

A

T. asa. EKC98308.1 HQTRREAAGVHYLRSWFLSNLAHPFFSRAERQKMASIASTTPRNVESSTFNWRRRSGWSAVRRKWWGGQ
T. asa. EJT51135.1 HQTRREAAGVHYLRSWFLSNLAHPFFSRAERQKMASIASTTPRNVESSTFNWRRRSGWSAVRRKWWGGQ
T. cor. 023_162 Sxi1 CQSHLEAVDVDYLRSWFLSNLAHPFFSRAERQKMASITNSTPRNVESSTFNWRRRSGWLTIRRRWGGQ
T. ink. 003_681 Sxi1 NGMQPTESSTDYLRSWFLANLASPFENRTERQKMAKLMGTTTRNVESHFTNWRRRSGWSTIKKKWGGG
C. muc. JCM9939 Sxi1 VAHEGKEADSRPLQAWFMANLAHPYFPLSVKRRFASELGLSLRNIDTQFTNWRRRSGWSAIKRRWADG
C. der. JCM11170 Sxi1 VAHEGKEADSRPLQAWFMANLAHPYFPLSVKRRFASELGLSLRNIDTQFTNWRRRSGWSAIKRRWADG
C. arb. JCM14201 Sxi1 EYDLGSRGQLNPLQRWFLDNLSPYFPLAVKRFQFSRELGLSLRNIDRRFTNWRRRTRWSDIKRWAGG
C. ole. Triol1|175080 NKTDDSRDATRHLRAWFKNLDHPYFPLSLRQRFASELGVVPRNINAQFTNWRRRTGWSHIRKAWAGN
C. cur. LLPE01 Sxi1 SDNDWDDDHQPLRDWFKHLDYFPPSRIEKRELAASLGLDARSIDSHLTNWRRRSGWNDIKRWATS
C. das. JCM11166 Sxi1 SGSDVDAHPPATLQQWFISHLSHPFPPSRSEKRELANSLSLTPRNIDSQFTNWRRRTGWSDIKRWGKG
V. hum. JCM1457 Sxi1 AQAKTECKSLLSLRSWFLQHLEDYFPPSPREKGEWAGLMGVTVRNVDSHFTNWRRRSGWNGIKQNWAHG
V. hum. UJ1 Sxi1 AQAKTECKSLLSLRSWFLQHLEDYFPPSPREKGEWAGLMGVTVRNVDSHFTNWRRRSGWNGIKQNWAHG
C. neo. Sxi1 AAN75718.1 PKPSEPPIDHTVRLWFLDNLAYPYFTAQQKDFLAKTAGIQRSDVSDLTNYRRRAGWTDIMNVWCGG
C. gat. AAV28797.1 PKPLESAPDHTIVRLWFLNLAHPYFTAQQKDSLAKYAGMQRGKVDSDLTNYRRRAGWTDIMNMWCGG
T. kor. JCM12878 Sxi1 DATPSQNVVRQLRRWFLDHLAWPYFTSSQKQILAKALSIAPKRVETQLTNWRRRSGWTDIKDLYAGG
N. alb. LKPZ01 Sxi1 DPTNKADEADEHLRDWFLHAYPFPPDKPTKAVLSSTGLDVRQLNTWFTNMRSSGWTDYLSYASG
N. alb. LLJT01 Sxi1 DPIDPADEADEHLRDWFLHAYPFPPDKPTKAVLSSTGLDVRQLNTWFTNMRSSGWTDYLSYASG
T. mel. Sxi1 ADO17677.1 QONPLFPPTDPIRTWFLHAYPFPPDKPTKAVLSSTGLDVRQLNTWFTNMRSSGWTDYLSYASG
K. hev. Sxi1 ACZ51516.1 SISRSPEPDHSLRIWFLHNSISYPYFTVSMKETLASKAGITRAKVDSDLTNFRRRAGWTEIMNEWCGG
X. den. XDEN_05476 RPRTEHPSSFRHLRDWFLIVHLDPYFSAQEKELALARNLTKNISINLWFTNMRSSGWMDFVRTHALN

helix I
 3 aa
 helix II
 helix III

B

C. neo. Sxi2 AAV98474.1 RPSPFAPETLHVLESAYSRCVLSAAESALIAEAAASITPQQVRTWFQNKRRNGKKTRITSTVTQQVPH
C. gat. Sxi2 AAV28762.1 RPSTFAPGTLNILESAYARCTILSAAETALIAEAAASITPQQVRTWFQNKRRNGKKTRITSSITQPVSH
T. fae. 002_950 Sxi2 RGANFRKRSLDVLEDAFARTPFLNKSECAMIARAAGLSSRQVRTWFQNKRRNVSKGS--ARKQA-KSQ
T. cor. Sxi2 LRPLTLKRSLDILEDAFERTPFLNKSECAMVARASGLSSRQVRTWFQNKRRNVSKGSDSARKQE-KTG
T. ovo. 001_797 Sxi2 RGASFNTRSLDVLEEAFAFARTPFLNKRECAMVARAAALSSRQVRTWFQNKRRNVSKPTGSARKKTGRVS
T. ovo. 014_242 Sxi2 RGASFSGHSLKVLEEAFAFARTPFLNKSECAMVARAAALSSRQVRTWFQNKRRNVSKPAASARKKAKKDC
C. muc. JCM9939 Sxi2 SNVQRGSSFKPILKDAFQRSQFLNKAECKLVAKAAGLSCQQVRTWFQNKRRNSSKSSSARRTSRTSR
C. cya. JCM31388 Sxi2 VRLLSGHKTKQVLEDAFTRSPFLNKAECRLVAKAAGISTQQVRTWFQNKRRNSPKRPIRRRLNNSKAA
A. dom. 002_744 Sxi2 SVRKCYAETQQVLEAFARSFPLNKAECALVARAANLSPQQVRTWFQNRRSRAKNDVTATFVPLESK
V. fra. JCM1530 Sxi2 TVADCLQRTKEMLEEAFAFARSFPLNKAECAMLAKASGLTARQLRTWFQNKRRNLKPEPPTTESLDAD
V. hum. CBS4282 Sxi2 SRPAARPREDDQTSIAAYTRAPTLLHSECKMVARASGLTHQQVRTWFQNKRRSRDKKQSRIRSMRSTYRR
K. hev. Sxi2 ACZ51517.1 KLSSFSSTLLVLDAAAYARSKLSQAETIIIAQAAGISPPQQVRTWFQNKRRNGKDKNPSTAAANRPVSS
T. tep. JCM11965 Sxi2 SVIQGQHTLAVLERSYARSRNLSQAECSLVAKAARISHHQVRTWFQNRNRREIRKSRKMTMTASASH
X. den. XDEN_05477 RRSSFTKNTIDTLQALYDLNQYPNPIELKTIIVKVGLOPKQIRAWFQNRNRSSPARSHKKPLKIST

helix I
 helix II
 helix III