

PmPPAE1	MKG--VTIVVLWVCVVAWAAAAVGD-----EQLSGKKREPOQP-----NENFGPN-----GSFRPSNNRPGFTPAGQSDCTGNRRN-----	68
LvPPAE1	MKG--VTIVALWVCVVAWAAAAVGD-----EQVSRKKREPOQP-----DENFGPD-----GSFRPSNN-PGFNPGG-PDCTGNRRN-----	66
PlPPAE	MKV--VVELLVLSLVTWAAVGVGVG-----VNVTOEEAHSRVKROF-----GFNRGRG-----GNPHRNNAFGHGHGCGFIPPGHQGG-----	72
PtSP	MRGRTVLVA AVLVVVLWAVVSACPAPLEEDLLEEEEEAEETLTVERQAQGGGRGNRGGGGGRNINCNRRKNRDKEECQGNNNRPNRPNRGNDRNDRPNRPGRRPNRPGRKPNK	112

PmPPAE1	---SRRCQNRPSGGQALGQGGG-----VSSAFQOIPWLSQLSRDQON--LLIPNLPKTPSGGAQNRFFLLGTGKPDVPFQQCVTPRFRERGHCRYLQHCTIQPEFANNFNVFLR	170
LvPPAE1	---SRRCQNRPTGGQVVGQGGG-----VSSAFQOIPWLSQLSSDQRN--LLIPNLPKTPSRGAQSRFFLLGTGKPDVPFQQCVTPKFRERGHCRYLQHCTIQPEFVNNFNVFLR	169
PlPPAE	---NLHNIGRPAGGRPSAQTLLGQ---GHNLNNQLSWFNDVVSGTNNNEITLKGLPRLPLRQAQNTFFQLGVGQPDVPFQQCRTPKGERGQCRFLQYCILPEFAQNFQAFILQ	177
PtSP	GKTGINCNRRQNRDLPECCADGPPSQDVEVLAGSVPWLTDVAAAGNV--VELQGLPNT--RMQSRRYQLAVNQPDLPFQSCRTPRREKCFCRYLQHCTILPEFVSGFTAYLP	220

PmPPAE1	YVCFIEGVYVGVCCPDTFNNNNATPPPPPTTPKPTTPRPVTPPSQSRGCGLIAKRPPTRIVGGKDADPQEWPPWMAALMRDGASSYCGGVLLITDSHILTAAHCVDFDRNTIT	282
LvPPAE1	YVCFIEGVYVGVCCPDTFNNNNVTPPPPPTTPRPPTTPRPVTPPSQSRGCGLIAKRPPTRIVGGKDADPQEWPPWMAALMRDGASSYCGGVLLITDSHILTAAHCVDFDRNTIT	281
PlPPAE	YVCFIQGTYYGACCPPTTVNNVGVTAAPPPPTTPAPTTPRPPTTPKSEANGCGLVAKRPPTRIVGGKPADPREWPPWVAALLRQGSTQYCGGVLLITNQHVLTAAHCVRGFDQTTIT	289
PtSP	YACLIDSKYLGACCPPTNFNSNNLQEPSTPNPVTAPPTPRPTTPPSSEARGCGLIAKPPTRIVGGKPADPKWPPWIAALLRNGATQFCGGTLLITNQHVLTAAHCIVDFTKESIT	332

PmPPAE1	VRLGEYTFDLADDTGHVDFKVDIRMHRSYDTTTYVNDIALITKLQGSTNFNVDIWPVCLPEGDESIECRTGTVTGWGTIYYGGPVSSNTLOEVTVPWIWINKACDDAYEQNIID	394
LvPPAE1	VRLGEYTFDRADDTGHVDFRVADIRMHSSYDTTTYVNDIALITKLQGSTNFNVDIWPVCLPEGDESIECRTGTVTGWGTIYYGGPVSSNTLOEVTVPWIWSNSDCDKAYEQNIID	393
PlPPAE	IRLGEYDFKQTS-TGAQTFGVLLKKEHEAYDTTTYVNDIALITLTKSTEFNADIWPICLPDGDETYVDRQGTVVGWGTIYYGGPVSSVLMVSVIPIWITNADCAAYGQDIID	400
PtSP	VRLGEYTFDETGESPHVDFKIKTMKPHEHYDTNTYVNDIALITLDRITDFNDIWPVCLPQSDSESYVCRDATVVGWGTIYFGGPVASTLOEVTIPVWINEECNAAYEQDIID	444

PmPPAE1	KQLCAGATDGGKDSCQGDSSGGPLLLOQGSENRWAVVGVVSWGIRCAEPGNPGVYTRVSKYVDWIKNNAV	: 463
LvPPAE1	KQLCAGATDGGKDSCQGDSSGGPLLLOQGAENRWAVAGVVSWGIRCAEPGNPGVYTRVSKYVDWIKNNAV	: 462
PlPPAE	KQLCAGDKAGGKDSCQGDSSGGPLMLQQGGANRWAVVGVVSWGIRCAEAASPGVYTRISKYTDWIRANQ-	: 468
PtSP	KQICAGAREGGKDSCQGDSSGGPLLLOQGGANRWAIAGVVSWGIRCAEPGNPGVYTRVSRYSQWIRNNAV	: 513