

	I	II	III	VIIb	VII	VIII	IX	X
ePK (33,220)	LGGEFG LGGEFG	VAYK VAYK	EE EE	HRDVK HRDVK	DFG DFG	APF APF	DVWS DVWS	PR PR
ROP11 (4)	LGAGAST LGAGAST	RVALRF RVALRF	EE EE	THDITPEIV THDITPEIV	GGFQH GGFQH	TDPR TDPR	VDANN VDANN	KRGAP KRGAP
ROP16 (4)	LGSGHFGE LGSGHFGE	LYAAKV LYAAKV	QEL QEL	ANGDVKNM ANGDVKNM	LWGS LWGS	WPEL WPEL	LDVWA LDVWA	EPEL EPEL
ROP17 (4)	LGGGFGL LGGGFGL	REALKI REALKI	DEF DEF	VHGDKLQNF VHGDKLQNF	SDFTQ SDFTQ	MSPEZ MSPEZ	ZDSNM ZDSNM	VRISP VRISP
ROP18 (2)	LGSGGFAT LGSGGFAT	ELAVKV ELAVKV	RES RES	VHTDIKPAIF VHTDIKPAIF	GDFGT GDFGT	EPPER EPPER	TDANQ TDANQ	KRILP KRILP
ROP19-29-38 (18)	LGSGSTGI LGSGSTGI	PLAOKI PLAOKI	ES ES	AHNDLKEIV AHNDLKEIV	QDFGE QDFGE	LDPOT LDPOT	RDWA RDWA	RRRPL RRRPL
ROP20 (4)	LASGSYIV LASGSYIV	PLAVRI PLAVRI	YS YS	VHODIKAEIE VHODIKAEIE	ADFDA ADFDA	SPPEY SPPEY	VDSHS VDSHS	TRCKA TRCKA
ROP21-27 (9)	LGAGCGV LGAGCGV	CAVAYK CAVAYK	SE SE	VHSDIKPAIV VHSDIKPAIV	GDSSL GDSSL	LPPEN LPPEN	KDWA KDWA	TRPTL TRPTL
ROP25 (4)	LGFGAYGV LGFGAYGV	TYAAKI TYAAKI	EEL EEL	SHNDVKQNF SHNDVKQNF	GDFAY GDFAY	SSPEL SSPEL	RDSWA RDSWA	KRATV KRATV
ROP28 (4)	LGVGGLGG LGVGGLGG	KFAGKI KFAGKI	EEI EEI	VHTDIKAEIF VHTDIKAEIF	ADLSM ADLSM	LDPNG LDPNG	RDAYA RDAYA	BRWTP BRWTP
ROP30 (4)	LGGSFAM LGGSFAM	LWAIKI LWAIKI	LQM LQM	LHNDLKEIVL LHNDLKEIVL	GDGGA GDGGA	LDPOS LDPOS	RDWA RDWA	TRKTP TRKTP
ROP31 (4)	LGCGTSS LGCGTSS	KVAYKI KVAYKI	REA REA	VHGDKPSIF VHGDKPSIF	GRFSY GRFSY	MSLEN MSLEN	HRSMY HRSMY	BRWTP BRWTP
ROP32 (3)	LGVGNGL LGVGNGL	VVALKI VVALKI	KEM KEM	LHGDKNEIF LHGDKNEIF	GDFEQ GDFEQ	CGPRR CGPRR	RDSWC RDSWC	BRWTP BRWTP
ROP33 (4)	TPSKELRA TPSKELRA	PLVYKA PLVYKA	LEV LEV	LHRDIKTIF LHRDIKTIF	ADFDG ADFDG	LAPEI LAPEI	SDVYA SDVYA	RRITL RRITL
ROP34 (4)	RPSAALLS RPSAALLS	GVVKA GVVKA	SEP SEP	AHRDLKEDIF AHRDLKEDIF	SDAAT SDAAT	MPPET MPPET	TDVYS TDVYS	KRPLT KRPLT
ROP35 (7)	HVSEALAD HVSEALAD	GVVYK GVVYK	SE SE	LHRDIKEIV LHRDIKEIV	ADFEQ ADFEQ	EAPEL EAPEL	SDVEA SDVEA	RRITL RRITL
ROP39 (3)	AGTGGVNI AGTGGVNI	NVSLRI NVSLRI	EAD EAD	VHSDIKPEIV VHSDIKPEIV	ADFDK ADFDK	ADPQT ADPQT	QDWA QDWA	NRLDV NRLDV
ROP41 (4)	LGVGNGIT LGVGNGIT	SLALKL SLALKL	NEM NEM	VHRDIKOSIF VHRDIKOSIF	GDFGL GDFGL	TDPSD TDPSD	ADLWA ADLWA	RRRLR RRRLR
ROP46 (4)	HMPPQLTA HMPPQLTA	GVNVKV GVNVKV	YEA YEA	VHGDKQNF VHGDKQNF	ADFGA ADFGA	IAPER IAPER	SDIWA SDIWA	ARPSV ARPSV
ROPK-Eten1 (3)	LGVGCGG LGVGCGG	ELAYK ELAYK	SE SE	CHVDIKPEIV CHVDIKPEIV	ADFGM ADFGM	MDPSH MDPSH	YDAWS YDAWS	KRPTP KRPTP