

a

A1	1	ECVTQLLKDTCT FE GGDIT TV FTPSAKY CQ VV CT YHPR CL LFTFT	44
A2	92	ACNKDIYVDLL MK GINYN SS VAKSAQE CQ ER CT DDVH CH FFTYA	135
A3	181	ACIRDI FPNTV FA DSNID SV MAPDAFV CG RI CT HHPG CL FFTF	224
A4	272	FCHSSFYHDTD FL GEELD IV AAKSHEA CQ KL CT NAVR CQ FFTYT	315



A1		AES P SED P TRWFT C VLKDSVTETLPR VM R-TAAISGYSFK C SHQIS	91
A2		TRQ F PSLEHRNI C LLKHTQTGTPT IT KLDKVVS G FS L KS C ALS N L	180
A3		SQEW P KESQRNI C LLK T SESGLPST RI KKSKALSG F SLQ S CRHSIPV	271
A4		PAQAS C NE G K G K C YLKLS S NGSP T KL H GRGGISGYTLRL C KMDNE	361



b

