

A—KAN B    uptag

KAN C —    D    downtag

A—D        A— uptag  
             D— downtag

reverse complement of sequence to match downtag

[http://www.bioinformatics.org/sms/rev\\_comp.html](http://www.bioinformatics.org/sms/rev_comp.html)

TEC 1-6, TEC 1 - D

Sequence ID: Query\_223227    Length: 74    Number of Matches: 1

Range 1: 1 to 74 [Graphics](#)

▼ Next Match    ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
137 bits(74)	2e-37	74/74(100%)	0/74(0%)	Plus/Minus
Query    486	CGAGCTCGAATTCATCGATAGTCATCCTCTAACTCAGGTCTACGAGACCGACACCGTAAA	545		
Sbjct    74	CGAGCTCGAATTCATCGATAGTCATCCTCTAACTCAGGTCTACGAGACCGACACCGTAAA	15		
Query    546	TGTCTACATACATA	559		
Sbjct    14	TGTCTACATACATA	1		

ASF 1-4 ASF 1- D

Sequence ID: Query\_16657    Length: 74    Number of Matches: 1

Range 1: 1 to 74 [Graphics](#)

▼ Next Match    ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
132 bits(71)	9e-36	73/74(99%)	0/74(0%)	Plus/Minus
Query    504	CGAGCTCGAATTTATCGATGTCCGTCGTTCTACATGCTGCTACGAGACCGACACCGTAAG	563		
Sbjct    74	CGAGCTCGAATTCATCGATGTCCGTCGTTCTACATGCTGCTACGAGACCGACACCGTAAG	15		
Query    564	AATTTATGGGTTAT	577		
Sbjct    14	AATTTATGGGTTAT	1		

ASF 1-3 Kan C

Sequence ID: Query\_53437 Length: 74 Number of Matches: 1

Range 1: 1 to 74 [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
132 bits(71)	8e-36	73/74(99%)	0/74(0%)	Plus/Plus
Query 237	ATAACCCATAAATTC	TTACGGTGT	CGGTCTCGTAGCAGCATGTAGAACGACGGACATCGA	296
Sbjct 1	ATAACCCATAAATTC	TTACGGTGT	CGGTCTCGTAGCAGCATGTAGAACGACGGACATCGA	60
Query 297	TAAATTCGAGCTCG			310
Sbjct 61	TGAATTCGAGCTCG			74

## ASF1-6 ASF1-D

Sequence ID: Query\_160661 Length: 74 Number of Matches: 1

Range 1: 1 to 74 [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
132 bits(71)	9e-36	73/74(99%)	0/74(0%)	Plus/Minus
Query 522	CGAGCTCGAATTTATCGATGTCCGTCGTTCTACATGCTGCTACGAGACCGACACCGTAAG			581
Sbjct 74	CGAGCTCGAATTCATCGATGTCCGTCGTTCTACATGCTGCTACGAGACCGACACCGTAAG			15
Query 582	AATTTATGGGTTAT			595
Sbjct 14	AATTTATGGGTTAT			1

## ASF 1-2 kan-B

Sequence ID: Query\_214093 Length: 74 Number of Matches: 1

Range 1: 1 to 74 [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
137 bits(74)	1e-37	74/74(100%)	0/74(0%)	Plus/Minus
Query 188	GTCGACCTGCAGCGTACGGCATATAGTGCCGTGTGCCTAGAGACCTCGTGGACATCCATC			247
Sbjct 74	GTCGACCTGCAGCGTACGGCATATAGTGCCGTGTGCCTAGAGACCTCGTGGACATCCATC			15
Query 248	TTTTCTATATCTTA			261
Sbjct 14	TTTTCTATATCTTA			1

## TEC1-1 TEC1-A

Sequence ID: Query\_155273 Length: 74 Number of Matches: 1

Range 1: 1 to 74 [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
137 bits(74)	1e-37	74/74(100%)	0/74(0%)	Plus/Plus
Query 324	GATACCTGTTTAACCATGGATGTCCACGAGGTCTCTATGCTACGGCCACTAGGTTGCGTA	383		
Sbjct 1	GATACCTGTTTAACCATGGATGTCCACGAGGTCTCTATGCTACGGCCACTAGGTTGCGTA	60		
Query 384	CGCTGCAGGTCGAC	397		
Sbjct 61	CGCTGCAGGTCGAC	74		

## TEC1-2 Kan B

Sequence ID: Query\_32753 Length: 74 Number of Matches: 1

Range 1: 1 to 74 [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
137 bits(74)	1e-37	74/74(100%)	0/74(0%)	Plus/Minus
Query 190	GTCGACCTGCAGCGTACGCAACCTAGTGCCGTAGCATAGAGACCTCGTGGACATCCATG	249		
Sbjct 74	GTCGACCTGCAGCGTACGCAACCTAGTGCCGTAGCATAGAGACCTCGTGGACATCCATG	15		
Query 250	GTTAAACAGGTATC	263		
Sbjct 14	GTTAAACAGGTATC	1		

## TEC1-5 TEC1-A

Sequence ID: Query\_58973 Length: 74 Number of Matches: 1

Range 1: 1 to 74 [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
137 bits(74)	2e-37	74/74(100%)	0/74(0%)	Plus/Plus
Query 300	GATACCTGTTTAACCATGGATGTCCACGAGGTCTCTATGCTACGGCCACTAGGTTGCGTA	359		
Sbjct 1	GATACCTGTTTAACCATGGATGTCCACGAGGTCTCTATGCTACGGCCACTAGGTTGCGTA	60		
Query 360	CGCTGCAGGTCGAC	373		
Sbjct 61	CGCTGCAGGTCGAC	74		

## TEC1-3 TEC1 Kan C

Sequence ID: Query\_227833 Length: 74 Number of Matches: 1

Range 1: 1 to 74 [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
137 bits(74)	2e-37	74/74(100%)	0/74(0%)	Plus/Plus
Query 187	TATGTATGTAGACATTTACGGTGTCTCGGTCTCGTAGACCTGAGTTAGAGGATGACTATCGA			246
Sbjct 1	TATGTATGTAGACATTTACGGTGTCTCGGTCTCGTAGACCTGAGTTAGAGGATGACTATCGA			60
Query 247	TGAATTCGAGCTCG	260		
Sbjct 61	TGAATTCGAGCTCG	74		