

Sh 1 MSPLCYLFVVSASVLLTLGDAEMFGAPRKLQPNNEATIEKFNHELVKVAHKFNSEHGNSL
Sm 1 MGPVCYLFVVSFVLLTSGNVGMFGAPRKLQLNNATIEKFGHELAKVAHKFNSEYGNSSL
Sj 1 ---MYFFLILPVLAFSLASGDGEMFGAPRKLQSNNEATLEKFSSELAKATHQFNREHGNHTF

Sh 61 HIITKLVNVTSQVRFCCLYKLSFLOVVQGILYTFYVKFSPTSCTTFANDNTHVLGDI FRNQ
Sm 61 HVITKLVNVTSQ-----VVQGI FYTFFVKFSPTSCTT-ANNNIHVLD TYF PNR
Sj 58 HIVTELINATSQ-----VVAGI IYKLFVKFT PASCTDFAEDKVS-LDNIVFSR

Sh 121 NSCDVTGGESKICKVTVWQRPWLQSDASEIIKIVNCSTDT-
Sm 108 DSCDLTDGESKICKVTLWDRPWLQSDFSKIIIRIVRCSNDTS
Sj 105 DSCDSGNNKSKICKVTIWKRPLASNESEIIKIVNCSDTS