

Gene name	Gene ID	Protein sequence
MsPAP1	MsG0180003365.01.T01	MRVSWVTEEKDSESLVEYGIKGGEYSKKAIGEHTSYRYFLYKSGKIHVV IGPLNPSTTYFYRCGSGPEFSFKTPPLKLPIEFVVVVDLGQTEWTKSTL KHIDSKDYDVFLPGDLSYADTHQPLWDSFGRLVEPYASQRPWMVTEGNH EIESIPIQPQAFRSYNARWLMPYNESGSTSNLYYSFEVASTHIIMLSY TDFDADSEQYKWLQSDLAKIDRK RTPWVITLLHAPWYNTNEAHEGEGEDM RQAMEDLLYEARVDLVFSGHVHAYERFTRIYDNKADPCGPLYVTIGDGGN REGLALKFKKPPSPLSLYREASFGHGRLRIVNETHANWSWHRNNDSEAFV ADDIWMKSLSNTKECWESLGQKNSHEEL*
		MDTSIPMGIRIVDTLESDIEIEFEDAEAEYTSQRIEFRILNRFLNMSD DRDVHPDCRNASNPHECTDYCFRVIAQAKLTQSGMHDDGPKPDENS DSE PDQPAPENNEDGSFPKLSARQKKWMELRAKMQEAKKRNQIEMANEKKRME APTESRGVSKQKWLD DRKKKIGKLLDANGLDMTKAYMLDTQEAAEEKYKK WEKDPAPFGWDVFNQRTLYNAYKKRTKNIEVDVEEYNRMKEADPEFYRDA SSLQYGKAPKTSEDKIDRMVQELKDRDEKRRAFSRRRTFREEKD VDSIND RNEHFNKKIERAFGKYTLEIKIISSEELHCRTDLLLQWCVLVSHCYSNAG KFKWWIAFSGVFDQMNVQKGVNMSLSDSDVFAVPSGYNAPQQVHITQGD LV GKAVIVSWVTEDEPGSNAVRYWSTDNTKQKKLAKGKIVTYRFFNYSSGFI HHTTIRNLEYNTKYYYEVGLGNTTRQFWFITPPEIGPDVPYTFGLIGDLD NFPNHDNVRWDTWGRFVERSVAYQPWIWTVGNHEIDFAPEIGETKPFKPY SHRYHTPYKASQSTSPFWYSIKRASAHIIVLASYSAYGKYTPQYQWLEQE LPKVNRTETPWLIVLMHSPWYNSNNQH YMEGETMRVMYEPWFVKYKVDVV YAGHVHAYERTERVSNIAYNVVGICTPIKDQSAPVYITIGDGGNLGGSE TNMTEPQPEYSAFREASFGHAIFDIMNRTHAHYSWHRNQDGY SVEADSHW FFNRFWHPVDDSTAHLVH*
MsPAP3	MsG0280008275.01.T01	MFGFGIEFCSDLNTTLFLKRVIQDENPDFIAFTGDNIFGPSSHDAAESMF RAFGPAMESGLPWAAILGNHDQESTLNREELMSLISLMDYSVSQINPSAD SLTDSVKGRKMSKIDGFGNYNLRVYGAPGSMMANSSVLNLFFLDSGDRVV YQGIRTYDWIRDSQLDWLRHVSREPQGQKQDPLHSTD RATSPITPPALAF FHIPIPEVRQLFYKQIVGQFQEGVACSRVNSAVLQTFVSMGDVKAVFVGH DHTNDFCGNLDGIWFCYGGGFGYHGYGKAGWPRRARIILAELQKGKASWT SVQKIMTWKRLDDEKMSKIDEQILWDHLHSREETKMAATSDEEMESLLST FNQIYEDVKNGISEIQSLQSKYSSELKLRESLQITCNNLKKENEELAKLY SESLKNVADQVLQSISSIIRCTDTS DPRLVRGLTCVRLDFRAKYMNLKEE LERSNNVISKEEGHRRALKLLEEEYNEKIARLEAQVKESLHEKATYEAT ISQLHGDIAAHKNHMQILANRLDQVHFEVESKYSSEIRDLKDCLMAEQEE KNDLNRKMKLLEKELLFKAKMVDQQEMTSNWQVETLKQKIMKLRKENE VLKRKFSHIEEGK*
		MEEVNPCKKLADRYLKREVLGEGTYGVVFK AIDTVQSCRETKGGEHVALI ADVSYMWMYNTGQMVAIKKIRNRIDEPIDGVNFTALREIKLLKELKHPNI VDLIDVFHYKQNLHLVFEFMETDLEAVIRDRNIFLSPADIKSYLLMILQG LAYCHKKWVLHRDVKPNNLLIGQNGQLKLADFGLSQIFGDQDHEFPDQAF ARWYRAPELLFGAKKYGSSVDVWATACVFAELLRRPFLEGSTDTHQTRK IFTAFGTPSPSQWPDMMYLKYYIQEKYIPAPPLRSLFPMASDDALDLSK MFTYDPNARISVQKALEHRYFSSAPPPTDPEKLPRVPKRESRVPDLNSF EGLSHIQLSPSRKIRRVMPRCDFEGNSLEGDKIDDNAVKKTVNKSFGGM RNLWQLSQGTCQRLAFMHLKQQLCSQIALGKHHNWGAHELIGVLYDQGKA DERSCTDGQGYDGASNMRGELNGLQDLILNECPYAYHVHISLAGDKHMRV TWITDDKSAPSVVEYGTLPGKYDNVAEGETTSYSYIFYSSGKIHHTVIGP LEPNSVYFYRCGGQGPELQLKTPPAQFPISFAVVGD LGQTGWTKSTLDHI DQCKYDVNLIPGDSLADYIQHRWDTFGRLVQPLASSRPWMVTQGNHEVE HIPLLDGFIYSNRWKMPFEESGSSSNLYYSFEVAGAHIIIMLSYDDYD VYSEQYKWLKTDLSKVDRKRTPWLLVIFHVPWYNSNTAHQGE GGDMMKTM EPLLYAASVDLVFAGHVHAYERSKRVYNGKLDPCGAVHITIGDGGNKEGL AHKYIDPQPKWSEFREASFGHGELKIVNTTHAFWSWHRNDDDEPVKSDDI WITSLVNSGCVAQKKTELEHALMTP*
MsPAP6	MsG0380014132.01.T01	MKSGIQVHISLAGDKHVRITWVTDDKSAPSVVEYGTLP GKYDSVAEGETT SYSYIFYSSGKIHHTVIGPLEPNSVYFYRCGGQGPELQLKTPPAQFPISF AVVGD LGQTGWTKSTLDHIDQCRYDVNLIPGDSLADYIQHRWDTFGRLV QPLASSRPWMVTQGNHEVEHIPLLDGFIYSNRWKMPFEESGSSSNLYY SFEVAGAHIIIMLSYDDYDVYSEQYKWLKMDLSKVDRKRTPWLLVIFHVP WYNSNTAHQGE GGDMMKTMEPLLYAASVDLVFAGHVHAYERSKRVYNGKL DPCGAVHVTIGDGGNKEGLAHKYIDPPKWSEFREASFGHGELKIVNSTH AFWSWHRNDDDEPVKSDDIWLTSLDSSGCVDQKRTELEHALMTP*
		MKSGIQVHISLAGDKHVRITWVTDDKSAPSVVEYGTLP GKYDSVAEGETT SYSYIFYSSGKIHHTVIGPLEPNSVYFYRCGGQGPELQLKTPPAQFPISF
MsPAP5	MsG0380014132.01.T02	MKSGIQVHISLAGDKHVRITWVTDDKSAPSVVEYGTLP GKYDSVAEGETT SYSYIFYSSGKIHHTVIGPLEPNSVYFYRCGGQGPELQLKTPPAQFPISF

		AVVVDLGQTGWTKSTLDHIDQCRYDVNLIPGDLSYADYIQHRWDTFGRLV QPLASSRPWMVTQGNHEVEHIPLLKDGFIYSNSRWKMPFEESGSSSNLYY SFEVAGAHIIMLGSYDDYDVYSEQYKWLKMDLSKVDKRKTPWLLVIFHVP WYNSNTAHQGEGGDMMKTMEPLLYAASVDLVFAGHVHAYERSKRVYNGKL DPCGAVHVTIGDGGNKEGLAHKYIDPPKWSEFREASFGHGELKIVNSTH AFWSWHRNDDDEPVKSDDIWLTSLDSSGCVDQKRTELEHALMTP*
MsPAP7	MsG0380015680.01.T01	MKGSSFFKINMILVILCFFTNLRMGLGDMNGIGEQLSKIAIHKITILALH SSASITASPFLLGIGEDTEWVTVEVESPEPTNEDWYKYANHSNPKYKKT GKNTLKFQLINQRADFSFALFSGGLSNPRLVAISNFIAFANPKAPVYPRL AHGKSWNEMTVTWTSGYDISEAVPFVEWGPKGKKQIQSAAGTLTFNRNSL CGEPARTVGWRDPGFIHTSFLKELWPNMRYTYRLGHFLSDGSYVWSKRY FKASPYPGQNSLQRVIIFGDMGKAERDGSNEYADYQPGSLNTTDQLINDL DNFDIVFHIGDLPYANGYISQWDQFTAQVQQIASKVPYMIASGNHERDWP NSGSFYDTPDSGGECGVP AETMYYP AENKAKFWYATDYG MFRFCIADSE HDWREGSEQYKFIEHCLATVDRKQQPWLIFAAHRPLGYSSNDWYAKEGSF QEPMGRESLQGLWQKYKVDIGFYGHVHNYERVCP IYQNQC VNNEKTHYSG TVNGTIHV VVG GGGSHLS DFTTAPPIWSIFRDRDYGFVKLTAFNHSYLLF EYKKSSDGKVYDSFTISR DYRDVLACVHDGCEKTTLAL*
MsPAP8	MsG0380015682.01.T01	MEGKLNMSLVILCLFITNLRICL GDMNGFGEQLSKIAIHKITILAIHDSA SVTASPFLLGSKGEDTEWVTVKLESPEPTNEDWVG VFTPANFNSSTCPPN PGGIGRVDTPFICSAPIKYKYANHSNPKYKKTGKTTLKFQLINQRADFSF ALFSGGLSNPKLVAVSNFIAFANPKAPVYPRLAHGKSWNEMTVTWTSGYD ISEAVPFVEWGPKGKKQIQSAAGTLTFNRNSMCGQPARTVGWRDPGFIHT GFLEELWPNMRYAYRLGHLLSDGSYVWSKRYSFKASPYPGQNSLQRVIIF GDMGKAERDGSNEYANYQPGSLNTTDQLIKDLNIDIVFHIGDLPYANGY ISQWDQFTAQVQQISSTVPYMIASGNHERSWPNSGSFYDTPDSGGECGVP AETMYYP AENKAKFWYATDYG MFRFCIADTEHDWREGSEQYKFIEHCLA TVDRKQQPWLIFAAHRPLGYSSNDWYAKEGSFE EPMGRESLQGLWQKYKV DIAFYGHVHNYERVCP IYQNQC VNNEKSHYSGTVNGTIHV VVG GGGSHLS DFTTAPPVWSIFRDKDYGF GKLTAFNHSYLLFEYKKSSDGKVYDSFTISR DYRDVLACVHDGCEKTTLAL*
MsPAP9	MsG0380016120.01.T01	MGFVLVSPHVVTLSLLLFS LCSILVHGVVPTLDGPFKPVTVPLDKSFRG NAVDIPD TDPLVQRNVEGFQPEQISLSLSTSHDSVWISWITGEFQIGENI EPLNPETVGSIVRYGRFGRSMNGQAVGYSLVYSQLYPFEG LHNYTSGIIH HVRITGLKPNTLYQYQCGDPSLSAMSDVHYFRTMPVSGPKSYPSRIAVVG DLGLTYNTTSTVNHMISNHPDLILLVGDASYANMYLTNGTGSDCYSCSFS NTPIHETYQPRWDYWGRYMEPLISSVPVMVIEGNHEIEEQAENKTFVAYS SRFAFPSEESGSSSTLYYSFNAGGIHFIMLGSIYSYDKSGDQYKWLEKDL ASLDREVTPWL VATWHAPWYSTYKSHYREAECMRVEMEDLLYKYGV DIVF NGHVHAYERSNRVYNYTLDPCGPVYITVGDGGNREKMAITHADEPGNCPE PLTTPDKFMRGFCAFNFSSSPATGKFCWDQ QPDYSAFRESSFGHGILEVK NETHALWIWNRNQDLYGTAGDEIYIVRQPDKCPPVKPEEVHKT*
MsPAP10	MsG0380016121.01.T01	MPVSGPKSYPSRIAVVGDLGLTYNTTSTVNHMTGNHPDLILLVGDVTYAN LYLTNGTGSDCYSCSFSNTPIQETYQPRWDYWGRYMEPLIASVPIMVLEG NHEIEEQLRTRHLLLIEYNKLSGRVINLQVK NETHALWIWHRNQDFYGSA GDEIYIVRQPDKCPPVKPEEVHKHEFGYYVQIILTIVF FILRDK*
MsPAP11	MsG0480019730.01.T01	MSDKSTAKAMFASLCSIMREQEVKKQRLSLLVHQYELFKMRMMKLVRRCT QVSNLSFWATDSKKS YLLIIRVNHSSFIQRQVIKTLKVVDLKRKNSQVQ IRTRSTEWPSLKQLQYLAKKNRKLARRGKYTPQYTWLEELPRVNRKKT PWLIVLMHSPWYNSNSYHYMEGETMRVMFESWFVKYKVDVVFAGHVHAYE RSERVSNIAYNIVNGICAPVKDLSAPVYINIGDGGNIEGLATKYTQPQPE YSAFREASFGHAIFDIKNRTHAYIAGIEIKMVMLLRVIPFGFQ*
MsPAP12	MsG0480019732.01.T01	MNHFELLIKSTTNLNLVQRHGPIWSFTLFASNDKLNRLVLNLVFCNGGT TSIFVRKVEKAIDMPLDSDVFKVPPGYNAPQVHITQGDHVGKALIVSWV TEDEPGSDAVRYWSENSKHKKLAKGKIFTYRYFNYSSGFIHHATIRNLKY NTKYYYEVGLKNTRQFWFTTPPAIGDPVPYTFGLIGDLGQTYDSNRTL HYQLNSTKGQTVLVFGDLSYADNYPNH DNVRWDTWGRFAERSVAYQPWIW TIGNHELDFAPEIGENEPFKPFSHRYHTPYKASQSTSPFWYSIKRASAHI IVLASYSAYGKYTPQYTWLEELPRVNRKKT PWLIVLMHSPWYNSNSYHY MEGETMRVMFESWFVKYKVDVVFAGHVHAYERSERVSNIAYNIVNGICAP VKDLSAPVYINIGDGGNIEGLATKYTQPQPEYSAFREASFGHAIFDIKNR THAYYSWHRNQGD A VKSDSLWFFNRFWNPVDDSKPHGEIKFKGWVQTHG FSQSINSFTIIIHTYAFASMPLEV FILLREIVGFYKEDASNACELFSLLL HSACHVVVFDMLIKVFASNSMLEHAYHVFVSAKDVGIEFNTMSCNFLLKC LVDANRVDDDDDRGVSVSADIRQASEILGKIYRSGETPNVVTYSTYIKGF SNAGSLGVAWKLICNLCRENQSINNHC FNAVMYGLCQRGLLDEASQVLEE

		MKSVGKLPDVYGYSLIDALCKNRDDEKAIDRLEDMNLNQIKPSIVSYTS FIRRLCKTMLMETAMNTFRVIGASGYKYDQTIYETEVDGFCRKGDMDSAG KLFEEMCSNNFTPSAFCYCSLIKGFYKLRQFANALKVYSIMQKRGIWPD IACNHILSIYCKKHDFNEALALLEEFQEHGLNPYSYNEFIHKLCRESFPK KALQLLPVILKRNVPPELLIIVLSFIALPNS*
MsPAP13	MsG0480019733.01.T01	MHKIALKCVVEIQNKVFEECGKMGLHSSLLAFGLVLNLVFCNGGRTST FVRKVEKTIDMPLDSDFDVPSPGYNAPQQVHITQGDHVGKAVIVSWVTEN EPGSNAVRYWSKNSKQKKLAKGKIVTYRFFNYTSGFIHHTTIRNLEYNTK YYYEVGLGNTTRQFWFTTPPEIGPDVPYTFGLIGDLGQSYDSNKTLSHYE LNPTNGQTVLFFVGDLSYADNYPNHDNVRWDTWGRFAERSVAYQPWIWTVG NHELDFAPEIIGFFWCCVTTWYNSSFCSGKYTPQYKWLEQELPKVNRTE PWLIVLMHSPWYNSYNYHYMEGESMRVMYEPWFVKYKVDVVYAGHVHAYE RSERVSNAVYNVVGICTPIKDQSAPVYITIGDGGNLEGLATNMTEPQPE YSAYREASFGHAIFDIKNRTHAHYSWHRNQDGYSVEADSHWFFNRFWHPV DDSTTHVSH*
MsPAP14	MsG0480022236.01.T01	MLSELNNESEAEMKSRQEVGNDNGGWSATHSFVSRNSDSNETIAFLFGDM GTTTAYNTYLRTQDESISTMKWILRDVEALGNKPAFISHIGDISYARGYA WLWDHFFAQIEPVATKVAYHVCIGNHEYDWPLQPWKPDWANYRTDGGGEC GVPYSLRFNMPGNSSEPTGTVAPATRNLYYSFDMGTVHFVYISTETNFLP GSNQYNFLKRDLESVDRNKTPFVVVQGHRPMYTTSSNEVRDAALRGKMVEH LEPLLVNNHVTLALWGHVHRYERFCPLNNYTCGNGVGRKAGEKGYTVHLV IGMAGQDWQPIWQPRPDHPDDPIYPQQRSLYRGGEFGYIRLVATKQKLV IYYVGNHDGEVHDTLEILESGEVVSGGGNDNVNGGIGSAKPEVQIKDPHC RGTTSENFVADSASVASSIKYHAEFTASFPEKFEPSKAYFATAESVRDS LIINWNATYEYYERVNVKQAYYMSMEYLQGRALLNAIGNLQLSGPYAEAL RKLGYNLEDVANQEPDAALGNGGGLGRLASCFLDSLATLNPWAGYGLRYR WEIPGKFRETSVSYPVRFYGEVISGPDGAKQWTGGESILAVAYDVPIPGY KTRTTINLRLWSSKVSTEEFDLKAFNTGDHAKAYAVMKNAEKVIFVPDYN VSVAEMLIPAELSQHISWDGGQWNKQHEIAMNGCVQIGTLDGANVEIREE VGEDNFFLFGARAEIAGLRKERAAGR*
MsPAP15	MsG0480022238.01.T01	MRVMYVTRDPKETVRYGERKCHMGGLAVARVKRYEREHMCAPANESVG WRDPGYIHDALITSLKKGRRYYYKFKGTDPCQTQTINGTKDVALREKM LEPLLVNNNVNLA LWGHVHRYERFCPLNNYTCGNGVGRRAGDKGYTVHLV IGMAGQDKQSIWKTRRGHPNDSIFPQPKQSLYRGGEFGYIRLVATKQKLV VSYVGNHDGEVHDTMEILASGELFNGNVNVDIGNAKPKGLIEELHYPSMS REEAYWCLGPLVWTFSPQLDAERLTNHSFTALGTVVS LGTFGTKLVSRM LIFFITQNAHDWINS AATALAKLLRRAFKEMAELLIRNVVKWNCNNHMG SILNIDGRCLGTPIRAGFSGVIRYNHGFYLSRFTGRIINSNDIFVELTAI HRGLCLAIDMGLDDLVS RGYGYDYKCWP IVQSSRVDMKIKSSSEN D MIKESNQ*
MsPAP16	MsG0480022891.01.T01	LAKWRWRILQNEVRFGRWLS CGDQILNRVDWGTDSFPYFLSRWWKDISAL DVPDGNWLDVFLVRPTAEVVS VEDLLVHLVALLSLSFLSLEEDKWVWGP DDGDSFTVK SAYS SLIAKVFTNEENLDV LNIFVTPSSFLDFQMGIVGKNL NIEFVISTGDNFYDDGLKGVDDPAFYESFVDIYTAPSLQ QIWIYNVLGNHDYRGDVEAQLGPILRQKDSRWVCLRSFILD TDNVEFFVDTTPFVEEYFTD PGKHTYDWKGVLP LESYRAELLKEVDSALVQSTAKWKIVVAHHPIKSAGP HGNTQELVEQLLPILKSNNV DAYINGHDH CLEHIIDKESGIHFFTSGGGS KAWGGDIKPWDPKELKLYYDGGQGFMSMQISKTNASIVFYD VFGKVLHTWSMSKKLKEAA*
MsPAP17	MsG0580026511.01.T01	MQEEVDGSNEYNNFQHGSINTTQQLIQDLENIDMVFHIGDISYANGYLSQ WDQFTAQVEPIASAVPYMIASGNHERDWPGSGSFYGNMDSGGECG VLAETMFYVPASNRAKFWYSIDYGMFRFCVADTEHDWREGTEQYK FIEHCLASVD RQKQPWLVLFAHRVLGYSSCICYAEEGSFAEPMGRESLQKLWQKYK VDIAIYGHVHNYERTCPIYQ NICTSEEKHN YKGTLN GTHIVAGGGGASLSTFT SLKTKWSIFKDYDYG FVKLTA FDHSNLLFEYKKS RDGKVYDSFKISR DYRDILACVTDSCPSATMAL*

MsPAP18	MsG0680030857.01.T01	MKICTFCMSLTIVLVIIANINMVVSKRHIPTTLDGPFKPMTRWFDSSLRR GSDDLPMTHPRLKMNVTNLNFPQIALAISSPTSMWISWITGKSQIGQNV PLDPASIGSEVVYGKESGKYTNVGKDSLVSQLYPFEGLLNYTSGIIHH VKLEGLEPGTRYYYNCGDSSIPAMSQENSFETFAKPSPKNYPARIAVIGD LGLTSNSSTTVDHLSYNDPSMILMIGDLTYANQYLTTGGKGASCFSCAFP DAPIRETYQPRWDGWGRFMQPLTSKIPMMVIEGNHEIEPQADGITFKSYL TRFAVPAEESGSKSNFYYSFDTGGIHFIMLGAYVDYNRTGAQFAWLKQDL QSVDRSVTPWL VATMHPPWYNSYASHYQEFECMRLEMEALLYQYRVDIIF NGHVHAYERMNRVYNYTLDPCGPVYITVGDGGNIEKVDVDHADEPGKCP PGDNIPEFGGVCHSNFTFGPAKGNFCWNKQPEWSAFRESSFGHGILEVMT LTFEASIFLFITSVDTKGFGFAAVSNPAFMNSGTSVARAVKPSRSALT*
MsPAP19	MsG0680034704.01.T01	MASFSAKSMTMFFLFTIIFGFGFLHASAELQRFTHTPKTDGSLNFLVVG WGRRGEYNQSDVAFQMGVVGEKLDIDFVVSTGDNFYDDGLTGEHDPNFEE SFSKIYTAKSLQKQWYSVLGNHDYRGNVEAQLSPFLRQIDNRWLC VDESELVEIFFVDTPFVEEYFTAPEHNYDWNGINPPKNYLANLLKDVEIA LRESRAKWKIVVGHHAIRSVGHHGDTKELVNLLLPILQANHVDFYMN HCLEHISDTNSPLQLVSGAGSKAWRGDVRDTTGNDVNFFYDGGQGFMSVQ LTGTDANIVFYDVTGNVLHKIASSKQLHSSI*
MsPAP20	MsG0680034704.01.T02	TIILCCKKCLVKIDIDPFFNIRYRIKTSCSKGDTPTSLNQVLSTFTRAMA SFSAKSMTMFFLFTIIFGFGFLHASAELQRFTHTPKTDGSLNFLVVG RRGEYNQSDVAFQMGVVGEKLDIDFVVSTGDNFYDDGLTGEHDPNFEE SKIYTAKSLQKQWYSVLGNHDYRGNVEAQLSPFLRQIDNRWLC SELVEIFFVDTPFVEEYFTAPEHNYDWNGINPPKNYLANLLKDVEIALR ESRAKWKIVVGHHAIRSVGHHGDTKELVNLLLPILQANHVDFYMN LEHISDTNSPLQLVSGAGSKAWRGDVRDTTGNDVNFFYDGGQGFMSVQLT GTDANIVFYDVTGNVLHKIASSKQLHSSI*
MsPAP21	MsG0780038493.01.T01	MNSLTSLQLFLLNLLPLFFTFSNCHIPTTLEGPFPLVTVPFDTSLRGD TEDLPDDDPVRRQVTGFQPEQISLSLSTTHHSVWLSWITGEYQIGNNIK PLDPKTVSSVRYGTSRLELVNEEKGESLVYSQLYPFEGLLNYTSGIIHH VRLTGLEPSTLYYYQCGDPSLQAMSDIYHFRTMPISGPQSYPRVAIVGD LGLTYNTTTTISHMTSNEPDLVLLIGDVTYANLYLTNGTGSNCYSCSFPQ TPIHETYQPRWDYWGFRMQNLVSRVPIMVVEGNHEIELQARNRTFVAYSS RFAFPSEESGSSSTFYYSFNAGGIHFIMLGAYIDYEKTAQQYKWLERDLA NVDRSLTPWL VATWHPPWYSSYKAHYREAECMRIEVEELLYSYGVDIVFN GHVHAYERFNRVYNYSLDPCGPVYITVGDGGNREKMSIPFADEPGNCPEP STTPDPYMGGF CATNFTFGPAAGKFCWDRQPDYSAFRESSFGYGIFV PLYPTT*
MsPAP22	MsG0780041108.01.T01	MRFKGTHFPLAFLILVCLGFDVAVYCYNRPPPRKTIFVPHDLDDSSPQV HISQVGQDKMRVSWITESPTPATVHYGPSSAANALSATGTTTSYHYALYE SGENEIHNVVIGPLKSNTVYYYRLGDSAKTYNFKTTPAQFPIKFGVVGAG DLGQTEWTVSTLKHLDGSNYDMLLPGDLSYADFVQNLWDSFGRLVKPYA SQRPWMVTTGNHDIEKIPGAMQGGKCHLKKVDQILYITILLMCLAFMLSC WVLIPILPRILHNINGFKDLQKVNMGKTPWVVVLVHAPWYNSNEAHQGE AESVDMKNAMEGLLCNARVDVVFTGHVHEECFNVSNELIN*
MsPAP23	MsG0780041115.01.T01	MRFKGTHFPLAFLILVCLGFDVAVYCYNRPPPRKTIFVPHDLDDSSPQV HISQVGQDKMRITWITESPTPATVHYGPSANALSATGTTTSYHYALYE SGEIHNVVIGPLKPNTVYYYRLGDSAKTYNFKTTPAQFPIKFGVVGDLGQ TEWTVSTLKHLDGSNYDMLLPGDLSYADFVQNLWDSFGRLVEPYASQRP WMVTTGNHDIEKIPVVHKEPFTAYNARWQMPFEESGSDSNLYYSFDVSGV HVIMLSYTDFAPDSSQYKWLQGDQKVNRGKTPWVVVLVHAPWYNSNEA HQGEAESVDMKNAMEGLLYNARVDVVFTGHVHAYERFTRVYKDKGDNCGP VHIVIGDGGNREGLATRYQDPKPEISLFREASFGHGVLEVVNASHALWSW HKNDNEEPVVS DSVWLTSLSSDPACKA*

MsPAP24	MsG0880042856.01.T01	MSGRLVKKILNEQHQLSQQQFIKEEEEEDDNEQEEGSTAPSTINPFDLLN DNDSEPENQGDSEADETSVRDDNKERTSALKSSAQVSTSNPKSKKKKNNKK KKSKDNAVSGKAVNAKDKSRVKEDAVSILQVVKSFENQNNNQPSSSRQM RGVRRVRHNLKKTVLVTPANTWLPDDSLSMEFLEIKNGYHYFRYVHSPS YSQYQKSFEAAKAINDINGVASILQHRPYHIDSLTMAEYFKGNCQLKYK HDTNKPLFTALFTRMKNLDRRGCHRSALEVCKLLLSLSDDDPMGAIFCID YFALRSEYAWLEKFSEAYKSDNSIWLLPNFSFSLAICRFYLERAASEDA CVDSKKSFSDDLMTQALMLHPSVIKKLVTKVPLKDRAWTDILKHAFFRSD QTGIPSQDHLINIYVERNYLIWRPLDLQKLLIGAAKQVMETLESNKSEVN DWSCVRKEAFSSEKNEYGHLLVSDFSDSVTAIPQENLQQFMGIPRAGEAM LDENQFVNQQGNGHAPRGVANRNALAVLFESMLPWVTYEEGGPDVNQPVM MQMIDPYWTVIPVMLVHYATHPLAQYDLWRSKIVILLSWVWSIRLTHNY FRRENGNGVLEKIGVSLRWVNSMENIGGGFHSLLFMSLSRLMFLIGLSLP LYVVHFVNKPLSILDLVAIVVCLSGIVIAVFADTQLHDFMSRNNKFKELG KPVIPVLDTAYGITAGVRITLVRRCGGDWLC LHGTLDMDGP LLELWMIL AEKPNLIVFTGDNIYGSDSLDSAKSMDAAFAPAIESNIPWVAVLGNHDQQ GSLSREGVMKYIVGMKNSLSKVNPPGVHIIDGFGNNNWRLVVFKKAYIKG PAPQKEAAPGLAYFHIPLPEYTSFDSSNMTGVKMETDGGDGISSASVNSG FFTTLVEAGDGSDTMLMERLDGLGGQEWVVASLEKTDKGSWGAVKSIKSW KRLDDQHLTGINGEVLWSKSTPVCNIFLFGVVTIEEFLAYFADTQLHDF MSRNNKLKGLGKPVIPVLDTGLWYYSRRPNYFGETLWWWGLVVFAWNLGH GWTFIGALVNTCVWLM*
MsPAP25	MsG0880042857.01.T01	MNLRKSFVFDTKRKMGLNFMVFVVMVSWFWSIPTTCALAAKQQENQKLRF DQNGEFKILQVADMHYANGKTTLC LDVLP SQNASCTDLNTTAFIHRMILA EKPNIIVFTGDNIYGYDSSSAKSMDLAFAPAIESNIPWVAVLGNHDQEG SLSREGVMKYIVGLKNSLSKVNPEVHIIDGFGNNNLEIGGVQGTA FENK SVLNLYFLDSGDYSKVPSPGYDWIKPSQQLWFERTSAKL RKAYIKGPAP QKEAAPGLAYFHIPLPEYTSFDSSNMTGVKMETDGGDGISSASVNSGFFT TLVGAGDVKAVFVGHDHLNDFCGKLMDIQLCYAGGFGYHAYGKAGWSRRA RVVVASLEKTDKGSWGAVKSIKSWKRLDDQHLTGIDGEVLWSKSTPDGVK TGSEELNHQFASSKSQMWSEAEAKNKLVEIKNLKEMQASVGFHIGSWKL*
MsPAP26	MsG0880044980.01.T01	MQPLFTNLLVLAIIHFHQQAVVSPQSHDLHQPLSKVAIHNTLFALHPDASI KATPNLLGFKGQNTIEWVTLKYNNPNPSIHDWIGVFSPANFSSSICPAENR LVNPPFLCSAPIKFQYANFSSHNYKITGKGLKLQLINQRSDFSALFTG GLTNPKLVAVSNKVSFINPNAPVYPRLAQGKTWDEITVTWTSGYGISEAE PFVEWGRKEGKLVQSPAGTLTFDRNTMCGAPARTVGWRDPGYIHTSFLKE LWPNKEYTYKLGHRLVNGTTIWSQEYQFKSSPYPGQNSVQRVVIFGDMGK AEADGSNEYNNFQPGSLNTTNQIIQDLKDIDIVFHIGDLCYANGYLSQWD QFTAQIEPIASKVPYMTASGNHERDWP GSGSFYGTLDSGGECGVLAQTMF YVPAENREKFWYSVDYGMFRFCIAHTELDWRKGTEQYEFIEKCLASVDRQ KQPWLIFLAHRVLGYSSADFYVAEGSFEEPMGREDLQSLWQKYKVDIAMY GHVHNYERSCPYQNICTDKEKHNYKGS LNGTIHVVVGGGAALAEFAPI NTTWSIFKDHDGFGVKLTAFDHSNLLLEYKKSSDGQVYDSFKISRDYRDI LACTVDSCQSTTLAS*
MsPAP27	MsG0880046225.01.T01	MKQESIRHKHNMIVLVATLAWLLLNSNIVLCSAHANGFGEQPLSKIAIHK TIVSLHSNASVTATPSILGTKGEDTQWVTVDIDFPDPSVDDWVGVFSPAN FNSSACPPVNDPKEQIPYICSAPIKYKFANYSNSRYTKKGKASLRFQLIN QRADFSFALFSGGISNPKLVAVSNFISFANPKAPLYPRLAQGKSWDEMTV TWTSGYDINEATPFVEWGPEGKTPVQSPAGTLTFGRNSMCGSPARTVGWR DPGFIHTSFLKNLWPNFVYTYRLGHLLPDGSYIWSKKYSFKSSPYPGQDS LQRVVIFGDMGKVILIVSKHNLYSREGRLSEIVFEKESNMLPGAIFCQIY DSANGNHERDWPNSGSFYDVTDSGGECGVLAETMFYVPAENRAKFWYATD YGMFRFCIADTEHDWREGSEQYKFIEHCLATVDRQKQPWLIFAAHRVLVI PLTLNQCVNTERSHYSGIVNGTIHVVGAGSHLSNFSQVTPKWSLYRDY DFGFVKLTAFNHSSLLFEYKKSSDGNVYDSFTVSRDYKDV LACVHDSCEA TTLAS*
MsPAP28	MsG0880046835.01.T01	MENLRITVHITQGDYDGKAVIISWVTPDEPGSSHVQFGTSENKFQSTAQG TVSNYTFGEYKSGYIIHCLVEGLEHSTKYYYRIGSGDSSREFWFETPPKV GPDATYKFGIIGNIYISGDLGQTFNSLTLEHYIESEAQTVLVFGDLSVG KWVGPIACDTKAISKPTHI*

MsPAP30	MsG0880046836.01.T01	MQRLLHLVLLASFVFFSRDVYAGITSSFVRSEFPSVDIPLNHPAFAVPK
		GHNAPQQVHITQGDYDGKAVIISWVTPDEPGSSHVQFGTSENKFQSTAQG
		TVSNYTFGEYKSGYIIHCLVEGLEHSTKYYYRIGSGDSSREFWFETPPKV
		GPDATYKFGIIGDLGQTFNSLSTLEHYIESEAQTVLFVGDLSYADRYQYT
		DVGLRWDTWARFVERSTAYQPWIWNTGNHEIEYFPYMGEVVPFKSYLQRY
		TPPYLASKSTSPLWYAIRRASAHIIVLSSYSPFGCVCFKFTKFIPRNNIP
		WNIKMGILFQKYTPQWKWLRDELPQVDREKTPWLIVLMHVPLYNSNEAH
		FMEGESMRVVYESWFIKYKVDVIFAGHVHAYERSYRFSNIDYNITTGNRY
		PVADKSAPVYITVGDDGNQEGLASRFRDPQPEYSAFREASYGHSTLEIKN
		RTHAVYHWNRNDDGKKVATDSFVLHNQYW*

S1 Protein sequences of *MsPAP* gene family members