

SeLOX

A search tool for recombinase lox-like target sites

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You looked for

A_G | A_G | A_T | T_C | A_G | G_T | A_T | A | A | G | G | A | A

28 lox-like Sequences found :

Dots on top of the nucleotides indicate mismatches with the query pattern, those right of the spacer being reverse complement mismatches. Dots below nucleotides indicate asymmetry in the right arm of the lox-site to the corresponding positions on the left arm of the lox-site

ACAGGGACTCGAA AGCGAAAG TTCCAGAGAAGTT

5 strains Score : 4.34

gi|13897568|gb|AF254674.1| HIV-1 clone NT3.3/ from Tanzania 5' long terminal repeat, complete sequence
gi|13897588|gb|AF254694.1| HIV-1 clone NT25.4/ from Tanzania 5' long terminal repeat, complete sequence
gi|13897608|gb|AF254714.1| HIV-1 clone NT51/.17 from Tanzania 5' long terminal repeat, complete sequence
gi|13897627|gb|AF254733.1| HIV-1 clone B66.1/ from Tanzania 5' long terminal repeat, complete sequence
gi|13897630|gb|AF254736.1| HIV-1 clone B36.2/ from Tanzania 5' long terminal repeat, complete sequence

TGAGGGAGAGAAC AACAGCCTA TTACACCCTATAT

2 strains Score : 3.0

gi|13897568|gb|AF254674.1| HIV-1 clone NT3.3/ from Tanzania 5' long terminal repeat, complete sequence
gi|13897630|gb|AF254736.1| HIV-1 clone B36.2/ from Tanzania 5' long terminal repeat, complete sequence

AGGGAGAGAACAA CAGCCTA TTACACCCTATAT

2 strains Score : 2.66

gi|13897568|gb|AF254674.1| HIV-1 clone NT3.3/ from Tanzania 5' long terminal repeat, complete sequence
gi|13897630|gb|AF254736.1| HIV-1 clone B36.2/ from Tanzania 5' long terminal repeat, complete sequence

AATGGATGATGAT GAGAGAGA AACATTAATGTGG

2 strains Score : 2.66

gi|13897568|gb|AF254674.1| HIV-1 clone NT3.3/ from Tanzania 5' long terminal repeat, complete sequence

gi|13897630|gb|AF254736.1| HIV-1 clone B36.2/ from Tanzania 5' long terminal repeat, complete sequence

GGATGGTGCTTCA AGCTAG TACCAGTTGATCC

2 strains Score : 1.0

gi|13897569|gb|AF254675.1| HIV-1 clone NT4.3/ from Tanzania 5' long terminal repeat, complete sequence

gi|13897588|gb|AF254694.1| HIV-1 clone NT25.4/ from Tanzania 5' long terminal repeat, complete sequence

CCAGGGCCAGGAA CCAGGT TTCCACTAACATT

1 strains Score : 6.32

gi|13897627|gb|AF254733.1| HIV-1 clone B66.1/ from Tanzania 5' long terminal repeat, complete sequence

GACTCGAAAGCGA AAGTAAAAG TTCCAGAGAAGTT

1 strains Score : 6.0

gi|88853341:1-750 Human immunodeficiency virus type 1 complete genome, subtype A4, isolate 97CD.KCC2

ACACAGAAGGGAC TTTCCGCTG GGACTTTCCACTG

1 strains Score : 6.0

gi|13897568|gb|AF254674.1| HIV-1 clone NT3.3/ from Tanzania 5' long terminal repeat, complete sequence

AGCTACTGAGGGA GAGAACAACA TCCTATTACACCC

1 strains Score : 5.32

gi|4336542|gb|AF096641.1| HIV-1 strain TZB0003 country Tanzania 5' long terminal repeat, complete sequence

TGAGGGAGAGGAT AACCAACCTA TTACACCCTATAT

1 strains Score : 5.0

gi|13897627|gb|AF254733.1| HIV-1 clone B66.1/ from Tanzania 5' long terminal repeat, complete sequence

GACTGGT[.]**GAGTAC**[.] **GCCAAGAA** **TTTTT**[.]**GACTAGCG**[.]

1 strains Score : 4.34

gi|13897569|gb|AF254675.1| HIV-1 clone NT4.3/ from Tanzania 5' long terminal repeat, complete sequence

GACTGGT[.]**GAGTAC**[.] **GCCAAAT** **TTTTT**[.]**GACTAGCG**[.]

1 strains Score : 4.34

gi|13897630|gb|AF254736.1| HIV-1 clone B36.2/ from Tanzania 5' long terminal repeat, complete sequence

ACAGGGACTCGAA **AGCGAAAG** **TTCCG**[.]**GAGAAAGTT**[.]

1 strains Score : 4.34

gi|4336542|gb|AF096641.1| HIV-1 strain TZB0003 country Tanzania 5' long terminal repeat, complete sequence

ACAGAGACTCGAA **AGCGAAAG** **TTCCAG**[.]**GAGAAAGTT**[.]

1 strains Score : 4.0

gi|13897569|gb|AF254675.1| HIV-1 clone NT4.3/ from Tanzania 5' long terminal repeat, complete sequence

CAC[.]**TGTTAAGCCT**[.] **CAATAAAGCT** **TGCCTT**[.]**GAGTGCC**[.]

1 strains Score : 3.98

gi|13897630|gb|AF254736.1| HIV-1 clone B36.2/ from Tanzania 5' long terminal repeat, complete sequence

AGAAGTTGCTGAC **AGGGACT** **TTCCG**[.]**CTGGGACT**[.]

1 strains Score : 3.32

gi|88853341:1-750 Human immunodeficiency virus type 1 complete genome, subtype A4, isolate 97CD.KCC2

TGAGGGAGAGAAC **AACATCCTA** **TTACAC**[.]**CCCTATAT**[.]

1 strains Score : 3.0

gi|4336542|gb|AF096641.1| HIV-1 strain TZB0003 country Tanzania 5' long terminal repeat, complete sequence

TGAGGGAGAGAAC AACAGCTTA TTACACCCTATAT

1 strains Score : 3.0

gi|13897588|gb|AF254694.1| HIV-1 clone NT25.4/ from Tanzania 5' long terminal repeat, complete sequence

CGAAGGAGAGAAC AACAGCCTA TTACACCCTATAT

1 strains Score : 3.0

gi|13897608|gb|AF254714.1| HIV-1 clone NT51/.17 from Tanzania 5' long terminal repeat, complete sequence

AAGGAGAGAACA CAGCCTA TTACACCCTATAT

1 strains Score : 3.0

gi|13897608|gb|AF254714.1| HIV-1 clone NT51/.17 from Tanzania 5' long terminal repeat, complete sequence

GGCTACTGAGGGA GAGAACAACA GCCTATTACACCC

1 strains Score : 2.98

gi|13897630|gb|AF254736.1| HIV-1 clone B36.2/ from Tanzania 5' long terminal repeat, complete sequence

GGCTAATGAGGGA GAGGATAACA ACCTATTACACCC

1 strains Score : 2.98

gi|13897627|gb|AF254733.1| HIV-1 clone B66.1/ from Tanzania 5' long terminal repeat, complete sequence

AGGGAGAGAACA CATCCTA TTACACCCTATAT

1 strains Score : 2.66

gi|4336542|gb|AF096641.1| HIV-1 strain TZB0003 country Tanzania 5' long terminal repeat, complete sequence

AGGGAGAGAACA CAGCTTA TTACACCCTATAT

1 strains Score : 2.66

gi|13897588|gb|AF254694.1| HIV-1 clone NT25.4/ from Tanzania 5' long terminal repeat, complete sequence

GGGGAGAGAACA TAGCCTG TTACACCCTATAT

1 strains Score : 2.32

gi|88853341:1-750 Human immunodeficiency virus type 1 complete genome, subtype A4, isolate 97CD.KCC2

AGAGAAACATTAA TGTGGAAGT TTGATAGCCGGCT

1 strains Score : 2.32

gi|13897630|gb|AF254736.1| HIV-1 clone B36.2/ from Tanzania 5' long terminal repeat, complete sequence

GGATGGTGTTTCA AGCTAG TACCAGTTGATCC

1 strains Score : 1.0

gi|13897627|gb|AF254733.1| HIV-1 clone B66.1/ from Tanzania 5' long terminal repeat, complete sequence

GGCTACTGGGGGA GAGAACAATA GCCTGTTACACCC

1 strains Score : 0.98

gi|88853341:1-750 Human immunodeficiency virus type 1 complete genome, subtype A4, isolate 97CD.KCC2
