057498.1
Bovine leukemia virus isolate COL30 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057495.1
Bovine leukemia virus isolate COL29 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057494.1
Bovine leukemia virus isolate COL28 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057493.1
Bovine leukemia virus isolate COL27 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057492.1
Bovine leukemia virus isolate COL26 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057491.1
Bovine leukemia virus isolate COL23 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057488.1
Bovine leukemia virus isolate COL22 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057487.1
Bovine leukemia virus isolate COL20 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057485.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Bovine leukemia virus isolate COL13 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057478.1
Bovine leukemia virus isolate COL10 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057475.1
Bovine leukemia virus isolate COL8 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057473.1
Bovine leukemia virus isolate COL1 tax protein (tax) gene, partial cds	374	374	98%	5e-100	100%	MH057466.1
Bovine leukemia virus DNA, complete sequence, strain: pvAN015	374	374	98%	5e-100	100%	AP018032.1
Bovine leukemia virus DNA, complete sequence, strain: pvAN014	374	374	98%	5e-100	100%	AP018031.1
Bovine leukemia virus DNA, complete sequence, strain: pvAN013	374	374	98%	5e-100	100%	AP018030.1
Bovine leukemia virus DNA, complete sequence, strain: pvAN011	374	374	98%	5e-100	100%	AP018029.1
Bovine leukemia virus DNA, complete sequence, strain: pvAN004	374	374	98%	5e-100	100%	AP018025.1
Bovine leukemia virus DNA, complete sequence, strain: pvAK011	374	374	98%	5e-100	100%	AP018023.1
Bovine leukemia virus DNA, complete sequence, strain: pvAK007	374	374	98%	5e-100	100%	AP018022.1
Bovine leukemia virus DNA, complete sequence, strain: pvAK006	374	374	98%	5e-100	100%	AP018021.1
Bovine leukemia virus DNA, complete sequence, strain: pvAK001	374	374	98%	5e-100	100%	AP018020.1
Bovine leukemia virus DNA, complete sequence, strain: pvAF902	374	374	98%	5e-100	100%	AP018018.1
Bovine leukemia virus DNA, complete sequence, strain: pvAF805	374	374	98%	5e-100	100%	AP018017.1
Bovine leukemia virus DNA, complete sequence, strain: pvAF784	374	374	98%	5e-100	100%	AP018016.1
Bovine leukemia virus DNA, complete sequence, strain: pvAF513	374	374	98%	5e-100	100%	AP018014.1
Bovine leukemia virus DNA, complete sequence, strain: pvAF481	374	374	98%	5e-100	100%	AP018013.1
Bovine leukemia virus DNA, complete sequence, strain: pvAF438	374	374	98%	5e-100	100%	AP018012.1
Bovine leukemia virus DNA, complete sequence, strain: pvAF266	374	374	98%	5e-100	100%	AP018010.1
Bovine leukemia virus DNA, complete sequence, strain: pvAF076	374	374	98%	5e-100	100%	AP018007.1
Bovine leukemia virus DNA, complete sequence, strain: pvAF060	374	374	98%	5e-100	100%	AP018006.1
Bovine leukemia virus DNA, complete sequence, strain: pvAN903	374	374	98%	5e-100	100%	LC164086.1
Bovine leukemia virus DNA, complete sequence, strain: pBLV-FLK	374	374	98%	5e-100	100%	LC164083.1
Bovine leukemia virus proviral DNA, complete genome, strain: par7	374	374	98%	5e-100	100%	LC080653.1
Bovine leukemia virus proviral DNA, complete genome, strain: asun5	374	374	98%	5e-100	100%	LC080652.1
Bovine leukemia virus proviral DNA, complete genome, strain: asun1	374	374	98%	5e-100	100%	LC080651.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Bovine leukemia virus DNA, complete proviral genome, strain: #469, deficient type	374	374	98%	5e-100	100%	LC005616.1
Bovine leukemia virus DNA, complete proviral genome, strain: #469, wild type	374	374	98%	5e-100	100%	LC005615.1
Bovine leukemia virus tax gene for Tax protein, partial cds, strain: #207	374	374	98%	5e-100	100%	AB662994.1
Bovine leukemia virus tax gene for Tax protein, partial cds, strain: #156	374	374	98%	5e-100	100%	AB662991.1
Bovine leukemia virus tax gene for Tax protein, partial cds, strain: #105	374	374	98%	5e-100	100%	AB662989.1
Bovine leukemia virus tax gene for Tax protein, partial cds, strain: #7	374	374	98%	5e-100	100%	AB662979.1
Bovine leukemia virus tax gene for Tax protein, partial cds, strain: #1	374	374	98%	5e-100	100%	AB662977.1
Bovine leukemia virus, complete proviral genome, isolate LS3	374	374	98%	5e-100	100%	HE967303.1
Bovine leukemia virus, complete proviral genome, isolate LS2	374	374	98%	5e-100	100%	HE967302.1
Bovine leukemia virus, complete proviral genome, isolate LS1	374	374	98%	5e-100	100%	HE967301.1
Bovine leukemia virus strain Arg-LP11pX pX region, partial sequence	374	374	98%	5e-100	100%	JF288773.1
Bovine leukemia virus strain Arg-LP06pX pX region, partial sequence	374	374	98%	5e-100	100%	JF288768.1
Bovine leukemia virus strain Arg-LP05pX pX region, partial sequence	374	374	98%	5e-100	100%	JF288767.1
Bovine leukemia virus strain Arg-LP04pX pX region, partial sequence	374	374	98%	5e-100	100%	JF288766.1
Bovine leukemia virus strain Arg-LP03pX pX region, partial sequence	374	374	98%	5e-100	100%	JF288765.1
Bovine leukemia virus isolate USCA-5 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428061.1
Bovine leukemia virus isolate USCA-4 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428060.1
Bovine leukemia virus isolate JPMI-5 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428059.1
Bovine leukemia virus isolate JPMI-4 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428058.1
Bovine leukemia virus isolate JPKA-5 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428057.1
Bovine leukemia virus isolate JPKA-4 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428056.1
Bovine leukemia virus isolate JPKA-3 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428055.1
Bovine leukemia virus isolate JPHY-3 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428052.1
Bovine leukemia virus isolate JPHY-2 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428051.1
Bovine leukemia virus isolate JPEH-5 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428047.1
Bovine leukemia virus isolate JPEH-4 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428046.1
Bovine leukemia virus isolate JPEH-3 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428045.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Bovine leukemia virus isolate JPAI-5 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428044.1
Bovine leukemia virus isolate JPAI-4 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428043.1
Bovine leukemia virus isolate JPAI-3 Tax (tax) gene, partial cds	374	374	98%	5e-100	100%	EF428042.1
Bovine leukemia virus cell-line FLK-BLV subclone pBLV913, complete genome	374	374	98%	5e-100	100%	EF600696.1
Bovine leukemia virus isolate JPAI-2 R3 protein (R3), G4 protein (G4), rex protein (rex), and tax protein (tax) genes, partial cds	374	374	98%	5e-100	100%	DQ975367.1
Bovine leukemia virus isolate JPMI-3 R3 protein (R3), truncated G4 protein (G4), rex protein (rex), and tax protein (tax) genes, partial cds	374	374	98%	5e-100	100%	DQ975366.1
Bovine leukemia virus isolate USWI R3, G4, Rex, and Tax genes, partial cds	374	374	98%	5e-100	100%	DQ412669.1
Bovine leukemia virus isolate USID R3, G4, Rex, and Tax genes, partial cds	374	374	98%	5e-100	100%	DQ412667.1
Bovine leukemia virus isolate USIA R3, G4, Rex, and Tax genes, partial cds	374	374	98%	5e-100	100%	DQ412666.1
Bovine leukemia virus isolate JPMI-2 R3, G4, Rex, and Tax genes, partial cds	374	374	98%	5e-100	100%	DQ412662.1
Bovine leukemia virus isolate JPMI-1 R3, G4, Rex, and Tax genes, partial cds	374	374	98%	5e-100	100%	DQ412661.1
Bovine leukemia virus isolate JPKA-2 R3, G4, Rex, and Tax genes, partial cds	374	374	98%	5e-100	100%	DQ412660.1
Bovine leukemia virus isolate JPKA-1 R3, G4, Rex, and Tax genes, partial cds	374	374	98%	5e-100	100%	DQ412659.1
Bovine leukemia virus isolate JPHY R3, G4, Rex, and Tax genes, partial cds	374	374	98%	5e-100	100%	DQ412658.1
Bovine leukemia virus isolate JPEH-2 R3, G4, Rex, and Tax genes, partial cds	374	374	98%	5e-100	100%	DQ412656.1
Bovine leukemia virus isolate JPEH-1 R3, G4, Rex, and Tax genes, partial cds	374	374	98%	5e-100	100%	DQ412655.1
Bovine leukemia virus isolate JPAI R3, G4, Rex, and Tax genes, partial cds	374	374	98%	5e-100	100%	DQ412654.1
Bovine leukemia virus isolate CRAS-2 R3, G4, Rex, and Tax genes, partial cds	374	374	98%	5e-100	100%	DQ412648.1
Bovine leukemia virus isolate CRAG R3, G4, Rex, and Tax genes, partial cds	374	374	98%	5e-100	100%	DQ412646.1
Bovine leukemia virus from USA tax gene, partial cds	374	374	98%	5e-100	100%	AY700378.1
Synthetic construct bovine leukemia virus, complete sequence	369	369	98%	2e-98	99%	KP113663.1

Alignments

Bovine leukemia virus isolate S6F15, complete genome

Sequence ID: **MH170028.1** Length: 8720 Number of Matches: 1
Range 1: 7270 to 7476

Score	Expect	Identities	Gaps	Strand	Frame
374 bits(414)	5e-100()	207/207(100%)	0/207(0%)	Plus/Plus	

Features:

```

Query 3      GGCCCCACTCTCTACATGCCTGCCCGGCCCTGGTTTTGTCCAATGATGTCACCATCGATG 62
Sbjct 7270    GGCCCCACTCTCTACATGCCTGCCCGGCCCTGGTTTTGTCCAATGATGTCACCATCGATG 7329
Query 63     CCTGGTGCCCCCTCTGCGGGCCCCATGAGCGACTCCAATTCGAAAGGATCGACACCACGC 122
Sbjct 7330    CCTGGTGCCCCCTCTGCGGGCCCCATGAGCGACTCCAATTCGAAAGGATCGACACCACGC 7389
Query 123    TCACCTGCGAGACCCACCGTATCAACTGGACCGCCGATGGACGACCTTGCGGCCTCAATG 182
Sbjct 7390    TCACCTGCGAGACCCACCGTATCAACTGGACCGCCGATGGACGACCTTGCGGCCTCAATG 7449
Query 183    GAACGTTGTTCCCTCGACTGCATGTCT 209
Sbjct 7450    GAACGTTGTTCCCTCGACTGCATGTCT 7476
    
```

Bovine leukemia virus isolate COL66 tax protein (tax) gene, partial cds

Sequence ID: **MH057531.1** Length: 314 Number of Matches: 1
 Range 1: 20 to 226

Score	Expect	Identities	Gaps	Strand	Frame
374 bits(414)	5e-100()	207/207(100%)	0/207(0%)	Plus/Plus	

Features:

```

Query 3      GGCCCCACTCTCTACATGCCTGCCCGGCCCTGGTTTTGTCCAATGATGTCACCATCGATG 62
Sbjct 20      GGCCCCACTCTCTACATGCCTGCCCGGCCCTGGTTTTGTCCAATGATGTCACCATCGATG 79
Query 63     CCTGGTGCCCCCTCTGCGGGCCCCATGAGCGACTCCAATTCGAAAGGATCGACACCACGC 122
Sbjct 80     CCTGGTGCCCCCTCTGCGGGCCCCATGAGCGACTCCAATTCGAAAGGATCGACACCACGC 139
Query 123    TCACCTGCGAGACCCACCGTATCAACTGGACCGCCGATGGACGACCTTGCGGCCTCAATG 182
Sbjct 140    TCACCTGCGAGACCCACCGTATCAACTGGACCGCCGATGGACGACCTTGCGGCCTCAATG 199
Query 183    GAACGTTGTTCCCTCGACTGCATGTCT 209
Sbjct 200    GAACGTTGTTCCCTCGACTGCATGTCT 226
    
```

Bovine leukemia virus isolate COL65 tax protein (tax) gene, partial cds

Sequence ID: **MH057530.1** Length: 314 Number of Matches: 1
 Range 1: 20 to 226

Score	Expect	Identities	Gaps	Strand	Frame
374 bits(414)	5e-100()	207/207(100%)	0/207(0%)	Plus/Plus	

Features:

```

Query 3      GGCCCCACTCTCTACATGCCTGCCCGGCCCTGGTTTTGTCCAATGATGTCACCATCGATG 62
Sbjct 20      GGCCCCACTCTCTACATGCCTGCCCGGCCCTGGTTTTGTCCAATGATGTCACCATCGATG 79
Query 63     CCTGGTGCCCCCTCTGCGGGCCCCATGAGCGACTCCAATTCGAAAGGATCGACACCACGC 122
Sbjct 80     CCTGGTGCCCCCTCTGCGGGCCCCATGAGCGACTCCAATTCGAAAGGATCGACACCACGC 139
Query 123    TCACCTGCGAGACCCACCGTATCAACTGGACCGCCGATGGACGACCTTGCGGCCTCAATG 182
Sbjct 140    TCACCTGCGAGACCCACCGTATCAACTGGACCGCCGATGGACGACCTTGCGGCCTCAATG 199
Query 183    GAACGTTGTTCCCTCGACTGCATGTCT 209
Sbjct 200    GAACGTTGTTCCCTCGACTGCATGTCT 226
    
```

Bovine leukemia virus isolate COL61 tax protein (tax) gene, partial cds

Sequence ID: **MH057526.1** Length: 314 Number of Matches: 1
 Range 1: 20 to 226

Score	Expect	Identities	Gaps	Strand	Frame
374 bits(414)	5e-100()	207/207(100%)	0/207(0%)	Plus/Plus	

Features:

```

Query 3      GGCCCCACTCTCTACATGCCTGCCCGGCCCTGGTTTTGTCCAATGATGTCACCATCGATG 62
Sbjct 20      GGCCCCACTCTCTACATGCCTGCCCGGCCCTGGTTTTGTCCAATGATGTCACCATCGATG 79
    
```

```

Query 63 CCTGGTGCCCCCTCTGCGGGCCCCATGAGCGACTCCAATTCGAAAGGATCGACACCACGC 122
Sbjct 80 CCTGGTGCCCCCTCTGCGGGCCCCATGAGCGACTCCAATTCGAAAGGATCGACACCACGC 139
Query 123 TCACCTGCGAGACCCACCGTATCAACTGGACCGCCGATGGACGACCTTGCGGCCTCAATG 182
Sbjct 140 TCACCTGCGAGACCCACCGTATCAACTGGACCGCCGATGGACGACCTTGCGGCCTCAATG 199
Query 183 GAACGTTGTTCCCTCGACTGCATGTCT 209
Sbjct 200 GAACGTTGTTCCCTCGACTGCATGTCT 226

```

Bovine leukemia virus isolate COL60 tax protein (tax) gene, partial cds

Sequence ID: **MH057525.1** Length: 314 Number of Matches: 1

Range 1: 20 to 226

Score	Expect	Identities	Gaps	Strand	Frame
374 bits(414)	5e-100()	207/207(100%)	0/207(0%)	Plus/Plus	

Features:

```

Query 3  GGCCCCACTCTCTACATGCCTGCCCGGCCCTGGTTTTGTCCAATGATGTCACCATCGATG 62
Sbjct 20  GGCCCCACTCTCTACATGCCTGCCCGGCCCTGGTTTTGTCCAATGATGTCACCATCGATG 79
Query 63  CCTGGTGCCCCCTCTGCGGGCCCCATGAGCGACTCCAATTCGAAAGGATCGACACCACGC 122
Sbjct 80  CCTGGTGCCCCCTCTGCGGGCCCCATGAGCGACTCCAATTCGAAAGGATCGACACCACGC 139
Query 123 TCACCTGCGAGACCCACCGTATCAACTGGACCGCCGATGGACGACCTTGCGGCCTCAATG 182
Sbjct 140 TCACCTGCGAGACCCACCGTATCAACTGGACCGCCGATGGACGACCTTGCGGCCTCAATG 199
Query 183  GAACGTTGTTCCCTCGACTGCATGTCT 209
Sbjct 200  GAACGTTGTTCCCTCGACTGCATGTCT 226

```

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