

Sequence of the sense strand DNA encoding your SELEX library:

CCGAAGCTTAATACGACTCACTATAGGGAGCTCAGAATAAACGCTCAA[N₁₋₅₀]TTCGACATGAGGCCCGGATCCGGC

The primers used for polymerase chain reaction (PCR) and reverse transcription (RT) have the following sequences:

5'-Primer

CCGAAGCTTAATACGACTCACTATAGGGAGCTCAGAATAAACGCTCAA

3'-Primer

GCCGGATCCGGCCTCATGTTCGAA

Notes

1. The initial library contains a 50 base long randomized region, designated as [N₁₋₅₀]. At the level of the library pool, there is an equal probability of finding any of the four bases at each position in this region. However, any single molecule derived from this pool has a unique base at each position derived from this region.

2. The T7 promoter is underlined. The first base to be incorporated into your RNA transcription product is the G shown in boldface. Therefore, an RNA transcript derived from this library will have the sequence:

GGGGAGCUCAGAAUAAACGCUCAA[N₁₋₅₀]UUCGACAUGAGGCCCGGAUCCGGC

The DNA sequence data for 30 different clones obtained at the end of your SELEX process to identify heme binding aptamers is given below. The sequence corresponds to the N₁₋₅₀ region only.

>Clone_6-3

TGGTTTCAGCGACAGGAGGGGTGATGCTGTCCTTTGCGTGT

>Clone_6-5

CTTATGCAGTTTTACAGGGGTGATATGACTGCACCAGTAGGGGGATGTTC

>Clone_8-1

TGCTAGTGTGTATGCACGTGGAGGAGGCGTACACTTGCTTTGTGGT

>Clone_8-3

TGCAGAAGTTGCGTGTGGAGGAGGTGGCATGACTGCTGTTAGGGTAGTTG

>Clone_8-50

GGGATCTGGTTGAAACTGGAGGCCTATAGAAGTTGGTTGTGTGTTTTGAG

>Clone_8-6

GTCCTGTGATGGTATTTTTTCGTTCCGCTTACTTCGACATGAGGCCCGGATCCATCTGAA

T

>Clone_8-7

GATTGACCGTATGGAGGATGCAAAGGGAGGGAGGTCACTTGAGTTAGTTA
>Clone_8-8
GCAGGATGTGGAGGAGGCATCTGCTGCAATCGGGACTTGTGTGCGAGTATC
>Clone_8-12
GCATTGTCTGCGTGTGGAGGCAGGAGGCAAGATAAGAGGTGATGCGGTTG
>Clone_8-13
CATGTTGGCGATACGTCTAAACGGTGGGTTGTGGAGGATTGATTTATACG
>Clone_8-19
AGTAGTGTGACCGTGTGGTGGAGGTTGGCGACATATGTAGGGTGCATG
>Clone_8-2
GGGTTCTGGTTGAAACTGGAGGCCTATAGAAGTTGGTTGTGTGTTTTGAG
>Clone_8-20
CGAAGGCACTTCATGGGGTGGAGGAGGCATGCGAGGTGTCCGGCGAGTGG
>Clone_8-10
TGCTAGTGTTGTATGCACGTGGAGGAGGAGGCGTACACTTGCTTTGTGGT
>Clone_8-18
GATTGACCGTATGGAGGATGCATAGGGAGGGAGGTCACTTGAATTAGTTA
>Clone_8-26
CACACGTGACTGTGGAGGCAGCGGAGGCGAGTTATGTGATGTTAAGAGGT
>Clone_8-28
TATGTTAAGAGGCCACTGATGCGCGTAGGTCTCTGGGGATTGAGGAAGGT
>Clone_8-30
AGGTTGCGCTAGGTGAGGAAGGAGGTGTAGGTACGGCCTATTGAGTGGGA
>Clone_8-31
CGTAGTCCATGAGTGTCTTTAGCTAACGGTTGGTAGTGAACCATATCCTG
>Clone_8-32
GCCAATGAGAGCTGTAGGAGGGCGGGACGTGCTTAGTGCGTGACACCGGA
>Clone_8-33
TTGTCCTGACTTGCTTGAACGTTAGCGTGATGCGTTATGCCCTGGATGGG
>Clone_8-16
GCATTGTCTGCGTGTGGAGGCAGGAGGCAAGATAAGAGGTGATGCGGTTG
>Clone_8-11
TGCTAGTGTTGTATGCACGTGGAGGAGGAGGCGTACACTTGCTTTGTGGT
>Clone_8-34
CACCAATGACGGGGGTTAAGACGGAGGGAGATGCATCGGTGTGAAGCTGA
>Clone_8-47
GGGATCTGGTTGAAACTGGAGGCCTATAGAAGTTGGTTGTGTGTTTTGAG
>Clone_8-38
TGCGCAATACACGGTGAGGAGGTGGAGAGATGTAGGTGCTTAGCAGTTGA
>Clone_8-17
GATTGACCGTATGGAGGATGCAAAGGGAGGGAGGTCACTTGAGTTAGTTA
>Clone_8-15
TGCTAGTGTTGTATGCACGTGGAGGAGGAGGCGTACACTTGCTTTGTGGT
>Clone_8-37
CGTGAACGCATGTGGTGGAGGAGGCGATTGCACGTGGGACCGAGCATTG
>Clone_8-42
TGGACCGCAGCACGGCGCTCGTGGTAAGGCCGTATGCCCATCGAATGAAG