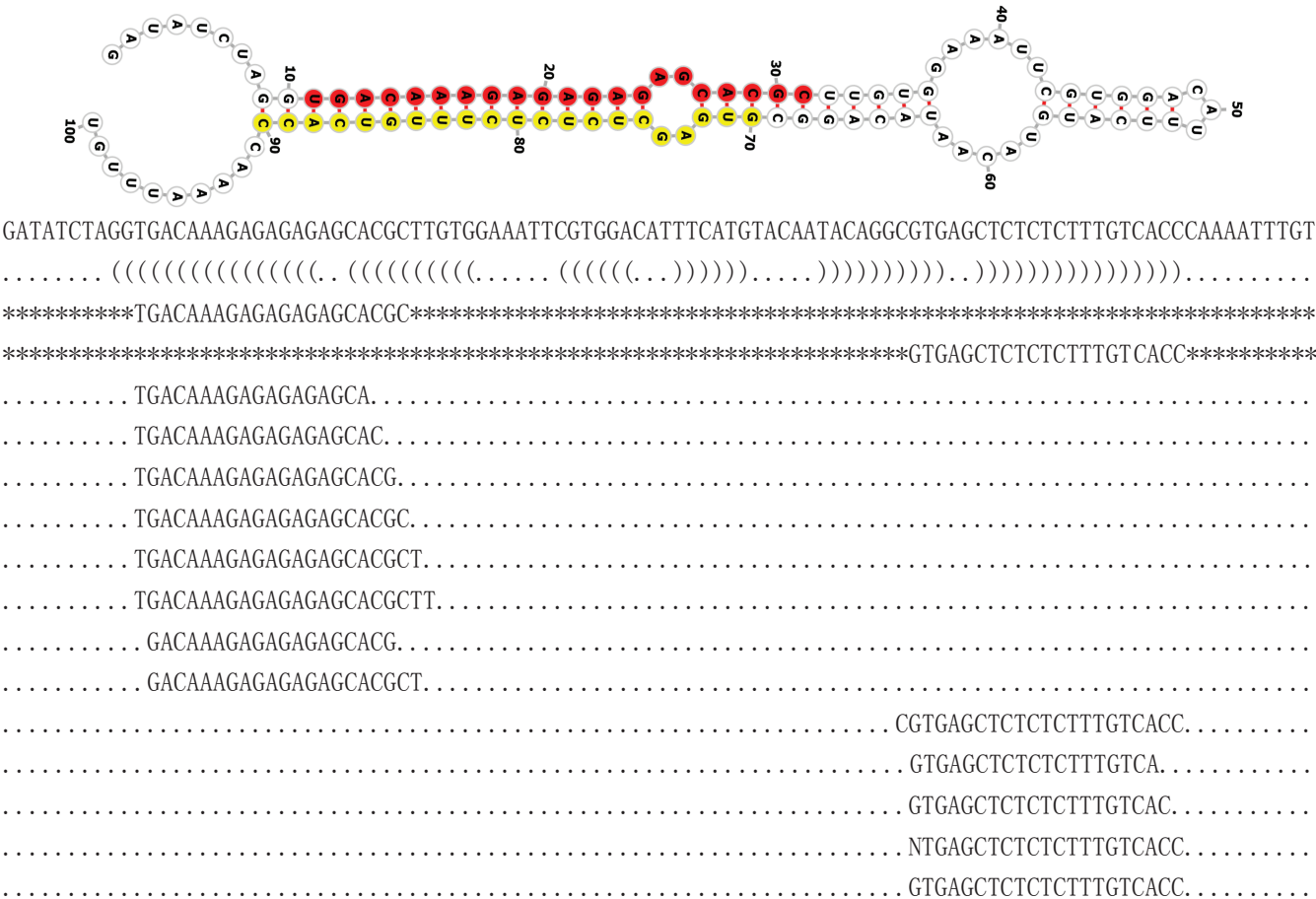


Precursor

Sequence and structure of each precursor

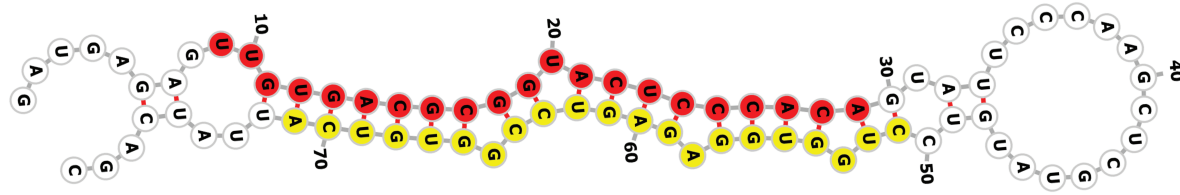
Reads

lka-PremiR-1
MFE -51.60 kcal/mol
LP 100 nt



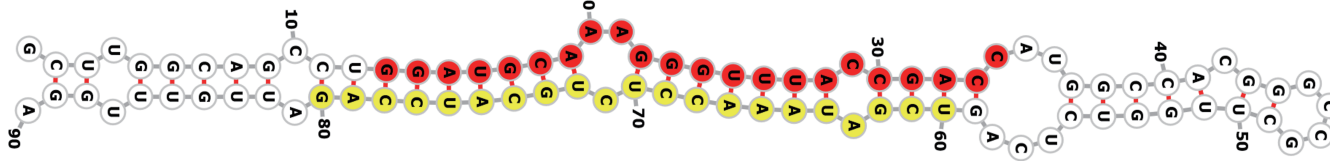
LP:length of precursor; MFE: minimal folding energy.

lka-PremiR-2
MFE -20.50 kcal/mol
LP 79 nt



GATGAGAGTTGTGACGCGGTACTCCCACAGTATTCCCAAGCTCGTATGTCCTGGTGGAGAGTCCGGTGTCA	0
..(((.....(((((((((((.....)))))).))))).))))).))))).))))).))))..	0
*****TTGTGACGCGGTACTCCCACA*****	0
*****CTGGTGGAGAGTCCGGTGTCA*****	0
.....TTGTGACGCGGTACTCCC.....	2
.....TTGTGACGCGGTACTCCCACA.....	24
.....AGCTCGTATGTCCTGGTGGAG.....	2
.....TCCTGGTGGAGAGTCCGGTGT.....	1
.....CTGGTGGAGAGTCCGGTGT.....	1
.....CTGGTGGAGAGTCCGGTGTCA.....	2
.....CTGGTGGAGAGTCCGGTGTCA.....	6

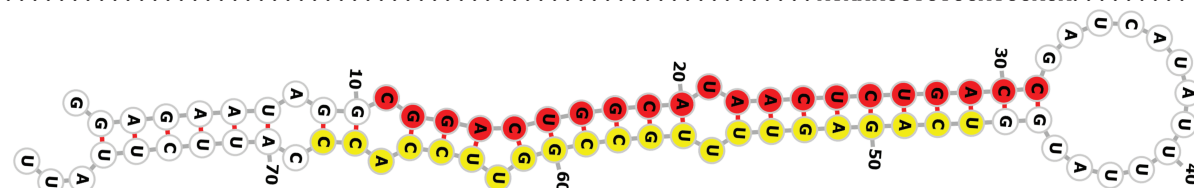
lka-PremiR-3
MFE -40.90 kcal/mol
LP 90 nt



GCTTGGCAGCCTGGATGCAAAGGTTTACCGACCATGGCCACGGGCCGCTTGGTCTCAGTCGATAAACCTCTGCATCCAGATTGTTTGGA	0
.(((((.(((((((((((.....)))))).))))).))))).))))).))))).))))).))))..	0
*****GGATGCAAAGGTTTACCGACC*****	0
*****TCGATAAACCTCTGCATCCAG*****	0
.....TGGATGCAAAGGTTTACCGAC.....	1
.....GGATGCAAAGGTTTACCGACC.....	7
.....GGATGCAAAGGTTTACCGACCATG.....	2
.....ATGGCCACGGGCCGCTTGGTCTCAG.....	1

..... GGTCTCAGTCGATAAACC.....	1
..... TCAGTCGATAAACCTCTGCATCCAG.....	5
..... CAGTCGATAAACCTCTGCATCCA.....	1
..... CAGTCGATAAACCTCTGCATCCAGA.....	1
..... AGTCGATAAACCTCTGCATCC.....	1
..... AGTCGATAAACCTCTGCATCCA.....	1
..... GTCGATAAACCTCTGCATCCA.....	4
..... TCGATAAACCTCTGCATC.....	53
..... TCGATAAACCTCTGCATCC.....	195
..... TCGATAAACCTCTGCATCCA.....	361
..... TCGATAAACCTCTGCATCCAG.....	7356
..... TCNATAAACCTCTGCATCCAG.....	2
..... TCGATAAACCTCTGCATCCAGA.....	15
..... CGATAAACCTCTGCATCC.....	1
..... CGATAAACCTCTGCATCCA.....	1
..... CGATAAACCTCTGCATCCAG.....	17
..... CGATAAACCTCTGCATCCAGA.....	2
..... GATAAACCTCTGCATCCAG.....	3
..... ATAAACCTCTGCATCCAG.....	2
..... ATAAACCTCTGCATCCAGA.....	3

lka-PremiR-4
MFE -40.20 kcal/mol
LP 78 nt



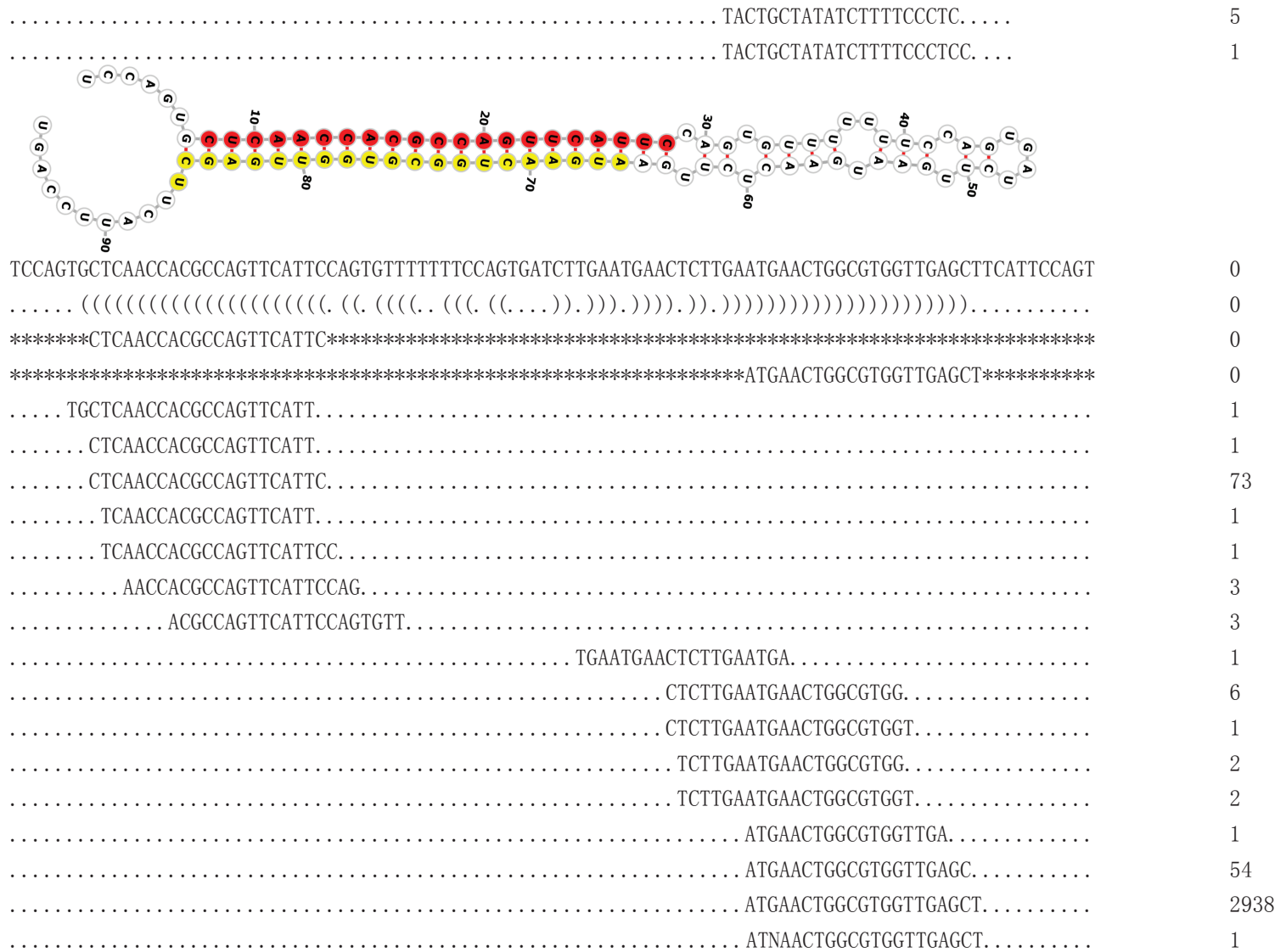
GGAGAATAGGCGGACTGGCATAACTCTGACCGATCATATTTATGGTCAGAGTTTGGCCGTTCCACCCATTCTTATT	0
. (((((((((((((((((((((((((((.....)))))))))).)))))).)))).))))))....	0

*****CGGACTGGCATAACTCTGACC*****	0
*****TCAGAGTTTGGCCGGTCCACC*****	0
... AATAGGCGGACTGGCATAACT...	1
..... GGCGGACTGGCATAACTCTGACC.....	1
..... GCGGACTGGCATAACTCTG.....	1
..... GCGGACTGGCATAACTCTGA.....	3
..... GCGGACTGGCATAACTCTGAC.....	5
..... GCGGACTGGCATAACTCTGACC.....	2
..... CGGACTGGCATAACTCTG.....	28
..... CGNACTGGCATAACTCTGA.....	1
..... CGGACTGGCATAACTCTGA.....	383
..... CGGACTGGCATAACTCTGAC.....	145
..... CGGACTGGCATAACTCTGACC.....	13714
..... CNGACTGGCATAACTCTGACC.....	1
..... CGGACTNGCATAACTCTGACC.....	1
..... CGGACTGGCATAACTCTGACCG.....	2
..... CGGACTGGCATAACTCTGACCGA.....	16
..... CGGACTGGCATAACTCTGACCGAT.....	27
..... CGGACTGGCATAACTCTGACCGATC.....	80
..... GGACTGGCATAACTCTGACC.....	13
..... NACTGGCATAACTCTGACC.....	1
..... GACTGGCATAACTCTGACC.....	5
..... GACTGGCATAACTCTGACCG.....	1
..... ACTGGCATAACTCTGACC.....	103
..... ACTGGCATAACTCTGACCG.....	11
..... ACTGGCATAACTCTGACCGA.....	7

..... ACTGGCATAACTCTGACCGATC.	1
..... ACTGGCATAACTCTGACCGATCA.	2
..... ACTGGCATAACTCTGACCGATCAT.	1
..... ACTGGCATAACTCTGACCGATCATA.	1
..... CTGGCATAACTCTGACCG.	3
..... CTGGCATAACTCTGACCGA.	2
..... TATTTTATGGTCAGAGTTTGC.	1
..... ATTTTATGGTCAGAGTTTGC.	1
..... TTATGGTCAGAGTTTGGCCGGTTCC.	1
..... TATGGTCAGAGTTTGGCCGGTTCCA.	2
..... ATGGTCAGAGTTTGGCCGGTTCCA.	3
..... TGGTCAGAGTTTGGCCGGTTCCA.	1
..... TGGTCAGAGTTTGGCCGGTTCCAC.	2
..... GGTTCAGAGTTTGGCCGGTTC.	6
..... GGTTCAGAGTTTGGCCGGTTCC.	2
..... GGTTCAGAGTTTGGCCGGTTCCA.	1
..... GGTTCAGAGTTTGGCCGGTTCCACC.	2
..... GTCAGAGTTTGGCCGGTTC.	3
..... GTCAGAGTTTGGCCGGTTCC.	4
..... GTCAGAGTTTGGCCGGTTCCA.	2
..... TCAGAGTTTGGCCGGTTC.	232
..... TCAGAGTTTGGCCGGTTCC.	758
..... TCAGAGTTTGGCCGGTTCCA.	177
..... TCAGAGTTTGGCCGGTTCCAC.	1788
..... TCAGAGTTTGGCCGGTTCCACC.	47266
..... TCAGAGTTTGGCCNGTTCCACC.	1

..... AAAAGATATAGCAGTCAAAGT.	12
..... AAAAGATATAGCAGTCAAAGTG.	1
..... AAAAGATATAGCAGTCAAAGTGC.	1
..... AAAGATATAGCAGTCAAAGTG.	7
..... AAGATATAGCAGTCAAAGTG.	1
..... CAAAGTGCTCTCATTGTTCTC.	1
..... TGAACTTTACTGCTATATC.	1
..... TGAACTTTACTGCTATATCT.	2
..... AACTTTACTGCTATATCTTT.	1
..... CTTTACTGCTATATCTTT.	1
..... CTTTACTGCTATATCTTTTC.	6
..... CTTTACTGCTATATCTTTTCC.	4
..... TTTTACTGCTATATCTTT.	9
..... TTTTACTGCTATATCTTTT.	12
..... TTTTACTGCTATATCTTTTC.	233
..... TTTTACTGCTATATCTTTTCC.	40487
..... TTTTACTGCTATATCTTTTCCC.	48
..... TTTTACTGCTATATCTTTTCCCT.	16
..... TTTACTGCTATATCTTTT.	1
..... TTTACTGCTATATCTTTTC.	4
..... TTTACTGCTATATCTTTTCC.	410
..... TTTACTGCTATATCTTTTCCC.	27
..... TTTACTGCTATATCTTTTCCCT.	1
..... TTACTGCTATATCTTTTCC.	23
..... TTACTGCTATATCTTTTCCCT.	3
..... TACTGCTATATCTTTTCC.	3

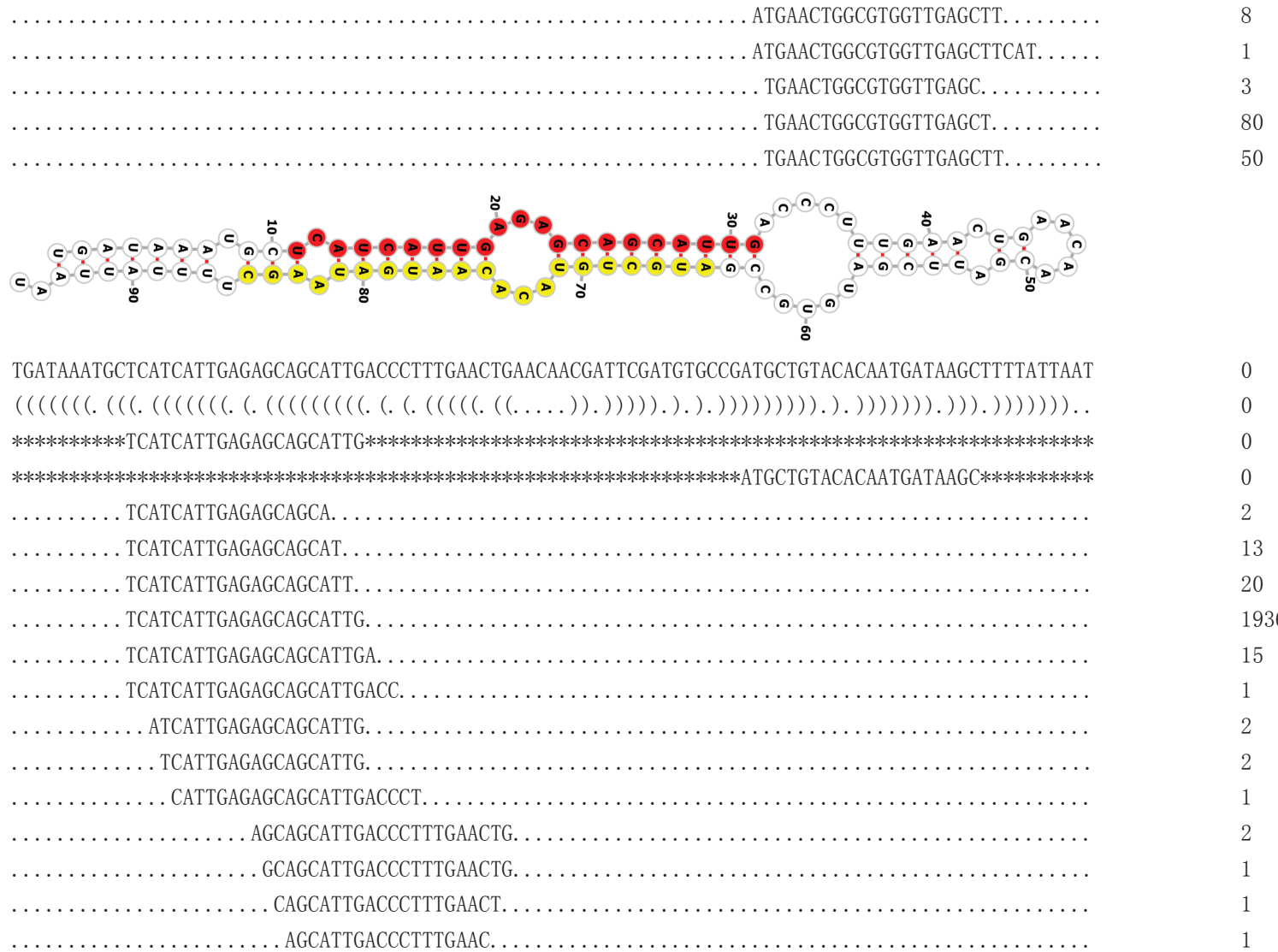
LP 96 nt



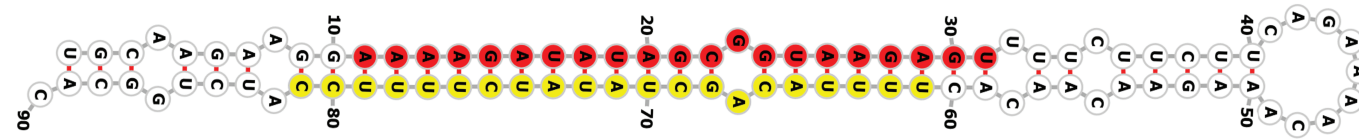
lka-PremiR-7

MFE -30.90 kcal/mol

LP 95 nt



..... ATTCGATGTGCCGATGCTGTA.	2
..... TTCGATGTGCCGATGCTGTACA.	1
..... GCCGATGCTGTACACAATGAT.	1
..... GCCGATGCTGTACACAATGATAAGC.	1
..... NATGCTGTACACAATGATAAG.	1
..... GATGCTGTACACAATGATAAG.	1
..... GATGCTGTACACAATGATAAGC.	4
..... ATGCTGTACACAATGATA.	1
..... ATGCTGTACACAATGATAAG.	7
..... ATGCTGTACACAATGATAAGC.	971
..... TGCTGTACACAATGATAAGC.	3
..... TGCTGTACACAATGATAAGCT.	1



lka-PremiR-8
MFE -38.10 kcal/mol
LP 90 nt

TGCAAGAAGGAAAAGATATAGCGGTAAGAGTTTTCTTCTTCAGAAAACAAAGAACAACACTTTTACAGCTATATCTTTCCATCTGGCAC	0
((. (((. ((((((((((((((((((. ((((((((((. ((((((((((.)))))).)).)))))))).)))))))).))))).)))).	0
*****AAAAGATATAGCGGTAAGAGT*****	0
*****TTTTACAGCTATATCTTTCC*****	0
..... AAGGAAAAGATATAGCGGTAA.	1
..... AGGAAAAGATATAGCGGT.	5
..... AGGAAAAGATATAGCGGTA.	11
..... AGGAAAAGATATAGCGGTAAG.	312
..... AGGAAAAGATATAGCGGTAAGA.	52
..... AGGAAAAGATATAGCGGTAAGAGT.	10

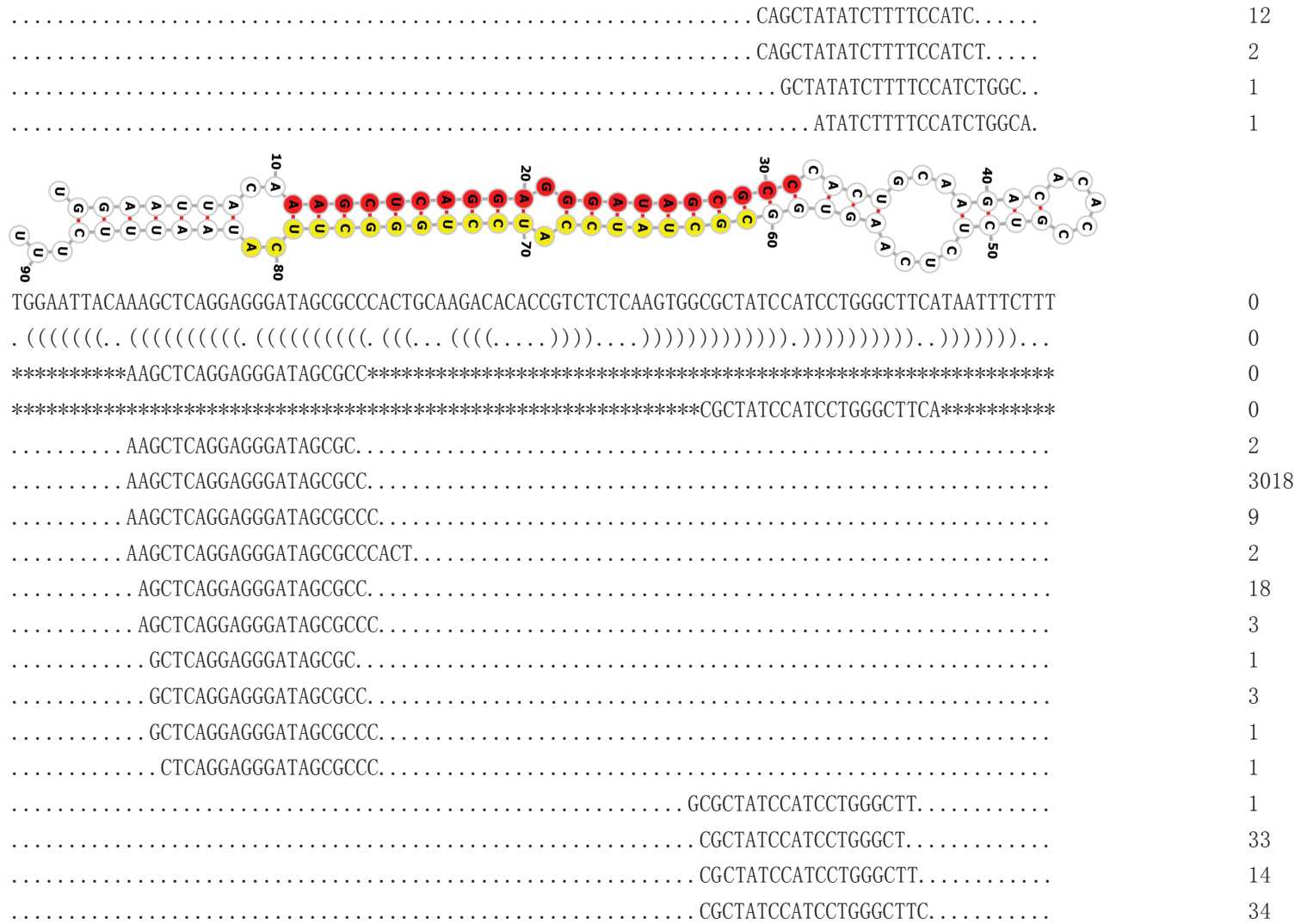
.....AGGAAAAGATATAGCGGTAAGAGTT.....	1
.....GGAAAAGATATAGCGGTA.....	1
.....GGAAAAGATATAGCGGTAAG.....	3
.....GGAAAAGATATAGCGGTAAGA.....	1
.....GAAAAGATATAGCGGTAAG.....	1
.....GAAAAGATATAGCGGTAAGA.....	3
.....GAAAAGATATAGCGGTAAGAG.....	37
.....GAAAAGATATAGCGGTAAGAGT.....	3
.....AAAAGATATAGCGGTAAG.....	11
.....AAAAGATATAGCGGTAAGA.....	4
.....AAAAGATATAGCGGTAAGAG.....	66
.....AAAAGATATAGCGGTAAGAGT.....	1216
.....AAAAGATATAGCGGTAAGAGTT.....	22
.....AAAAGATATAGCGGTAAGAGTTT.....	1
.....AAAGATATAGCGGTAAGA.....	2
.....AAAGATATAGCGGTAAGAG.....	26
.....AAAGATATAGCGGTAAGAGT.....	13
.....AAAGATATAGCGGTAAGAGTT.....	175
.....AAAGATATAGCGGTAAGAGTTT.....	1
.....AAAGATATAGCGGTAAGAGTTTTC.....	1
.....ATAGCGGTAAGAGTTTCTTC.....	1
.....TCAGAAAACAAAGAACAACACTT.....	1
.....CACTTTTACAGCTATATCTTT.....	1
.....CTTTTACAGCTATATCTTTTC.....	23
.....TTTTACAGCTATATCTTT.....	1
.....TTTTACAGCTATATCTTTT.....	1

..... TTTTACAGCTATATCTTTTC.	26
..... TTTTACAGCTATATCTTTTCC.	6804
..... TTTTACAGCTATATCTTTTCCA.	1
..... TTTTACAGCTATATCTTTTCCAT.	6
..... TTTTACAGCTATATCTTTTCCATC.	25
..... TTTTACAGCTATATCTTTTCCATCT.	1
..... TTTACAGCTATATCTTTTC.	6
..... TTTACAGCTATATCTTTTCC.	49
..... TTTACAGCTATATCTTTTCCA.	335
..... TTTACAGCTATATCTTTTCCAT.	4
..... TTTACAGCTATATCTTTTCCATC.	4
..... TTTACAGCTATATCTTTTCCATCT.	1
..... TTACAGCTATATCTTTTC.	1
..... TTACAGCTATATCTTTTCC.	17
..... TTACAGCTATATCTTTTCCA.	26
..... TTACAGCTATATCTTTTCCAT.	19
..... TTACAGCTATATCTTTTCCATC.	7138
..... TTACAGCTATATCTTTTCCATCT.	18
..... TACAGCTATATCTTTTCC.	14
..... TACAGCTATATCTTTTCCA.	23
..... TACAGCTATATCTTTTCCAT.	27
..... TACAGCTATATCTTTTCCATC.	10011
..... TACAGCTATATCTTTTCCATCT.	15
..... ACAGCTATATCTTTTCCATC.	24
..... ACAGCTATATCTTTTCCATCT.	2
..... CAGCTATATCTTTTCCAT.	1

lka-PremiR-9

MFE -49.40 kcal/mol

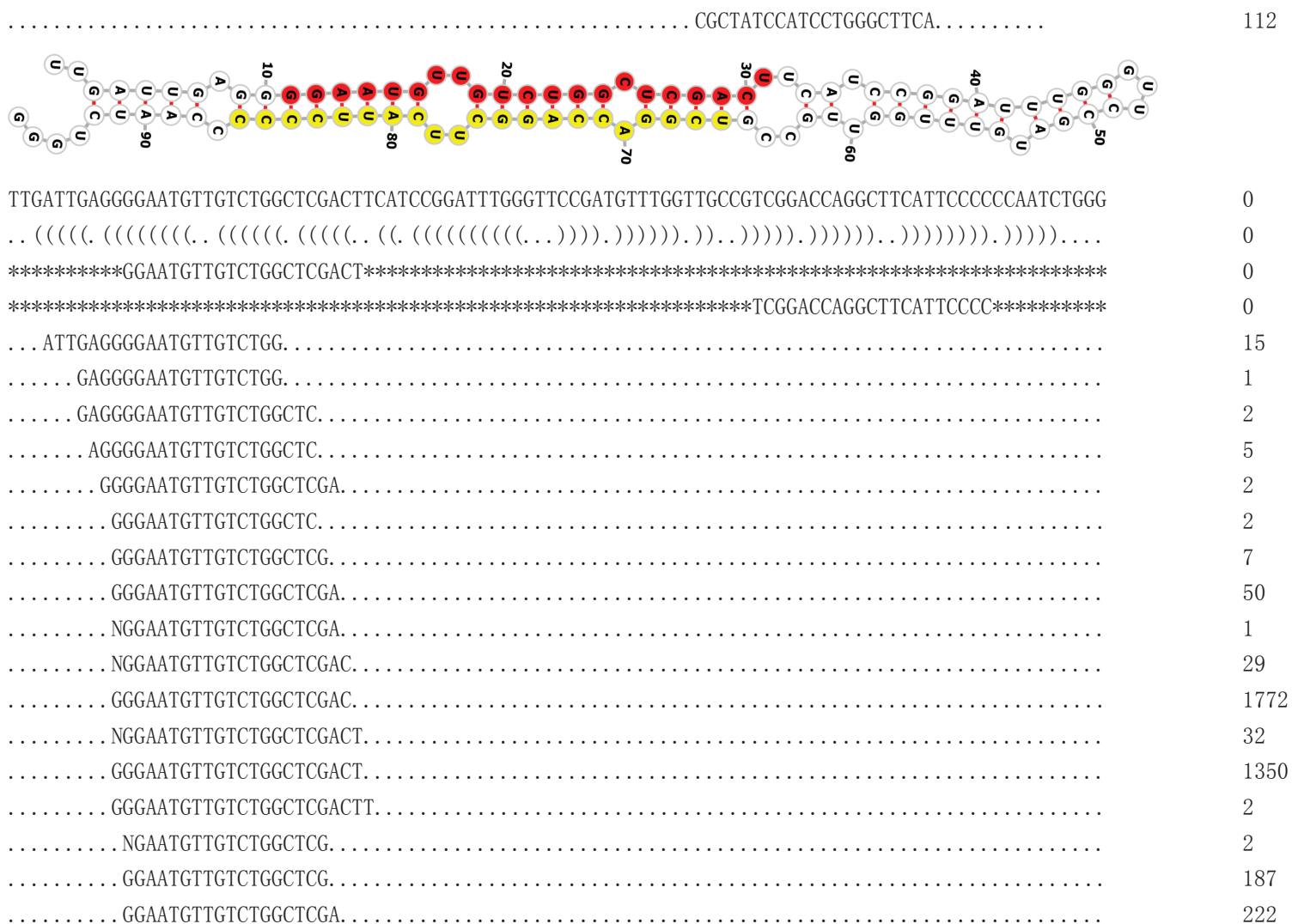
LP 91 nt



lka-PremiR-10

MFE -48.60 kcal/mol

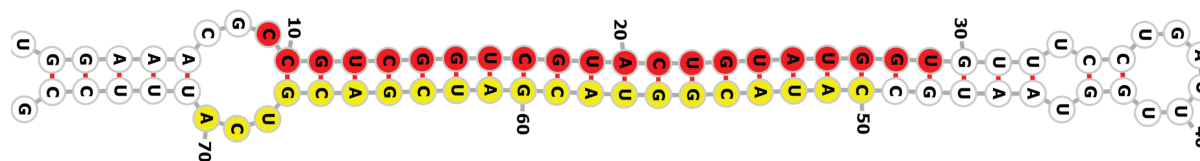
LP 96 nt



..... NGAATGTTGTCTGGCTCGA.....	6
..... GGAATGTTGTCTGGCTCGAC.....	593
..... NGAATGTTGTCTGGCTCGAC.....	7
..... NGAATGTTGTCTGGCTCGACT.....	142
..... GGAATGTTGTCTGGCTCGACT.....	9646
..... GNAATGTTGTCTGGCTCGACT.....	1
..... GGAATGTTGTCTGGCTCGACTT.....	8
..... GGAATGTTGTCTGGCTCGACTTC.....	5
..... GAATGTTGTCTGGCTCGA.....	6
..... GAATGTTGTCTGGCTCGAC.....	1
..... GAATGTTGTCTGGCTCGACT.....	5
..... GAATGTTGTCTGGCTCGACTT.....	6
..... AATGTTGTCTGGCTCGACT.....	12
..... ATGTTGTCTGGCTCGACT.....	5
..... GTCCGATGTTTGTTGCC.....	1
..... TCCGATGTTTGTTGCC.....	1
..... TTTGGTTGCCGTCGGACCAGGCT.....	1
..... TGCCGTCGGACCAGGCTTCATTCCC.....	1
..... CCGTCGGACCAGGCTTCATTCC.....	1
..... CCGTCGGACCAGGCTTCATTCCCC.....	25
..... CGTCGGACCAGGCTTCATTCC.....	7
..... GTCGGACCAGGCTTCATTCC.....	1
..... NTCGGACCAGGCTTCATTCC.....	3
..... GTCGGACCAGGCTTCATTCCC.....	197
..... NTCGGACCAGGCTTCATTCCC.....	16
..... GTCGGACCAGGCTTCATTCCCC.....	21

.....NTCGGACCAGGCTTCATTCCCC.....	84
.....TCGGACCAGGCTTCATTCC.....	821
.....TCGGACCAGGCTTCATTCC.....	13688
.....TCNGACCAGGCTTCATTCC.....	2
.....TCGGACCANGCTTCATTCC.....	1
.....TCGGACCAGGCTTCATTCCC.....	17145
.....TCNGACCAGGCTTCATTCCC.....	3
.....TCGGACCANGCTTCATTCCCC.....	70
.....TCGNACCAGGCTTCATTCCCC.....	41
.....TCNGACCAGGCTTCATTCCCC.....	944
.....TCGGACCAGGCTTCATTCCCC.....	6596666
.....TCGGACCAGGCTTCATTCCCCC.....	2025
.....TCGGACCAGGCTTCATTCCCCCC.....	3
.....TCGGACCAGGCTTCATTCCCCCA.....	1
.....CGGACCAGGCTTCATTCC.....	3
.....CGGACCAGGCTTCATTCCC.....	16
.....CGGACCAGGCTTCATTCCCC.....	301
.....CGGACCAGGCTTCATTCCCCC.....	7689
.....CGNACCAGGCTTCATTCCCCC.....	1
.....CGGACCAGGCTTCATTCCCCCC.....	13
.....GGACCAGGCTTCATTCCC.....	8
.....NGACCAGGCTTCATTCCCC.....	1
.....GGACCAGGCTTCATTCCCC.....	253
.....GGACCAGGCTTCATTCCCCC.....	11
.....GGACCAGGCTTCATTCCCCCC.....	1
.....GACCAGGCTTCATTCCCC.....	4

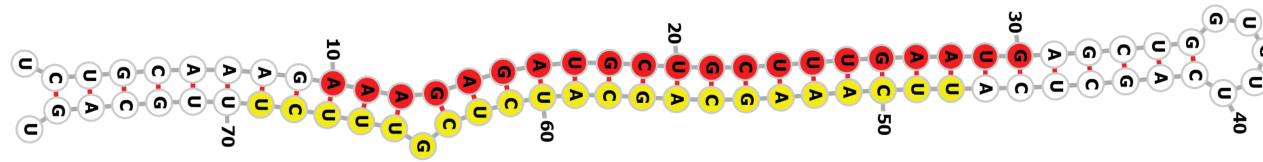
LP 76 nt



TGGAAACGCCGTCGGTCGTATGTTTCCCTGATTGGAATGCCATACGGTACGATCGACGTCATTTCGG	0
. (((((((. ((((((((((((((((((((((((((((.))).)))))))))))))))))).).)))).	0
*****CCGTCGGTCGTACTGTATGGT*****	0
*****CATACGGTACGATCGACGTCA*****	0
. GGAAACGCCGTCGGTCGTA.	1
. GGAAACGCCGTCGGTCGTAC.	1
. . . AAACGCCGTCGGTCGTACTGTA.	1
. . . . AACGCCGTCGGTCGTACTGTA.	2
. . . . AACGCCGTCGGTCGTACTGTATGG.	8
. GCCGTCGGTCGTACTGTATGG.	7
. CCGTCGGTCGTACTGTATG.	21
. CCGTCGGTCGTACTGTATGG.	35
. CCGTCGGTCGTACTGTATGGT.	870
. CCGTCGGTCGTACTGTATGGTG.	8
. CGTCGGTCGTACTGTATG.	19
. CGTCGGTCGTACTGTATGG.	2
. CGTCGGTCGTACTGTATGGT.	25
. CGTCGGTCGTACTGTATGGTG.	13
. GTCGGTCGTACTGTATGG.	1
. GTCGGTCGTACTGTATGGT.	1
. GTCGGTCGTACTGTATGGTGTT.	1
. GTACTGTATGGTGTTCCT.	1

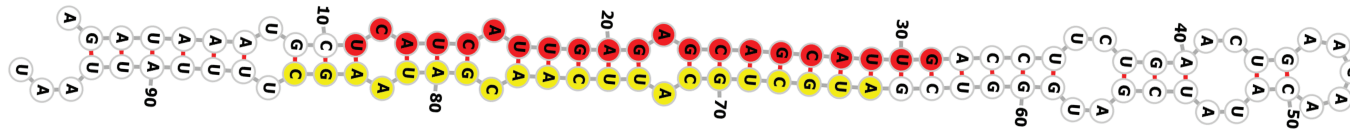
..... TACTGTATGGTGTTCCT.	2
..... TACTGTATGGTGTTCCTG.	3
..... TACTGTATGGTGTTCCTGAT.	1
..... GTTTCCTGATTGGTAATG.	1
..... TGCCATACGGTACGATCGACGT.	1
..... TGCCATACGGTACGATCGACGTC.	10
..... TGCCATACGGTACGATCGACGTCA.	3
..... GCCATACGGTACGATCGACG.	1
..... CCATACGGTACGATCGAC.	7
..... CCATACGGTACGATCGACGT.	2
..... CCATACGGTACGATCGACGTC.	310
..... CATACGGTACGATCGACG.	9
..... CATACGGTACGATCGACGT.	21
..... CATACGGTACGATCGACGTC.	436
..... CATACGGTACGATCGACGTCA.	141
..... CATACGGTACGATCGACGTCAT.	3
..... CATACGGTACGATCGACGTCATT.	1
..... ATACGGTACGATCGACGT.	5
..... ATACGGTACGATCGACGTC.	108
..... ATACGGTACGATCGACGTCA.	27
..... ATACGGTACGATCGACGTCAT.	18
..... ATACGGTACGATCGACGTCATT.	13
..... TACGGTACGATCGACGTC.	3
..... TACGGTACGATCGACGTCAT.	2

LP 76 nt



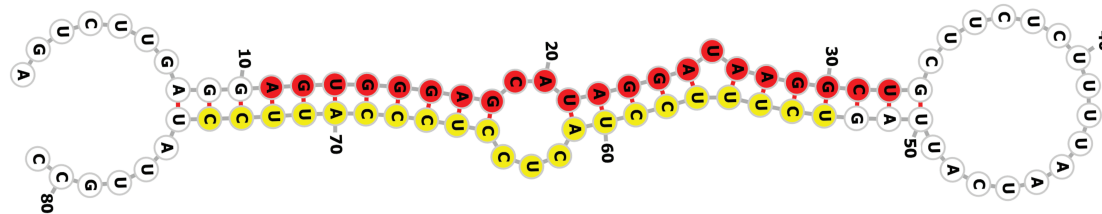
TCTGCAAAGAAAGAGATGCTGCTTTGAATGAGCTGGTGTTCAGCTCATTCAAAGCAGCATCTCGTTTCTTTGCAGT	0
. (((...))))))))))))))))))).)))))))).	0
*****AAAGAGATGCTGCTTTGAATG*****	0
*****TTCAAAGCAGCATCTCGTTTCT*****	0
..... AAAGAGATGCTGCTTTGAA.	4
..... AAAGAGATGCTGCTTTGAATG.	181
..... AAAGAGATGCTGCTTTGAATGA.	3
..... AAAGAGATGCTGCTTTGAATGAG.	12
..... AAGAGATGCTGCTTTGAA.	2
..... AAGAGATGCTGCTTTGAAT.	1
..... AAGAGATGCTGCTTTGAATG.	9
..... AAGAGATGCTGCTTTGAATGA.	8
..... AGAGATGCTGCTTTGAATG.	2
..... GCTGCTTTGAATGAGCTG.	1
..... TCATTCAAAGCAGCATCTCGT.	3
..... ATTCAAAGCAGCATCTCGTT.	1
..... ATTCAAAGCAGCATCTCGTTTC.	3
..... TTCAAAGCAGCATCTCGT.	3
..... TTCAAAGCAGCATCTCGTT.	1
..... TTCAAAGCAGCATCTCGTTT.	7
..... TTCAAAGCAGCATCTCGTTTC.	183
..... TTCAAAGCAGCATCTCGTTTCT.	2397
..... TTCAAAGCAGCATCTCGTTTCTT.	20

LP 95 nt



AGATAAATGCTCATCATTGAGAGCAGCATTGACCTTCTGAACTGAACAACATATCGATGGGTCGATGCTGCATTCAACGATAAGCTTTTATTAAT	0
. ((((((. (((. (((. (((((. ((((((((((((((. (((. ((. (...)).)).)).)))))))))))))).))))).)).)).))))). . .	0
*****TCATCATTGAGAGCAGCATTG*****	0
*****ATGCTGCATTCAACGATAAGC*****	0
..... TCATCATTGAGAGCAGCA.	2
..... TCATCATTGAGAGCAGCAT.	13
..... TCATCATTGAGAGCAGCATT.	20
..... TCATCATTGAGAGCAGCATTG.	1936
..... TCATCATTGAGAGCAGCATTGA.	15
..... TCATCATTGAGAGCAGCATTGACC.	1
..... ATCATTGAGAGCAGCATTG.	2
..... TCATTGAGAGCAGCATTG.	2
..... AGCAGCATTGACCTTCTG.	2
..... GCATTGACCTTCTGAACTGAACAA.	1
..... TGGGTCGATGCTGCATTCAACGATA.	2
..... GATGCTGCATTCAACGATAAGC.	2
..... ATGCTGCATTCAACGATAAGC.	52

LP 81 nt



AGTCTTGAGGAGTGGGAGCATAGGATAAGGCTGCTTCTCTTTTAATCATTAGTCTTTCCTACTCCTCCCATTCTTATGCC	0
. ((... ((((((((((. ((((((((((((.....)))))))))))). ...)))))))))). ...)).	0
*****AGTGGGAGCATAGGATAAGGCT*****	0
*****TCTTTCCTACTCCTCCCATTCC*****	0
..... AGTGGGAGCATAGGATAAGGCT.....	37
..... AGTGGGAGCATAGGATAAGGCTG.....	2
..... AGTGGGAGCATAGGATAAGGCTGC.....	2
..... AGTGGGAGCATAGGATAAGGCTGCT.....	7
..... GTGGGAGCATAGGATAAGGCTG.....	1
..... TGGGAGCATAGGATAAGGCTG.....	1
..... GGGAGCATAGGATAAGGCTG.....	4
..... GGGAGCATAGGATAAGGCTGC.....	1
..... AGCATAGGATAAGGCTGCT.....	1
..... AAGGCTGCTTCTCTTTTAATCATT.....	1
..... CTGCTTCTCTTTTAATCATT.....	1
..... CTGCTTCTCTTTTAATCATTAGTC.....	1
..... CTTCTCTTTTAATCATTAGTC.....	1
..... TTCTCTTTTAATCATTAGTC.....	1
..... TTTTAATCATTAGTCTTTCCTACTC.....	1
..... ATTAGTCTTTCCTACTCCTCCCATT.....	1
..... TAGTCTTTCCTACTCCTCCCATT.....	2
..... GTCTTTCCTACTCCTCCCA.....	1
..... TCTTTCCTACTCCTCCCA.....	7
..... TCTTTCCTACTCCTCCCAT.....	2
..... TCTTTCCTACTCCTCCCATT.....	21
..... TCTTTCCTACTCCTCCCATTCT.....	7

..... TGCTCTTCCACAGCTTTCTTG.....	51
..... TCTTCCACAGCTTTCTTGA.....	1
..... TCTTCCACAGCTTTCTTGAAC.....	16
..... TCTTCCACAGCTTTCTTGAAC.....	6
..... TCTTCCACAGCTTTCTTGAAC.....	1
..... TCTTCCACAGCTTTCTTGAAC.....	6
..... CTTCACAGCTTTCTTGAAC.....	14
..... TTCCACAGCTTTCTTGAAC.....	23
..... TTCCACAGCTTTCTTGAAC.....	2087
..... TTCCACAGCTTTCTTGAAC.....	20237
..... TTCCACAGCTTTCTTGAAC.....	8
..... TTCCACAGCTTTCTTGAAC.....	172181
..... TTCCACAGCTTTCTTGAAC.....	21
..... TTCCACAGCTTTCTTGAAC.....	2
..... TTCCACAGCTTTCTTGAAC.....	2
..... TTCCACAGCTTTCTTGAAC.....	1
..... TCCACAGCTTTCTTGAAC.....	21
..... TCCACAGCTTTCTTGAAC.....	140
..... TCCACAGCTTTCTTGAAC.....	171
..... CCACAGCTTTCTTGAAC.....	58
..... CCACAGCTTTCTTGAAC.....	11
..... CACAGCTTTCTTGAAC.....	94
..... CACAGCTTTCTTGAAC.....	1
..... GCTTTCTTGAAC.....	1
..... TTTCTTGAAC.....	1
..... TTCTTGAAC.....	1

..... TTCTTGAAC TAAGAGTCGAT.	1
..... TTCTTGAAC TAAGAGTCGATC.	6
..... TCTTGAAC TAAGAGTCGATCGG.	2
..... TCTTGAAC TAAGAGTCGATCGGA.	1
..... AACTAAGAGTCGATCGGATCCGGT.	1
..... TAAGAGTCGATCGGATCCGGTC.	1
..... AAGAGTCGATCGGATCCGGT.	2
..... AAGAGTCGATCGGATCCGGTC.	1
..... AAGAGTCGATCGGATCCGGTCAGT.	1
..... GAGTCGATCGGATCCGGTCAGTTCA.	1
..... TCGGATCCGGTCAGTTCAGAGC.	2
..... TCGGATCCGGTCAGTTCAGAGCTCA.	1
..... CGGATCCGGTCAGTTCAGA.	1
..... GGATCCGGTCAGTTCAGA.	3
..... GGATCCGGTCAGTTCAGAGC.	1
..... GGATCCGGTCAGTTCAGAGCTCA.	2
..... GGATCCGGTCAGTTCAGAGCTCAAG.	1
..... TCCGGTCAGTTCAGAGCTCAAGA.	1
..... TCCGGTCAGTTCAGAGCTCAAGAAA.	1
..... CCGGTCAGTTCAGAGCTCAAGA.	1
..... CCGGTCAGTTCAGAGCTCAAGAA.	1
..... CGGTCAGTTCAGAGCTCAAGAAAG.	2
..... CGGTCAGTTCAGAGCTCAAGAAAGC.	8
..... GTTCAGAGCTCAAGAAAGCTG.	1
..... TTCAGAGCTCAAGAAAGCT.	2
..... TCAGAGCTCAAGAAAGCTGTGGG.	1

.....AGCTCAAGAAAGCTGTGGGA.....	1
.....GCTCAAGAAAGCTGTGGG.....	8
.....GCTCAAGAAAGCTGTGGGA.....	50
.....GCTCAAGAAAGCTGTGGGAA.....	28
.....GCTCAANAAAGCTGTGGGAAA.....	1
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.....GCTCAAGAAAGCTGTGGGAAA.....	1683
.....CTCAAGAAAGCTGTGGGA.....	75
.....CTCAAGAAAGCTGTGGGAA.....	105
.....CTCAAGAAAGCTGTGGGAAA.....	1444
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.....TCAAGAAAGCTGTGGGAAA.....	44
.....TCAAGAAAGCTGTGGGAAAA.....	5
.....TCAAGAAAGCTGTGGGAAAAC.....	9
.....CAAGAAAGCTGTGGGAAA.....	1
.....CAAGAAAGCTGTGGGAAAA.....	1
.....AAGAAAGCTGTGGGAAAAC.....	3
.....AAGAAAGCTGTGGGAAAACA.....	22
.....AAGAAAGCTGTGGGAAAACAT.....	1
.....AGAAAGCTGTGGGAAAAC.....	1