

**Supplementary Information: “Rationally Designed DNA Looping Peptides Control DNA Topology,” by Gowetski, Kodis, and Kahn. *Nucleic Acids Research*, 2013.**

**Additional files provided in a zip archive: PDB files for models of LZD73 and LZD87 bound to DNA, PDB files for models of minicircle topoisomers formed from DNA loops, Microsoft Excel spreadsheet with the topoisomer distributions for the experiment of Figure 4.**

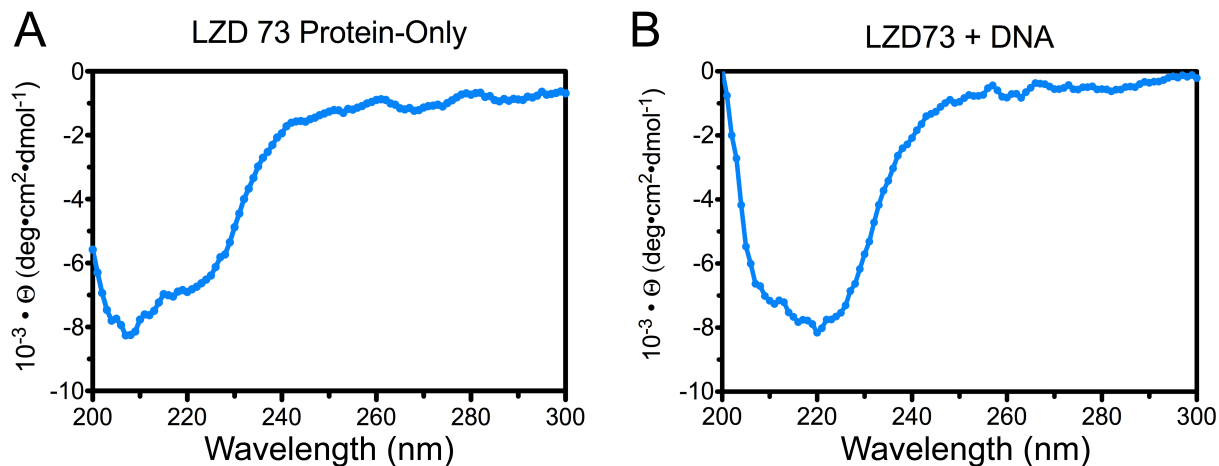
### **SI Materials and Methods:**

#### **Protein Expression and Purification**

The gene for LZD73 was synthesized commercially (BioMatik Inc.) and was cloned into pRSET A (Invitrogen/Life Technologies) using BamHI and EcoRI restriction sites. The gene for LZD87 was cloned using standard methods by inserting an additional 42 bp (coding for 14 aa, two coiled coil turns) into the plasmid containing *Lzd73*. The peptides were expressed in *E. coli* BL21 DE3 (pLysS) cells, grown in LB media with ampicillin (100 µg/ml) and chloramphenicol (40 µg/ml) at 37 °C, induced with 0.5 mM IPTG during a 14 hour induction. Cells were lysed by French press in 10 mM MES pH 6.0, 0.5 M NaCl, 20 mM imidazole. The peptides were purified from the soluble supernatant by FPLC with a Co<sup>2+</sup>-charged HiTrap chelating affinity column (GE Healthcare) utilizing a 20-400 mM imidazole gradient. The peak elution fractions were concentrated using a Centricon Ultra 4000 (Millipore), and were buffer exchanged into a storage buffer of 10 mM Tris HCl pH 7.7, 150 mM NaCl, and 10 % glycerol using Biospin 6 columns (BioRad). The proteins were quantitated by UV absorption using an estimated  $\epsilon(280\text{ nm}) = 8480\text{ M}^{-1}\text{cm}^{-1}$  from the ProtParam tool (ExpASY). Peptide molecular weight and purity (est. > 98 % based on Coomassie staining) was confirmed using SDS PAGE.

The expected  $\alpha$ -helical folding of the coiled-coil was verified by circular dichroism (CD) as shown in Fig. S1.

**Supplementary Figure S1: CD analysis of the LZD73 peptide.** (A) LZD73 peptide alone (1.2 µM) in 20 mM Tris-HCl (pH 8.0 @ 25°C), 50 mM NaCl, 2 mM CaCl<sub>2</sub>. (B) LZD73 (1.2 µM) with 58mer CREB site dsDNA (1 µM). The two dips at 210 nm and 220 nm are indicative of  $\alpha$ -helical folding. An increase in the amplitude of the 220 nm signal is observed upon DNA addition, consistent with additional folding of the basic region upon DNA binding.



### ***DNA Sequences Used in Cyclization Assays***

The DNA fragments below were made by PCR, subjected to XhoI digestion, and gel purified as described in the text. Each sequence contains one CREB site (5'-ATGACGTCAT-3') and one Inv-2 site (5' -GTCATATGAC-3'), which are **highlighted**, and two XhoI sites (5' -CTCGAG-3'), which are underlined.

Vx (448) 212

AATGTGTGCCTGGCGATCTCGAGTGCAGCTGGAAGACAAGGTGGAGGAACTGCTGAGCAAGAAC  
TACCACCTGGAGAACGAAGTTGCGCGCCTGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCAT  
GCGCGGGATCCGAATTCTCCGGATCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTC  
CCAACAGTTGCGCAGCCTGAATGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGCG  
GGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCG  
CTTTCTTCCCTTCCCTTTCTCGCCACGTTCCGCCGCTTTCCCGTCAAGCTCTAAATCGGGGGCT  
CCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGAT  
GGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCACGT  
TCTTTAATAGTGGACTCTTGTTCCAACTGGAACAACACTCAACCCTATCTCGCGTCATATGAC  
CAAGCTTGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAG  
CAATAACTAGCATAAACCCTTTTGCAGCTTTTCTCGAGTCAAGACCCGTTTAGAGGCC

Vx (153) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCGCTGCTCTGAAG  
CGAGCTCGGAACACTGAAGCTGCTCGACGGAGCCGAGCTCGGAAGCTGCAACGAATGAAGCAGC  
TGGAAGACAAGGTGGAGGAACTGCTGAGCAAGAACTACCACCTGGAGAACGAAGTTGCGCGCCT  
GAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGGGATCCGAATTCTCCGGATCTGG  
CGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAAT  
GGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGCGGGTGTGGTGGTTACGGTCATATGACCAAG  
CTGAATTCGCGCGCTGACCTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTTATTTTTCTAAAT  
ACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAA  
AGGAAGAGTATGAGTATTCAACATTTCCGTGTGCGCCCTTATTCCCTTTTTTTCGGGCATTTTGCC  
TTCCTGTTTCTCGAGTTGCAGCTTTT

Vx (202) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCAGCTGCTCTGAA  
GCGAGCTCGGAACACTGAAGCTGCTCGACGGAGCCGAGCTCGGAAGCTGCAACGAATGAAGCAG  
CTGGAAGACAAGGTGGAGGAACTGCTGAGCAAGAACTACCACCTGGAGAACGAAGTTGCGCGCC  
TGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGGGATCCGAATTCTCCGGATCTG  
GCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAA  
TGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCG  
CTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGGTCATATGACCAAGCTGAATTCGCGCGC  
TGACCTCGGAAATGTGCGCGGAACCCCTATTTGTTTTATTTTTCTAAATACATTCAAAATATGTAT  
CCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTA  
TTCAACATTTCCGTGTGCGCCCTTATTCCCTTTTTTTCGGGCATTTTGCCTTCTGTTTCTCGAGT  
TGCAGCTTTT

Vx (254) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCAGCTGCTCTGAA  
GCGAGCTCGGAACACTGAAGCTGCTCGACGGAGCCGAGCTCGGAAGCTGCAACGAATGAAGCAG

CTGGAAGACAAGGTGGAGGAACTGCTGAGCAAGAACTACCACCTGGAGAACGAAGTTGCGCGCC  
TGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGCGGATCCGAATTCTCCGGATCTG  
GCGTAATAGCGAAGAGGCCCGCACCCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAA  
TGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGGCGGGTGTGGTGGTTACGCGCAGCGTGACCG  
CTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCTTTCTCGCCACGTT  
CGCCGGCTTTCCCGTCAACGTCCGTCATATGACCAAGCTGAATTCGCGCGCTGACCTCGGAAA  
TGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGA  
CAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCC  
GTGTCGCCCTTATTCCCTTTTTTGCGGCATTTCCTGTTTCTCGAGTTGCAGCTTTT

Vx (310) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCAGCTGCTCTGAA  
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TGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGCGGATCCGAATTCTCCGGATCTG  
GCGTAATAGCGAAGAGGCCCGCACCCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAA  
TGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGGCGGGTGTGGTGGTTACGCGCAGCGTGACCG  
CTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCTTTCTCGCCACGTT  
CGCCGGCTTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTA  
CGGCACCTCGACCCCTGTCATATGACCAAGCTGAATTCGCGCGCTGACCTCGGAAATGTGCGCG  
GAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACC  
CTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCC  
CTTATTCCCTTTTTTGCGGCATTTCCTGTTTCTCGAGTTGCAGCTTTT

Vx (376) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCAGCTGCTCTGAA  
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CTGGAAGACAAGGTGGAGGAACTGCTGAGCAAGAACTACCACCTGGAGAACGAAGTTGCGCGCC  
TGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGCGGATCCGAATTCTCCGGATCTG  
GCGTAATAGCGAAGAGGCCCGCACCCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAA  
TGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGGCGGGTGTGGTGGTTACGCGCAGCGTGACCG  
CTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCTTTCTCGCCACGTT  
CGCCGGCTTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTA  
CGGCACCTCGACCCCAAAAACCTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGAT  
AGACGGTTTTTTCGCCCTGTCATATGACCAAGCTGAATTCGCGCGCTGACCTCGGAAATGTGCG  
CGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAA  
CCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCG  
CCCTTATTCCCTTTTTTGCGGCATTTCCTGTTTCTCGAGTTGCAGCTTTT

Vx (448) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCGACGATAAGGAT  
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GAGCTCGGAAGCTGCAACGAATGAAGCAGCTGGAAGACAAGGTGGAGGAACTGCTGAGCAAGAA  
CTACCACCTGGAGAACGAAGTTGCGCGCCTGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCAT  
TGCGCGCGGATCCGAATTCTCCGGATCTGGCGTAATAGCGAAGAGGCCCGCACCCGATCGCCCTT  
CCCAACAGTTGCGCAGCCTGAATGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAAGCGGGC  
GGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTT

GCTTTCTTCCCTTCCCTTTCTCGCCACGTTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGC  
TCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGA  
TGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACG  
TTCTTTAATAGTGGACTCTTGTTCCAAACCTGGAACAACACTCAACCCTATCTCGCGTCATATGA  
CCAAGCTGAATTCGCGCGCTGACCTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTTATTTTTC  
TAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATT  
GAAAAAGGAAGAGTATGAGTATCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTTCGGGCATT  
TTGCCTTCCTGTTTCTCGAGTTGCAGCTTTT

Vx (435) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCAGCTGCTCTGAA  
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TGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGCGGATCCGAATTCTCCGGATCTG  
GCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAA  
TGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCG  
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CGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGAT  
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AATGTGCGCGGAACCCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGA  
GACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATCAACATTT  
CCGTGTCGCCCTTATTCCCTTTTTTTCGGGCATTTTGCCTTCTGTTTCTCGAGTTGCAGCTTTT

Vx (438) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCAGCTGCTCTGAA  
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CTGGAAGACAAGGTGGAGGAACTGCTGAGCAAGAACTACCACCTGGAGAACGAAGTTGCGCGCC  
TGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGCGGATCCGAATTCTCCGGATCTG  
GCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAA  
TGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCG  
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CGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTA  
CGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGAT  
AGACGGTTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAAC  
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AATGTGCGCGGAACCCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGA  
GACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATCAACATTT  
CCGTGTCGCCCTTATTCCCTTTTTTTCGGGCATTTTGCCTTCTGTTTCTCGAGTTGCAGCTTTT

Vx (440) 414

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TGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGCGGATCCGAATTCTCCGGATCTG  
GCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAA

TGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGGCGGGTGTGGTGGTTACGCGCAGCGTGACCG  
CTACACTTGCCAGCGCCCTATCGCCCGCTCCTTTTCGCTTTCTTCCCTTCCCTTTCTCGCCACGTT  
CGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCGGATTTAGTGCTTTA  
CGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGAT  
AGACGGTTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAAC  
TGGAACAACACTCAACCCGTCATATGACTATAAGCTTAAGCTGAATTCGCGCGCTGACCTCGGA  
AATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGA  
GACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTT  
CCGTGTCGCCCTTATTCCCTTTTTTTGCGGCATTTTGCCTTCTGTTTCTCGAGTTGCAGCTTTT

Vx (443) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCAGCTGCTCTGAA  
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CTGGAAGACAAGGTGGAGGAACTGCTGAGCAAGAACTACCACCTGGAGAACGAAGTTGCGCGCC  
TGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGCGGATCCGAATTCTCCGGATCTG  
GCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAA  
TGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGGCGGGTGTGGTGGTTACGCGCAGCGTGACCG  
CTACACTTGCCAGCGCCCTATCGCCCGCTCCTTTTCGCTTTCTTCCCTTCCCTTTCTCGCCACGTT  
CGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCGGATTTAGTGCTTTA  
CGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGAT  
AGACGGTTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAAC  
TGGAACAACACTCAACCCATGTCATATGACAAGCTTAAGCTGAATTCGCGCGCTGACCTCGGA  
AATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGA  
GACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTT  
CCGTGTCGCCCTTATTCCCTTTTTTTGCGGCATTTTGCCTTCTGTTTCTCGAGTTGCAGCTTTT

Vx (445) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCAGCTGCTCTGAA  
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CTGGAAGACAAGGTGGAGGAACTGCTGAGCAAGAACTACCACCTGGAGAACGAAGTTGCGCGCC  
TGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGCGGATCCGAATTCTCCGGATCTG  
GCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAA  
TGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGGCGGGTGTGGTGGTTACGCGCAGCGTGACCG  
CTACACTTGCCAGCGCCCTATCGCCCGCTCCTTTTCGCTTTCTTCCCTTCCCTTTCTCGCCACGTT  
CGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCGGATTTAGTGCTTTA  
CGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGAT  
AGACGGTTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAAC  
TGGAACAACACTCAACCCATAAGTCATATGACGCTTAAGCTGAATTCGCGCGCTGACCTCGGA  
AATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGA  
GACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTT  
CCGTGTCGCCCTTATTCCCTTTTTTTGCGGCATTTTGCCTTCTGTTTCTCGAGTTGCAGCTTTT

Vx (450) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCAGCTGCTCTGAA  
GCGAGCTCGGAACACTGAAGCTGCTCGACGGAGCCGAGCTCGGAAGCTGCAACGAATGAAGCAG  
CTGGAAGACAAGGTGGAGGAACTGCTGAGCAAGAACTACCACCTGGAGAACGAAGTTGCGCGCC  
TGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGCGGATCCGAATTCTCCGGATCTG

GCGTAATAGCGAAGAGGGCCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAA  
TGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGGCGGTGTGGTGGTTACGCGCAGCGTGACCG  
CTACACTTGCCAGCGCCCTATCGCCCGCTCCTTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTT  
CGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTCCGATTTAGTGCTTTA  
CGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGAT  
AGACGGTTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAAC  
TGGAACAACACTCAACCCTATAAGCTTAGTCATATGACAGCTGAATTCGCGCGCTGACCTCGGA  
AATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGA  
GACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTT  
CCGTGTCGCCCTTATTCCCTTTTTTTCGCCATTTTGCCTTCTGTTTCTCGAGTTGCAGCTTTT

Vx (453) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCAGCTGCTCTGAA  
GCGAGCTCGGAACACTGAAGCTGCTCGACGGAGCCGAGCTCGGAAGCTGCAACGAATGAAGCAG  
CTGGAAGACAAGGTGGAGGAACTGCTGAGCAAGAACTACCACCTGGAGAACGAAGTTGCGCGCC  
TGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGCGGATCCGAATTCTCCGGATCTG  
GCGTAATAGCGAAGAGGGCCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAA  
TGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGGCGGTGTGGTGGTTACGCGCAGCGTGACCG  
CTACACTTGCCAGCGCCCTATCGCCCGCTCCTTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTT  
CGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTCCGATTTAGTGCTTTA  
CGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGAT  
AGACGGTTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAAC  
TGGAACAACACTCAACCCTATAAGCTTAAGCTCATATGACTGAATTCGCGCGCTGACCTCGGA  
AATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGA  
GACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTT  
CCGTGTCGCCCTTATTCCCTTTTTTTCGCCATTTTGCCTTCTGTTTCTCGAGTTGCAGCTTTT

Vx (455) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCAGCTGCTCTGAA  
GCGAGCTCGGAACACTGAAGCTGCTCGACGGAGCCGAGCTCGGAAGCTGCAACGAATGAAGCAG  
CTGGAAGACAAGGTGGAGGAACTGCTGAGCAAGAACTACCACCTGGAGAACGAAGTTGCGCGCC  
TGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGCGGATCCGAATTCTCCGGATCTG  
GCGTAATAGCGAAGAGGGCCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAA  
TGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGGCGGTGTGGTGGTTACGCGCAGCGTGACCG  
CTACACTTGCCAGCGCCCTATCGCCCGCTCCTTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTT  
CGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTCCGATTTAGTGCTTTA  
CGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGAT  
AGACGGTTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAAC  
TGGAACAACACTCAACCCTATAAGCTTAAGCTGGTCATATGACAATTCGCGCGCTGACCTCGGA  
AATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGA  
GACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTT  
CCGTGTCGCCCTTATTCCCTTTTTTTCGCCATTTTGCCTTCTGTTTCTCGAGTTGCAGCTTTT

Vx (458) 414

AATGTGTGCCTGGCGATCTCGAGGAGGATAAGGATCGATGGGGATCCGATCCAGCTGCTCTGAA  
GCGAGCTCGGAACACTGAAGCTGCTCGACGGAGCCGAGCTCGGAAGCTGCAACGAATGAAGCAG  
CTGGAAGACAAGGTGGAGGAACTGCTGAGCAAGAACTACCACCTGGAGAACGAAGTTGCGCGCC

TGAAGAAGCTGGTGGGTGAACTGCAGATGACGTCATGCGCGCGGATCCGAATTCTCCGGATCTG  
GCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAA  
TGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCG  
CTACACTTGCCAGCGCCCTATCGCCCGCTCCTTTCGCTTCTTCCCTTCCTTCTCGCCACGTT  
CGCCGGCTTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTA  
CGGCACCTCGACCCCAAAAACCTTGATTAGGGTGTGGTTCACGTAGTGGGCCATCGCCCTGAT  
AGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTCCAAAC  
TGGAACAACACTCAACCCTATAAGCTTAAGCTGAATGTCATATGACTCGCGCGCTGACCTCGGA  
AATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGA  
GACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTT  
CCGTGTGCCCTTATTCCTTTTTTGCGGCATTTCCTTCTGTTTCTCGAGTTGCAGCTTTT

**Primers used for PCR:**

XhoI sites (underlined) were introduced with a mismatched sequence on the primers.

Vx(448)212 forward primer

5'-AATGTGTGCCTGGCGATCTCGAGCAGCTGGAAGACAAGGTGGAGGAAC-3'

Vx(448)212 reverse primer

5'-AAAAGCTGCAACTCGAGGGGTTATTGTCTCATGAGCG-3'

Vx(XXX)414 forward primer

5'-AATGTGTGCCTGGCGATCTCGAGGAGGATAAAGGATCGATGGGGATCCGATCC-3'

Vx(XXX)414 reverse primer

5'-AAAAGCTGCAACTCGAGAAACAGGAAGGCAAAATGCCGC-3'