RcSAPK1	MERYEILKDIGSGNFGVAKLVRDRWTKELFAVKFIERGOKIDE	43
LcSnRK2		43
GmSAPK2	MERYEILKDIGSGNFAVAKLVRDNYTNELFAVKFIERGOKIDE	43
ZmSnRK2.2	KERYEVIKDIGSGNFGVAKLVRDVRTKELFAVKFIERGMKIDE	43
AtSnRK2.2	MDPATNSPIMPIDLPIMHDSDRYDFVKDIGSGNFGVARLMTDRVTKELVAVKYIERGEKIDE	62
	1	
RcSAPK1	HVQREIMNHRSLKHPNIVRFKEV <mark>R</mark> LTPTHLAIVMEYAAGGELFERI <mark>S</mark> NAGRFSEDEARFFFQ	105
LcSnRK2		105
GmSAPK2		105
ZmSnRK2.2		105
AtSnRK2.2	NVQRE I I NHRSLRHPN I VRFKEV ILTP <mark>S</mark> HLA I VMEYAAGGELYER I CNAGRF SEDEARFFFQ	124
RcSAPK1		160
LcSnRK2		160
GmSAPK2		160
ZmSnRK2.2		160
AtSnRK2.2	QLISGVSYCH <mark>A</mark> MQICHRDLKLENTLLDGS <mark>PAPRL</mark> KICDFGYSKVLFISLKSSVLHSQPKSTV	186
RcSAPK1		222
LcSnRK2		222
GmSAPK2		222
ZmSnRK2.2		222
AtSnRK2.2	GTPAYIAPE <mark>IL</mark> LRQEYDGKLADVWSCGVTLYVMLVGAYPFEDPQEPRDYRKTIQRILSV <mark>T</mark> YS	248
200		
RcSAPK1		282
LcSnRK2		282
GmSAPK2	VPDYVRVSMECRHLLSOIFVASPEKRITIPEIKNHPWFLRNLPMELTEG GSWOMNDVNNP	282
ZmSnRK2.2		284
AtSnRK2.2	IPEDLHLSPECRHLISRIFVADPATRITIPEITSDKWFLKNLPGDLMDENRMGSQFQEPEQP	310
B. CARVA	SON I E E VVS I I O E A RKA V V L PK SG NNL L E G SM D L DDAD A DAD CED I E T SG D F V C P L	000
RcSAPK1	SQNIEEVVSIIQEARKAVVLPKSGNNLLEGSMDLDDADADADCEDIETSGDFVCPL SQSLEEVLSIIQEASKPIEASRVEGHLLGSSMDLDDLDADVDVEDIETSGDFVCPL	338
LcSnRK2	SQNVEEVLSTIGEASKPIEASRVEGHLLGSSMDLDDLDADVDVEDTETSGDFVCPL SQNVEEVLSTIGEASKSLNVPKVGGLLTGGSMDLDDFDADEDLEDLETSGEFVCPT	338
GmSAPK2	SQSLEEIMSIILEARKPGDGLKHAGQLPGL GSMELDDTDVDD IDVEDSGDFVCAL	338
ZmSnRK2.2	MQSLDTIMQIISEATIPTVRNRCLDDFMADNLDLDDDMDDFDSESE-IDVDSSGEIVYAL	339 369
AtSnRK2.2	3	309
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