

```
>test
aataactccctccgctccctaataatttgagcgcgttgactttttaaacaatatttgacgcttctgtatttcaaaaaaattaagtaattattaattcctttcctatcatttga
ttcattgttaataatactttttatgtatacatatagttttacataatcacaagaagttttgataagacgaacggtcaaacatgttataaaaagtcaacggcgtcaaatatt
tagggaaggaggagtagCTTACCTCGCTTGTCTCAAgcgaaaaccaagtgCTTACCTCGCTTGTCTCAAgcgaaaaccaatccacaacatgttcacatgtttggggac
gaaggtgtcgataaaaacataatacggacatgagggcatcatgatcacacatagaacgaatataatcataaaatattctatgggaaagtaacaattccttcagaaagcaaa
catgaagcaaaaacctaccgagaagtaaccaacaacagtcocatagtcattgaagcaattgtaatttatcacaacatcagaaagagtcaataaagagcttgaaggcaaac
cacatactcaatcatctcttttgtttccacaattcttacaactcacgtggtactcatggtgtcaaagtttcagctcagaggaagataggggcttatagtttggctccca
cggtttacctcaagggtaaagtcaacaacaataaaacatgagtactcctcctcgttccaaaatagatgactcaactttgtactaacttttagtaaaaagtagtataaggttg
ggtcatctattttggaacggatgtcgcgaccttatgagccgacgaaaccatcatcttagggtggcgttgagctttctaatcgcacctgtggatagatagatagatagata
gatagatagatagatagatagatcatctcgtgcaacgaccttatgagccgacgaaaccatcatctatggtggcgttgagctttctgactcgccccatcctgtcgcgacct
tatgagccgacgaatccgctcagcttatggtggcgttgagctttctgactcgccccatcctgtcgcgaccttatgagaacgctcgcgacgcttgactttttaaagcagcga
cgcgcaaacatcatctt
```

In silico Primer(s) search:

2 5'-cttacctcgcttgtcctcaa

Position: 243->262 20bp 100% Tm = 54,1°C

```
5-cttacctcgcttgtcctcaa->
|||||
tcgaatggagcgaacaggagttcgct
```

Position: 277->296 20bp 100% Tm = 54,1°C

```
5-cttacctcgcttgtcctcaa->
|||||
Acgaatggagcgaacaggagttcgct
```

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 Last update: 17/03/10

Primer design results

Selected regions were (0 569)-(569 1139)

No	Sc	Primer sequences	Pos	Plen	%GC	Tm	CpG	Sa	Sea	Pa	Pea	Len
1.	11.95	TTTAGGGAAGGAGGGAGTAG	222	20	50.0	60.8	11	8	0	10	4	514
		CTATTTTGAACGGAGGGGAG	736	20	50.0	62.3		20	6	Details	FPCR	
2.	12.87	TTTAGGGAAGGAGGGAGTAG	222	20	50.0	60.8	11	8	0	10	4	510
		TTTGGAACGGAGGGAGTAAC	732	20	50.0	63.6		16	6	Details	FPCR	
3.	13.41	TTTAGGGAAGGAGGGAGTAG	222	20	50.0	60.8	10	8	0	16	4	462
		TTGAGGTAACCGTTGGGAG	684	20	50.0	63.6		20	4	Details	FPCR	
4.	13.58	CTCCCTCCGTCCTAAATAT	4	20	50.0	62.2	18	16	6	16	4	651
		TAAGCCCCTATCTTCTCTG	655	20	50.0	60.8		16	4	Details	FPCR	
5.	14.57	CTCCCTCCGTCCTAAATAT	4	20	50.0	62.2	27	16	6	16	4	881
		TCTATCTATCCACATGGGCG	885	20	50.0	61.4		20	4	Details	FPCR	
6.	15.40	CTTACCTCGCTTGTCTCAA	276	20	50.0	63.4	7	16	8	18	4	379
		TAAGCCCCTATCTTCTCTG	655	20	50.0	60.8		16	4	Details	FPCR	
7.	15.40	CTTACCTCGCTTGTCTCAA	242	20	50.0	63.4	9	16	8	18	4	413
		TAAGCCCCTATCTTCTCTG	655	20	50.0	60.8		16	4	Details	FPCR	
8.	15.55	TTTAGGGAAGGAGGGAGTAG	222	20	50.0	60.8	8	8	0	6	0	385
		CGTAGTTGTAAGAAATTGTGG	607	21	42.9	60.9		20	4	Details	FPCR	
9.	16.04	TTTAGGGAAGGAGGGAGTAG	222	20	50.0	60.8	16	8	0	18	6	621
		CCTAAGATGATGGTTTCGTC	843	20	45.0	59.8		20	6	Details	FPCR	
10.	16.17	ATACTCCCTCCGTCCTAAA	1	20	50.0	63.2	31	16	2	18	2	973
		CAAGGCCACCATAGATGAT	974	20	50.0	63.0		20	4	Details	FPCR	
11.	16.40	TCACATGTTTGGGGACGAAG	320	20	50.0	62.7	7	20	4	16	4	416
		CTATTTTGAACGGAGGGGAG	736	20	50.0	62.3		20	6	Details	FPCR	
12.	16.56	CATAATACGGACATGAGGGC	352	20	50.0	61.6	16	20	4	18	8	622
		CAAGGCCACCATAGATGAT	974	20	50.0	63.0		20	4	Details	FPCR	
13.	16.68	CCTCAAGCGAAAACCAATCC	290	20	50.0	63.8	6	16	4	16	4	368
		CTATAAGCCCCTATCTTCTC	658	21	47.6	60.4		20	4	Details	FPCR	
14.	16.70	TTTAGGGAAGGAGGGAGTAG	222	20	50.0	60.8	9	8	0	14	4	448
		TGGGAGGCAAACTATAAGC	670	20	45.0	61.7		16	8	Details	FPCR	
15.	16.81	CCTCAAGCGAAAACCAATCC	290	20	50.0	63.8	15	16	4	18	8	595
		TCTATCTATCCACATGGGCG	885	20	50.0	61.4		20	4	Details	FPCR	
16.	17.33	TCACATGTTTGGGGACGAAG	320	20	50.0	62.7	7	20	4	16	4	412
		TTTGGAACGGAGGGAGTAAC	732	20	50.0	63.6		16	6	Details	FPCR	
17.	17.45	GAAGTAACCAACAACAGTCC	470	20	45.0	59.2	1	20	4	18	4	185
		TAAGCCCCTATCTTCTCTG	655	20	50.0	60.8		16	4	Details	FPCR	
18.	17.60	CCTCAAGCGAAAACCAATCC	290	20	50.0	63.8	19	16	4	18	4	684
		CAAGGCCACCATAGATGAT	974	20	50.0	63.0		20	4	Details	FPCR	
19.	17.62	ATGTTTGGGGACGAAGGTGT	324	20	50.0	64.1	7	20	6	14	2	412
		CTATTTTGAACGGAGGGGAG	736	20	50.0	62.3		20	6	Details	FPCR	