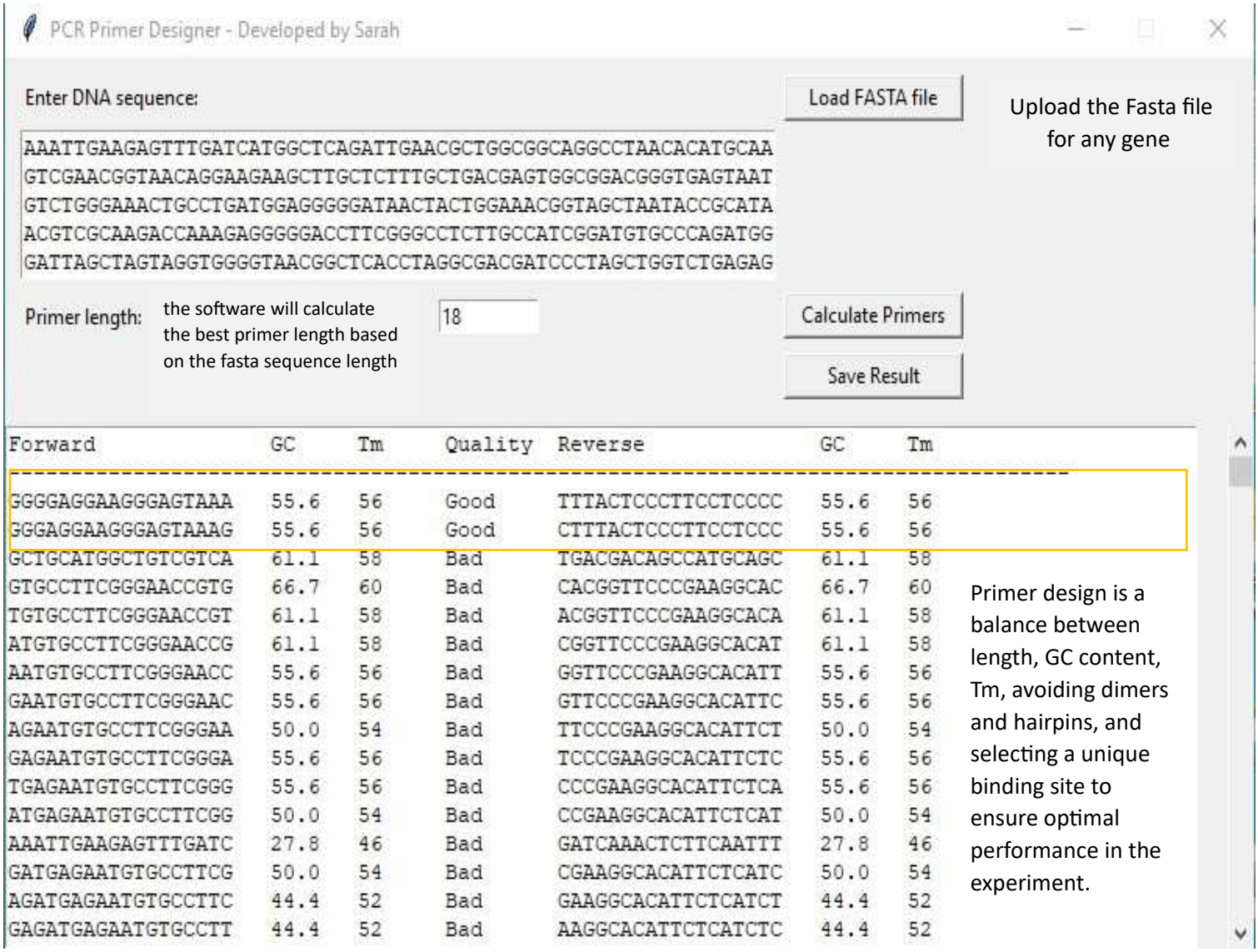
PCR Primer Designer - Developed by Sarah
Enter DNA sequence:
Load FASTA file
AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAA
GTCGAACGGTAACAGGAAGAAGCTTGCTCTTTGCTGACGAGTGGCGGACGGGTGAGTAAT
GTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATA
ACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCGGATGTGCCCAGATGG
GATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAG
Upload the Fasta file for any gene
Primer length:
the software will calculate the best primer length based on the fasta sequence length
18
Calculate Primers
Save Result
Forward GC Tm Quality Reverse GC Tm
GGGGAGGAAGGGAGTAAA 55.6 56 Good TTTACTCCCTTCCTCCCC 55.6 56
GGGAGGAAGGGAGTAAAG 55.6 56 Good CTTTACTCCCTTCCTCCC 55.6 56
GCTGCATGGCTGTCGTCA 61.1 58 Bad TGACGACAGCCATGCAGC 61.1 58
GTGCCTTCGGGAACCGTG 66.7 60 Bad CACGGTTCCCGAAGGCAC 66.7 60
TGTGCCTTCGGGAACCGT 61.1 58 Bad ACGGTTCCCGAAGGCACA 61.1 58
ATGTGCCTTCGGGAACCG 61.1 58 Bad CGGTTCCCGAAGGCACAT 61.1 58
AATGTGCCTTCGGGAACC 55.6 56 Bad GGTTCCCGAAGGCACATT 55.6 56
GAATGTGCCTTCGGGAAC 55.6 56 Bad GTTCCCGAAGGCACATTC 55.6 56
AGAATGTGCCTTCGGGAA 50.0 54 Bad TTCCCGAAGGCACATTCT 50.0 54
GAGAATGTGCCTTCGGGA 55.6 56 Bad TCCCGAAGGCACATTCTC 55.6 56
TGAGAATGTGCCTTCGGG 55.6 56 Bad CCCGAAGGCACATTCTCA 55.6 56
ATGAGAATGTGCCTTCGG 50.0 54 Bad CCGAAGGCACATTCTCAT 50.0 54
AAATTGAAGAGTTTGATC 27.8 46 Bad GATCAAACTCTTCAATTT 27.8 46
GATGAGAATGTGCCTTCG 50.0 54 Bad CGAAGGCACATTCTCATC 50.0 54
AGATGAGAATGTGCCTTC 44.4 52 Bad GAAGGCACATTCTCATCT 44.4 52
GAGATGAGAATGTGCCTT 44.4 52 Bad AAGGCACATTCTCATCTC 44.4 52
Primer design is a balance between length, GC content, Tm, avoiding dimers and hairpins, and selecting a unique binding site to ensure optimal performance in the experiment.