

A. *LdSNXi* cDNA Sequence (*L.donovani* strain LG13)

ATGGCCGCCGGCAACTCCATCTCTGTAAAGGTGGATGTGCCGTCCCAGG
TGAAGGGCCAGGGCACTCTGGAGATGTCTGTAACATCTACCCCATCAC
GATGCGCTTGCCCTGGCTTTATGAGCGATGCTCGGTTCAACCGGCGGTAC
ACCGACTTTGAGACTCTGCGCGGCCAGCTGTGTGCGACCTACTGGTACT
GCATTGTGCCACCCATTCCAGAGAAGGAGTCGGTGCAGGATAAGCTGGG
AAAGCTGCCACGCATGGTGGCGTCGGCGAAGGAGACGACCGCCTCCGAG
GGCGACCTGCTCGAGTACCGTCTGATCAGCCTGCGGCGCTTCCTGCAGC
GGCTTGCCCTACCACCCCATCCTGGGCAAGTCTGACCTTCTACAGAAGTT
CACGAACGATAACGAGTGGCGCCAGTGCCTCGCGACCCGGTGAAGCCG
CCTCGCTTTATCGTGTCTGTCGTCGCTGGAGGAGATCGCCAGATCATGGG
CTCCGTCAAGCAGTGCCTCTGGCGCCGGTACTCAAGGTAGCGGTGGCGC
TGCCGGGGGTGGTGGCGTTAGCCAAACCGGAGCGGCGTATCAGTTGGCA
CTGACTCAAGAGCCAGTGGATGAGGCGACGTGGAGGGCGACAAGCGAGT
ACATTGGTGAGCTGGAGTCTAACCTCAAGAGCATGCGCAACCTGCTGGA
GGCACTCGTGGATCGTCACCGGCGCGCCGCTCCGCCGTGAGCAACTTC
GCCGCCTCTTTTGGGCTGCTTGCGGAAGGCGAAGAGGATGCCGAGCTGC
GCGGCGCCATCGAAGGGGTGCGCGACTGCGGTGCGAAAGTGGCAGATGT
CTACAGCAAACACGCTGACAACGAGTCGACGCGGCTTGTCAGCACGTTA
AGCTTTTACGTGGGTATGTGTGCCGCCGTGCGGGAGACTCTGAGCCACA
TGTTTCAGCGCCCGCCAGTATCTGCGCAACTTGCAGAAGAAGGGCCAGGA
ACTGCAGGCGTTCGGCGATGCGGGCACAGTCGGCCAACCAGGTGCAGCTG
CAGAGCGAGCTGCACTTCGTGAATGAGCAGCGGGCCACCTCGAGGAAG
ACCTCATGGGCGCCGAGAAGACCTTCAGCGAGGAATTTATTCTCTTCCA
CGAAAACAAGCAATATGACGCCAAGGATATGCTGAAGAAGTTTGGCATG
CTGGAGCTCAGCTTCTCTGAGTCGATGAAGCAGGAGTGGGACGCCCTGC
GGCCAATGTTGGAGTCCCTTGGCACATAG

B. *LdSNXi* Amino acid Sequence (*L.donovani* strain LG13)

MAAGNSISVKVDVPSQVKGQGTLEMSYYIYPITMRLPGFMSDARFNRRY
TDFETLRGQLCATYWYCIVPPIPEKESVQDKLGKLPRMVASAKETTASE
GDLLEYRRISLRRFLQRLAYHPILGKSDLLQKFTNDNEWQCTRDPVKP
PRFIVSSSLEEIARSWAPSSSASGAGTQGS GGAAGGGGVSQTGAAYQLA
LTQEPVDEATWRATSEYIGELESNLKSMRNLLEALVDRHRRRAASAVSNF
AASFGLLAEGEEDAELRGAI EGVRDCGRKVADVYSKHADNESTRLVSTL
SFYVGMCAAVRETL SHMFSARQYLRNLQKKQELQASAMRAQSANQVQL
QSELHFVNEQRAHLEEDLMGAEKTFSEEFILFHENKQYDAKDMLKKFGM
LELSFSESMKQEWDA LRPMLES LGT

CLUSTAL O(1.2.4) multiple sequence alignment
DNA Sequence

LdSNXi	ATGGCCGCCGGCAACTCCATCTCTGTAAAGGTGGATGTGCCGTCCCAGGTGAAGGGCCAG	60
LDBPK_352470.1	ATGGCCGCCGGCAACTCCATCTCTGTAAAGGTGGATGTGCCGTCCCAGGTGAAGGGCCAG *****	60
LdSNXi	GGCACTCTGGAGATGTCGTACTACATCTACCCCATCACGATGCGCTTGCCTGGCTTTATG	120
LDBPK_352470.1	GGCACTCTGGAGATGTCGTACTACATCTACCCCATCACGATGCGCTTGCCTGGCTTTATG *****	120
LdSNXi	AGCGATGCTCGGTTCAACCGGCGGTACACCGACTTTGAGACTCTGCGCGGCCAGCTGTGT	180
LDBPK_352470.1	AGCGATGCTCGGTTCAACCGGCGGTACACCGACTTTGAGACTCTGCGCGGCCAGCTGTGT *****	180
LdSNXi	GCGACCTACTGGTACTGTCATTGTGCCACCCATTCCAGAGAAGGAGTCGGTGCAGGATAAG	240
LDBPK_352470.1	GCGACCTACTGGTACTGTCATTGTGCCACCCATTCCAGAGAAGGAGTCGGTGCAGGATAAG *****	240
LdSNXi	CTGGGAAAGCTGCCACGCATGGTGGCGTCGGCGAAGGAGACGACCGCTCCGAGGGCGAC	300
LDBPK_352470.1	CTGGGAAAGCTGCCACGCATGGTGGCGTCGGCGAAGGAGACGACCGCTCCGAGGGCGAC *****	300
LdSNXi	CTGCTCGAGTACCGTCGTATCAGCCTGCGGCGCTTCCTGCAGCGGCTTGCCTACCACCCC	360
LDBPK_352470.1	CTGCTCGAGTACCGTCGTATCAGCCTGCGGCGCTTCCTGCAGCGGCTTGCCTACCACCCC *****	360
LdSNXi	ATCCTGGGCAAGTCTGACCTTCTACAGAAGTTCACGAACGATAACGAGTGGCGCCAGTGC	420
LDBPK_352470.1	ATCCTGGGCAAGTCTGACCTTCTACAGAAGTTCACGAACGATAACGAGTGGCGCCAGTGC *****	420
LdSNXi	ACTCGGACCCGGTGAAGCCGCCTCGCTTTATCGTGTCTGTCGTCTGGAGGAGATCGCC	480
LDBPK_352470.1	ACTCGGACCCGGTGAAGCCGCCTCGCTTTATCGTGTCTGTCGTCTGGAGGAGATCGCC *****	480
LdSNXi	AGATCATGGGCTCCGTCAAGCAGTGCCCTCTGGCGCCGGTACTCAAGGTAGCGGTGGCGCT	540
LDBPK_352470.1	AGATCATGGGCTCCGTCAAGCAGTGCCCTCTGGCGCCGGTACTCAAGGTAGCGGTGGCGCT *****	540
LdSNXi	GCCGGGGGTGGTGGCGTTAGCCAAACCGGAGCGCGTATCAGTTGGCACTGACTCAAGAG	600
LDBPK_352470.1	GCCGGGGGTGGTGGCGTTAGCCAAACCGGAGCGCGTATCAGTTGGCACTGACTCAAGAG *****	600
LdSNXi	CCAGTGGATGAGGCGACGTGGAGGGCGACAAGCGAGTACATTGGTGAGCTGGAGTCTAAC	660
LDBPK_352470.1	CCAGTGGATGAGGCGACGTGGAGGGCGACAAGCGAGTACATTGGTGAGCTGGAGTCTAAC *****	660
LdSNXi	CTCAAGAGCATGCGCAACCTGCTGGAGGCACTCGTGGATCGTCACCGCGCGCCGCTCC	720
LDBPK_352470.1	CTCAAGAGCATGCGCAACCTGCTGGAGGCACTCGTGGATCGTCACCGCGCGCCGCTCC *****	720
LdSNXi	GCCGTGAGCAACTTCGCCGCTCTTTTGGGCTGCTTGCAGGAGGCGAAGAGGATGCCGAG	780
LDBPK_352470.1	GCCGTGAGCAACTTCGCCGCTCTTTTGGGCTGCTTGCAGGAGGCGAAGAGGATGCCGAG *****	780
LdSNXi	CTGCGCGGCGCCATCGAAGGGGTGCGCGACTGCGGTGCGAAAGTGGCAGATGTCTACAGC	840
LDBPK_352470.1	CTGCGCGGCGCCATCGAAGGGGTGCGCGACTGCGGTGCGAAAGTGGCAGATGTCTACAGC *****	840
LdSNXi	AAACACGCTGACAACGAGTCGACGCGGCTTGTGAGCACGTTAAGCTTTTACGTGGGTATG	900
LDBPK_352470.1	AAACACGCTGACAACGAGTCGACGCGGCTTGTGAGCACGTTAAGCTTTTACGTGGGTATG *****	900
LdSNXi	TGTGCCGCCGTGCGGGAGACTCTGAGCCACATGTTGAGCGCCCGCCAGTATCTGCGCAAC	960
LDBPK_352470.1	TGTGCCGCCGTGCGGGAGACTCTGAGCCACATGTTGAGCGCCCGCCAGTATCTGCGCAAC *****	960
LdSNXi	TTGCAGAAGAAGGGCCAGGAACGTCAGGCGTCGGCGATGCGGGCACAGTCGGCCAACCAG	1020
LDBPK_352470.1	TTGCAGAAGAAGGGCCAGGAACGTCAGGCGTCGGCGATGCGGGCACAGTCGGCCAACCAG *****	1020
LdSNXi	GTGCAGCTGCAGAGCGAGCTGCACTTCGTGAATGAGCAGCGGGCCACCTCGAGGAAGAC	1080
LDBPK_352470.1	GTGCAGCTGCAGAGCGAGCTGCACTTCGTGAATGAGCAGCGGGCCACCTCGAGGAAGAC *****	1080
LdSNXi	CTCATGGGCGCCGAGAAGACCTTCAGCGAGGAATTTATTCTCTTCCACGAAAACAAGCAA	1140
LDBPK_352470.1	CTCATGGGCGCCGAGAAGACCTTCAGCGAGGAATTTATTCTCTTCCACGAAAACAAGCAA *****	1140
LdSNXi	TATGACGCCAAGGATATGCTGAAGAAGTTTGGCATGCTGGAGCTCAGCTTCTCTGAGTCG	1200
LDBPK_352470.1	TATGACGCCAAGGATATGCTGAAGAAGTTTGGCATGCTGGAGCTCAGCTTCTCTGAGTCG *****	1200
LdSNXi	ATGAAGCAGGAGTGGGACGCCCTGCGGCCAATGTTGGAGTCCCTTGGCACATAG	1254
LDBPK_352470.1	ATGAAGCAGGAGTGGGACGCCCTGCGGCCAATGTTGGAGTCCCTTGGCACATAG *****	1254

CLUSTAL O(1.2.4) multiple sequence alignment Amino acid Sequence

LdSNXi	MAAGNSISVKVDVPSQVKGQGTLEMSYIYPITMRLPGFMSDARFNRRYTDFETLRGQLC	60
LDBPK_352470.1	MAAGNSISVKVDVPSQVKGQGTLEMSYIYPITMRLPGFMSDARFNRRYTDFETLRGQLC	60

LdSNXi	ATYWYCIVPPIPEKESVQDKLGKLPRMVASAKETTASEGDLLEYRRISLRRFLQRLAYHP	120
LDBPK_352470.1	ATYWYCIVPPIPEKESVQDKLGKLPRMVASAKETTASEGDLLEYRRISLRRFLQRLAYHP	120

LdSNXi	ILGKSDLLQKFTNDNEWRQCTRDVPVKPPRFIVSSSLEEIARSWAPSSSASGAGTQGS GGA	180
LDBPK_352470.1	ILGKSDLLQKFTNDNEWRQCTRDVPVKPPRFIVSSSLEEIARSWAPSSSASGAGTQGS GGA	180

LdSNXi	AGGGGVSQTGAAYQLALTQEPVDEATWRATSEYIGELESNLKSMRNLLEALVDRHRRRAAS	240
LDBPK_352470.1	AGGGGVSQTGAAYQLALTQEPVDEATWRATSEYIGELESNLKSMRNLLEALVDRHRRRAAS	240

LdSNXi	AVSNFAASFGLLAEGEEDAELRGAIEGVRDCGRKVADVYSKHADNESTRLVSTLSFYVGM	300
LDBPK_352470.1	AVSNFAASFGLLAEGEEDAELRGAIEGVRDCGRKVADVYSKHADNESTRLVSTLSFYVGM	300

LdSNXi	CAAVRETLSHMFSARQYLRNLQKKGQELQASAMRAQSANQVQLQSELHFVNEQRAHLEED	360
LDBPK_352470.1	CAAVRETLSHMFSARQYLRNLQKKGQELQASAMRAQSANQVQLQSELHFVNEQRAHLEED	360

LdSNXi	LMGAECTFSEEFILFHENKQYDAKDMLKKFGMLELSFSESMKQEWDALRPMLES LGT	417
LDBPK_352470.1	LMGAECTFSEEFILFHENKQYDAKDMLKKFGMLELSFSESMKQEWDALRPMLES LGT	417
