

GPPS-I nucleotide sequences alignment

MpGPPS-1 Unigene0045757	ATGAGTCTCTGTAAATCCCTGTCGGAAATGGCCTCAGACCATCGGCGTTAGATGTTACACGGCGCCGGAGCGGAGATCCAGATCC ATGAGTCTCTGTAAATCCCTGTCGGAAATGGCCTCAGACCATCGGCGTTAGATGTTACACGGCGCCGGAGCGGAGATCCAGATCC	90 90
MpGPPS-1 Unigene0045757	ACTCTTTTCATCTCATCCACTCCGCTGTAATGTCCTTCTCTCTACTTCTCATCCCGCTCAAGGCTCCGCCACTTTTTCGGTT ACTCTTTTCATCTCATCCACTCCGCTGTAATGTCCTTCTCTCTACTTCTCAAGCCCTCAAGGCTCTGCCACTTTTTCGGTT	180 180
MpGPPS-1 Unigene0045757	TCTGCAGTTTATACCAAGAGCGCAGCGAAATTAGGCTAAAGATCCGGCCCTTCGACTTCGCGCGCGTTCGATTTCCAGCGCTACATG TCTGCAGTTTATACCAAGAGCGCAGCGAAATTAGGCTAAAGATCCGGCCCTTCGACTTCGCGCGCGTTCGATTTCCAGCGCTACATG	270 270
MpGPPS-1 Unigene0045757	CTCCGSAAGCGAAATCCCTGACCAAGGCGTTGGAAGCGCGCTGAGATGAAGAGCCCGCTGAAGATCCACGAGTCCATCGGTACTCC CTCCGSAAGCGAAATCCCTGACCAAGGCGTTGGAAGCGCGCTGAGATGAAGAGCCCGCTGAAGATCCACGAGTCCATCGGTACTCC	360 360
MpGPPS-1 Unigene0045757	CTCTCGCCGGCGCAAGAGAGTGCCTCATCTGTGCATCCGCTCGAGCTCGCTCGGCGGACGAGTCAACGCGGATGCGCGCG CTCTCGCCGGCGCAAGAGAGTGCCTCATCTGTGCATCCGCTCGAGCTCGCTCGGCGGACGAGTCAACGCGGATGCGCGCG	450 450
MpGPPS-1 Unigene0045757	GCCTGGCCGTCGAGATGATCCACAGATGTGCTGATGACAGACGACCTCCCTGTCATGGACAACGACGACCTCCGCGCGGCAAGCCG GCCTGGCCGTCGAGATGATCCACAGATGTGCTGATGACAGACGACCTCCCTGTCATGGACAACGACGACCTCCGCGCGGCAAGCCG	540 540
MpGPPS-1 Unigene0045757	ACGAACCACTGCTTCGGCGAGAGCTGGCGTCTCTCCGCGGAGCCCTCTCTCTCTCGCTTCGAGCAGTGGCGCGCGGAGCC ACGAACCACTGCTTCGGCGAGAGCTGGCGTCTCTCCGCGGAGCCCTCTCTCTCTCGCTTCGAGCAGTGGCGCGCGGAGCC	630 630
MpGPPS-1 Unigene0045757	AAAGCGCGCCCGGAGCGGATCTGAGGTCCTCGGCGAGCTGGCTCTCGATCGGCTCGGAGGGCTGTGGCGGGCAGGCTGTG AAAGCGCGCCCGGAGCGGATCTGAGGTCCTCGGCGAGCTGGCTCTCGATCGGCTCGGAGGGCTGTGGCGGGCAGGCTGTG	720 720
MpGPPS-1 Unigene0045757	GACTCTGTCTCGGAGGGATGGCGAGGTGGCTGGACCACTCGAGTCAITCCACCACCACAAGACGCGCGCTGTGCAGGCTTCG GACTCTGTCTCGGAGGGATGGCGAGGTGGCTGGACCACTCGAGTCAITCCACCACCACAAGACGCGCGCTGTGCAGGCTTCG	810 810
MpGPPS-1 Unigene0045757	GTGGTTTGGGGGCGATTGGCGCGCGGAAAGSAGGAGGAGTGGCGAGCTGAGAAATTCGCGAATTCGATCGGATTGCTGTTCAG GTGGTTTGGGGGCGATTGGCGCGCGGAAAGSAGGAGGAGTGGCGAGCTGAGAAATTCGCGAATTCGATCGGATTGCTGTTCAG	900 900
MpGPPS-1 Unigene0045757	GTCGTGGACGATATCCAGATGTGACGAAATCGTCAAGGAATGGGGAAGACGCGGGGAAGGATCTGTGGCGGTAAGAACACATAT GTCGTGGACGATATCCAGATGTGACGAAATCGTCAAGGAATGGGGAAGACGCGGGGAAGGATCTGTGGCGGTAAGAACACATAT	990 990
MpGPPS-1 Unigene0045757	CCGAGCTATAGCTGTGGAGAATTCGAGGAATTCGCGATCGGTTGAAAGGGAGGCGCTGGACAGTCTCCATTTTATCTCTCAT CCGAGCTATAGCTGTGGAGAATTCGAGGAATTCGCGATCGGTTGAAAGGGAGGCGCTGGACAGTCTCCATTTTATCTCTCAT	1080 1080
MpGPPS-1 Unigene0045757	AGGGCAGCTCCATTGATGCTCTCCCAATTAATTTGCTTATAGCAGACAAATG AGGGCAGCTCCATTGATGCTCTCCCAATTAATTTGCTTATAGCAGACAAATG	1133 1133

GPPS-I nucleotide sequences alignment

MpGPPS-1 Unigene0045757	MSLVLNPLKRWPTIGVSDVHGRRRRSRSTLPSHPLRHEMPPSLVFSSELAHAFPSVSAVVTKESEIRLKDPAESSPAFDFDGYM MSLVLNPLKRWPTIGVSDVHGRRRRSRSTLPSHPLRHEMPPSLVFSSELAHAFPSVSAVVTKESEIRLKDPAESSPAFDFDGYM	90 90
MpGPPS-1 Unigene0045757	LRLKAKSVNKALEAAVEMKEPLKIHESMRYSLLAGGKRVRFMLCIAACELVGGDESTAMPAACAVEMIHMTSLMHDDLPCMDNDLRRGKP LRLKAKSVNKALEAAVEMKEPLKIHESMRYSLLAGGKRVRFMLCIAACELVGGDESTAMPAACAVEMIHMTSLMHDDLPCMDNDLRRGKP	180 180
MpGPPS-1 Unigene0045757	TNRHVFGESEAVLAGDALLSFAPFHVAATKGAFTERIVRVLGBLAVSIGSEGLVAGQVWDCSEGMAEVGLBHLRHHHKTAALLQGS TNRHVFGESEAVLAGDALLSFAPFHVAATKGAFTERIVRVLGBLAVSIGSEGLVAGQVWDCSEGMAEVGLBHLRHHHKTAALLQGS	270 270
MpGPPS-1 Unigene0045757	VVLGAILGGKBEVAQLRKFANCIQLLPQWDDILDVTKSKELGKTAGKDLVADKTTYPKLIGVERSKFADRIAREANQQLLHPFH VVLGAILGGKBEVAQLRKFANCIQLLPQWDDILDVTKSKELGKTAGKDLVADKTTYPKLIGVERSKFADRIAREANQQLLHPFH	360 360
MpGPPS-1 Unigene0045757	RAAPLIALANYIAYRD RAAPLIALANYIAYRD	376 376

GPPS-s nucleotide sequences alignment

MpGPPS-s Unigene0038587	ATGGCCATTAATCTCTCCCAATCAACTCCAAAACATGTTTCCCTCTCAAAAACAGATCTGATCTCAGCGGCTTCTCTCCGCGCGTGC	90
	ATGGCCATTAATCTCTCCCAATCAACTCCAAAACATGTTTCCCTCTCAAAAACAGATCTGATCTCAGCGGCTTCTCTCCGCGCGTGC	90
MpGPPS-s Unigene0038587	ATGGCAACTGCCCGCTGCCGCTTCCCACACTATGCCACGCCGCCCAAAGTCAGCCGTACTGGGCCGCATCCGAGCCGACATAGAG	180
	ATGGCAACTGCCCGCTGCCGCTTCCCACACTATGCCACGCCGCCCAAAGTCAGCCGTACTGGGCCGCATCCGAGCCGACATAGAG	180
MpGPPS-s Unigene0038587	AGATACCTGAAGAAATCCATGCAATAAGGCCCGCCGGAGAGTGTTCGGGCCCATGCACCACCTCACCTTCGCCGCCCCAGCCACCGCC	270
	AGATACCTGAAGAAATCCATGCAATAAGGCCCGCCGGAGAGTGTTCGGGCCCATGCACCACCTCACCTTCGCCGCCCCAGCCACCGCC	270
MpGPPS-s Unigene0038587	GCTCTCCACTATGCTTGGCGGGGTGGAGCTCGTCCGCGCGGACCGAAGCCAAAGCCATGGCAGCGCGGGCGGATCCATCTCGTCCAC	360
	GCTCTCCACTATGCTTGGCGGGGTGGAGCTCGTCCGCGCGGACCGAAGCCAAAGCCATGGCAGCGCGGGCGGATCCATCTCGTCCAC	360
MpGPPS-s Unigene0038587	GCGGCAGCCTACGTCCACGCACTCCCTTAACCGACGGTGGAGGCCATCCAAAGCCGCAATCCAGCACAAGTACGGCCCGAAC	450
	GCGGCAGCCTACGTCCACGCACTCCCTTAACCGACGGTGGAGGCCATCCAAAGCCGCAATCCAGCACAAGTACGGCCCGAAC	450
MpGPPS-s Unigene0038587	GTCCAGCTCCTCACCGGAGACGGGATTGTCCCGTTCGGGTTTGAGTGTCTGGCCGGTCACTGGACCCGGCCCGAACAGACGACCCGGAT	540
	GTCCAGCTCCTCACCGGAGACGGGATTGTCCCGTTCGGGTTTGAGTGTCTGGCCGGTCACTGGACCCGGCCCGAACAGACGACCCGGAT	540
MpGPPS-s Unigene0038587	AGGATCTGAGAGTTAATAAGAGATCAGTCGGCCCGCGCGCCGGAGGAATGATAAGCGGCTGCATAGGGAGAGAAATGTTTGAT	630
	AGGATCTGAGAGTTAATAAGAGATCAGTCGGCCCGCGCGCCGGAGGAATGATAAGCGGCTGCATAGGGAGAGAAATGTTTGAT	630
MpGPPS-s Unigene0038587	GGAAATACGAGTTTAGACTTCATTGAATATGTGTCAAGAAAAAATACGGCGAGATGCATGCTTGGCGCGCGGCTTGTGAGCCATATTC	720
	GGAAATACGAGTTTAGACTTCATTGAATATGTGTCAAGAAAAAATACGGCGAGATGCATGCTTGGCGCGCGGCTTGTGAGCCATATTC	720
MpGPPS-s Unigene0038587	GCGCGCGCACTCCGAGCAGGAGATTCAGAAGCTGAGGAATTTCCGGCTTATCAAGGAACCTCTCAGAGGAATGATGGAATGAAAAATTC	810
	GCGCGCGCACTCCGAGCAGGAGATTCAGAAGCTGAGGAATTTCCGGCTTATCAAGGAACCTCTCAGAGGAATGATGGAATGAAAAATTC	810
MpGPPS-s Unigene0038587	CATCAATTAATTGATGAGAAATAAATGGAAAAATGAAAGAATTGGCTCTCGAGGAGTTGGGAGGCTTCACGGGAAGAACGCTGAGCTG	900
	CATCAATTAATTGATGAGAAATAAATGGAAAAATGAAAGAATTGGCTCTCGAGGAGTTGGGAGGCTTCACGGGAAGAACGCTGAGCTG	900
MpGPPS-s Unigene0038587	ATGTCGAGCCTTGTAGCCGAGCCGAGCCTTACCGCGCTTA	941
	ATGTCGAGCCTTGTAGCCGAGCCGAGCCTTACCGCGCTTA	941

GPPS-s amino acid sequences alignment

MpGPPS-s Unigene0038587	MAINLSHINSKTCFPLKTRSDLRSSSVRCMPTAAAAPFTTATAAOSOPYWAAIADIDRVLKKSITRPPETVFGPMHHLTFAAFATA	90
	MAINLSHINSKTCFPLKTRSDLRSSSVRCMPTAAAAPFTTATAAOSOPYWAAIADIDRVLKKSITRPPETVFGPMHHLTFAAFATA	90
MpGPPS-s Unigene0038587	ASDLCLAAECBLVGGDRSQAMAAAAATHLVHAAAYVHEHLPLTDGSRFVSKPAIQHKYGNVELLTGDGIVPFGPELLAGSVDPARTDDPD	180
	ASDLCLAAECBLVGGDRSQAMAAAAATHLVHAAAYVHEHLPLTDGSRFVSKPAIQHKYGNVELLTGDGIVPFGPELLAGSVDPARTDDPD	180
MpGPPS-s Unigene0038587	RILRVIIBTSRAGGPEGMISGLHREBEIVDGNLSLDFIEVVKRKYGEMHACGAACGAILGGATLEETQKLRNFGLYQGLRGMEMKNS	270
	RILRVIIBTSRAGGPEGMISGLHREBEIVDGNLSLDFIEVVKRKYGEMHACGAACGAILGGATLEETQKLRNFGLYQGLRGMEMKNS	270
MpGPPS-s Unigene0038587	ESLIDENIIGKIKELALEELGGFHKNALMSSSLVAEPSLYA	312
	ESLIDENIIGKIKELALEELGGFHKNALMSSSLVAEPSLYA	312

LS nucleotide sequences alignment

MpLS Unigene0018537	ATGGCTCTCAGAGTGTTAGAGTGTGCAATGCAAAATCCAACTTCTAAGCACTAACCAGCCTATCTCAACCCCTCACACTGAAATCTCTCT ATGGCTCTCAGAGTGTTAGAGTGTGCAATGCAAAATCCAACTTCTAAGCACTAACCAGCCTATCTCAACCCCTCACACTGAAATCTCTCT	90 90
MpLS Unigene0018537	CCTAAATTCGCTCTTAACACTAAGGGTACTAGTCCCTCTCGCTCCGTGTGTCTGTCTCTCTCCGCAACTACTACCCGAAAGAGCATCC CCTAAATTCGCTCTTAACACTAAGGGTACTAGTCCCTCTCGCTCCGTGTGTCTGTCTCTCTCCGCAACTACTACCCGAAAGAGCATCC	180 180
MpLS Unigene0018537	CGAARCTACAAACCTTCTCGTGGATGTGACTTTATCCAAACCGCTCCAGTGATTATAAGGACGAGAGCATGCGAGAAGGGCTCTC CGAARCTACAAACCTTCTCGTGGATGTGACTTTATCCAAACCGCTCCAGTGATTATAAGGACGAGAGCATGCGAGAAGGGCTCTC	270 270
MpLS Unigene0018537	GAGCTGTGACCTTTGGTGAAGATGGAATTGGAGAAGAAACCGGATCAAAATTCGACAGCTTGAATGATGATGACTTGCAGAGGATGGGG GAGCTGTGACCTTTGGTGAAGATGGAATTGGAGAAGAAACCGGATCAAAATTCGACAGCTTGAATGATGATGACTTGCAGAGGATGGGG	360 360
MpLS Unigene0018537	CTGTCCGATCATTTCCAGAACGAGTTCAAAGAAATCTTGTCTCTGTATATCTCGACCATCCCTATTACAGAATCTGATCCAAAGAA CTGTCCGATCATTTCCAGAACGAGTTCAAAGAAATCTTGTCTCTGTATATCTCGACCATCCCTATTACAGAATCTGATCCAAAGAA	450 450
MpLS Unigene0018537	GAAAGGGATCTATACTCCACATCTCTGCATTTAGGCTCCTCGAGAACATGGGTTTCAAGTGTCTCAAGAGGATATCCAGGTTTCAAG GAAAGGGATCTATACTCCACATCTCTGCATTTAGGCTCCTCGAGAACATGGGTTTCAAGTGTCTCAAGAGGATATCCAGGTTTCAAG	540 540
MpLS Unigene0018537	AACGAGGAGGTGAGTTCAAAGAAAGCCCTTACGACGACACACAGAGGATGTTGCAACTGTACGAAGCTCTTTCTGTGTGACGGAAAGC AACGAGGAGGTGAGTTCAAAGAAAGCCCTTACGACGACACACAGAGGATGTTGCAACTGTACGAAGCTCTTTCTGTGTGACGGAAAGC	630 627
MpLS Unigene0018537	GAAACGACGCTCGACTCAGCGAGAGAAATTCGCCACAAATTTCTGGAAGAAAGAGTGAATGAGGGTGGTGTGATGAAACCTTTTAAACA GAAACGACGCTCGACTCAGCGAGAGAAATTCGCCACAAATTTCTGGAAGAAAGAGTGAATGAGGGTGGTGTGATGAAACCTTTTAAACA	720 717
MpLS Unigene0018537	AGAATCGCATATCTTTAGAAATCCCACTTCATTGGAGGATTAAGAGGCCAAATGCACCTGTGTGGATCGATTCGTATAGGAAGAGCCCC AGAATCGCATATCTTTAGAAATCCCACTTCATTGGAGGATTAAGAGGCCAAATGCACCTGTGTGGATCGATTCGTATAGGAAGAGCCCC	810 807
MpLS Unigene0018537	AACATGAATCCAGTAGTGTGAGCTTGCCTACTCGACTTAAATATTGTTCAAGCTCATTTTCAAGAACTCAAAGAACTCAAAGAACTCTTCGG AACATGAATCCAGTAGTGTGAGCTTGCCTACTCGACTTAAATATTGTTCAAGCTCATTTTCAAGAACTCAAAGAACTCAAAGAACTCTTCGG	900 897
MpLS Unigene0018537	TGGTGGAAATACTGGGTTTGTGAGAAGCTGCCCTTCGCAAGGGAAGACTGTGGAATGCTACTTTTGAATACTGGGATCATCGAG TGGTGGAAATACTGGGTTTGTGAGAAGCTGCCCTTCGCAAGGGAAGACTGTGGAATGCTACTTTTGAATACTGGGATCATCGAG	990 987
MpLS Unigene0018537	CCAGTCCAGCTGCAAGTCCAGAGTAATGATGGGCAAGTCAACGCTCTGATACGGTGATAGATGATATTTATGATGTCTATGTTAC CCAGTCCAGCTGCAAGTCCAGAGTAATGATGGGCAAGTCAACGCTCTGATACGGTGATAGATGATATTTATGATGTCTATGTTAC	1080 1077
MpLS Unigene0018537	TTAGAAGAACTCGAACACTTACAGACCTCATTCGGAGATGGGATATAGACTCAATCGACCAACTTCCCGATTACATGCAACTGTGCTTT TTAGAAGAACTCGAACACTTACAGACCTCATTCGGAGATGGGATATAGACTCAATCGACCAACTTCCCGATTACATGCAACTGTGCTTT	1170 1167
MpLS Unigene0018537	CTCGCACTCAACAACCTTCGTGATGACATCTTACGATGTTATGAAGAGAAAGCGCTCAACGTTATACCTTACCTCCCAACTTCGTGG CTCGCACTCAACAACCTTCGTGATGACATCTTACGATGTTATGAAGAGAAAGCGCTCAACGTTATACCTTACCTCCCAACTTCGTGG	1260 1257
MpLS Unigene0018537	GTGGATTTGGCGGATAAGTAAATGTGAGAGGACCGTGTCTACGGCCGACAAACCAAGTTTGAAGAGATTTTGGAAACTCATGG GTGGATTTGGCGGATAAGTAAATGTGAGAGGACCGTGTCTACGGCCGACAAACCAAGTTTGAAGAGATTTTGGAAACTCATGG	1350 1347
MpLS Unigene0018537	ATGTGATTAAGTGGGCTCCATGTTGACACATATTTTCGAGTAAAGGATTCATTCACAAAGGAGAGCTGCGACAGTTTGTACAAAG ATGTGATTAAGTGGGCTCCATGTTGACACATATTTTCGAGTAAAGGATTCATTCACAAAGGAGAGCTGCGACAGTTTGTACAAAG	1440 1437
MpLS Unigene0018537	TACCACGATTTAGTTCCTGTCATCTCTGTTTTCGCACTTCTGTAAGATTTGGGAACCTGATGGAAAGAGGTGAGCAGAGGCGATG TACCACGATTTAGTTCCTGTCATCTCTGTTTTCGCACTTCTGTAAGATTTGGGAACCTGATGGAAAGAGGTGAGCAGAGGCGATG	1530 1527
MpLS Unigene0018537	CCGAAATCACTTCAGTCTACATGATGACTACAATGCTTCGGAGGCGGAGGCGCCAAAGCACGTGAAATGGCTGATAGCAGAGTGTGG CCGAAATCACTTCAGTCTACATGATGACTACAATGCTTCGGAGGCGGAGGCGCCAAAGCACGTGAAATGGCTGATAGCAGAGTGTGG	1620 1617
MpLS Unigene0018537	AAGAAGATGAATCCAGAGGGTTCGAAGGATTCCTCATTTGGCAAGATTTTATAGGATGTGCAGTGTATTCGGAAGGATGGCCGAC AAGAAGATGAATCCAGAGGGTTCGAAGGATTCCTCATTTGGCAAGATTTTATAGGATGTGCAGTGTATTCGGAAGGATGGCCGAC	1710 1707
MpLS Unigene0018537	TTGATGTACCATAAAGGAGATGGGCTTGGCACACACATCTATATACATCAACAAATGACCCGACCTTATTCGAGCCCTTTGCATG TTGATGTACCATAAAGGAGATGGGCTTGGCACACACATCTATATACATCAACAAATGACCCGACCTTATTCGAGCCCTTTGCATG	1799 1796

LS amino acid sequences alignment

MpLS Unigene0018537	MALIVFSGAMOMIPSLTLYLQPSHLNSPKLLSNTKGTSRSLRVSCSSQLTERRSGNYNPSRWDFIQTLHSDYKDKHARRAS MALIVFSGAMOMIPSLTLYLQPSHLNSPKLLSNTKGTSRSLRVSCSSQLTERRSGNYNPSRWDFIQTLHSDYKDKHARRAS	90 90
MpLS Unigene0018537	ELVTLVKMELEKETDQIROLELIDDLQRMGLSDHFQNEFKELLSSVYLDHRYKNPDPKBEERDLYSTLSLAFRLLRHGFQVAQEVFVDFK ELVTLVKMELEKETDQIROLELIDDLQRMGLSDHFQNEFKELLSSVYLDHRYKNPDPKBEERDLYSTLSLAFRLLRHGFQVAQEVFVDFK	180 180
MpLS Unigene0018537	NESEFKESLSDDRGLLQLYEASFLITBGETTLESAREFATKFLERVNEGGDENLLTRIAYSLEIPLHWRIKRPNAPVWIDSYRKP NESEFKESLSDDRGLLQLYEASFLITBGETTLESAREFATKFLERVNEGGDENLLTRIAYSLEIPLHWRIKRPNAPVWIDSYRKP	270 269
MpLS Unigene0018537	NMNPVLELAILDLNIVOAHQELKESFRWRNTGFVKLFPARDRLVECFWNTGIIIEPRQHASARIMMKVNALITVDDIYDVTG NMPVLELAILDLNIVOAHQELKESFRWRNTGFVKLFPARDRLVECFWNTGIIIEPRQHASARIMMKVNALITVDDIYDVTG	360 359
MpLS Unigene0018537	LEELFETDLIRRWIDSIDQLPDWMLCFLALNPFVETSYDVMKEKGVNIPVLRQSWVDLADKYMVEARWFGGHKPSLEEVLENSW LEELFETDLIRRWIDSIDQLPDWMLCFLALNPFVETSYDVMKEKGVNIPVLRQSWVDLADKYMVEARWFGGHKPSLEEVLENSW	450 449
MpLS Unigene0018537	MSISGPCMLTHIFFRVDSFTKETVDSLYKYHDLVRWSSFLRLADDLGTVEEVSRGDVPSLQCYMSDYNASEBARKHVKWLIAEYW MSISGPCMLTHIFFRVDSFTKETVDSLYKYHDLVRWSSFLRLADDLGTVEEVSRGDVPSLQCYMSDYNASEBARKHVKWLIAEYW	540 539
MpLS Unigene0018537	KKMNARVSKDSPFGKDFIGCAVDLGRMAQLMYHNGDGHGTQHPILIHQVMTLEPEFP KMNARVSKDSPFGKDFIGCAVDLGRMAQLMYHNGDGHGTQHPILIHQVMTLEPEFP	598 597

L3OH nucleotide sequences alignment

MpL3OH-PM2 Unigene0052571	ATGGAGCTCCTCCAGCTTTGGTCCGGCGTTATAATCCCTCGTGTAACTAGCCCATATCTCTCTTAATCAACCAATGGCGAAAACCGAAA	90
	ATGGAGCTCCTCCAGCTTTGGTCCGGCGTTATAATCCCTCGTGTAACTAGCCCATATCTCTCTTAATCAACCAATGGCGAAAACCGAAA	90
MpL3OH-PM2 Unigene0052571	CCCCAAGCGAAGTTCCTCCCGGGCCCGCGAAGCTGCCGCTGATCGGGCACTCCACCTCTGTGGGGGAAGCTGCCGAGCAGCCGCTG	180
	CCCCAAGCGAAGTTCCTCCCGGGCCCGCGAAGCTGCCGCTGATCGGGCACTCCACCTCTGTGGGGGAAGCTGCCGAGCAGCCGCTG	180
MpL3OH-PM2 Unigene0052571	GCCAGCGTGGCAAGGAGTACGCCCGCTGCCCAAGCTGCAGCTGGTGGGTGTCTCCGCTGCTCTTGTGTCGGGGAGGCGACGAAAG	270
	GCCAGCGTGGCAAGGAGTACGCCCGCTGCCCAAGCTGCAGCTGGTGGGTGTCTCCGCTGCTCTTGTGTCGGGGAGGCGACGAAAG	270
MpL3OH-PM2 Unigene0052571	GAGGCGATGAAGCTGGTGAACCGCGCTGCCGCAACCGTTCGAGAGCATCGGGACGAGGATCATGTGTACGACACAGGAGCATCATC	360
	GAGGCGATGAAGCTGGTGAACCGCGCTGCCGCAACCGTTCGAGAGCATCGGGACGAGGATCATGTGTACGACACAGGAGCATCATC	360
MpL3OH-PM2 Unigene0052571	TTTCAGCCCTCAGAGCGAGCTGGCCGAGATGCGCAAGATCTGGGCTCCGAGCTCTCTCTCTCCCGCAAGCTCCGCTCTCCGCTCTC	450
	TTTCAGCCCTCAGAGCGAGCTGGCCGAGATGCGCAAGATCTGGGCTCCGAGCTCTCTCTCTCCCGCAAGCTCCGCTCTCCGCTCTC	450
MpL3OH-PM2 Unigene0052571	ATCCGGCAGGACGAGGCTCCGCGCTCTCCGCCACTCCGCTCTCCGAGGGCGGCCGTGCACATGACGAGGAGGATAGAGACGCTA	540
	ATCCGGCAGGACGAGGCTCCGCGCTCTCCGCCACTCCGCTCTCCGAGGGCGGCCGTGCACATGACGAGGAGGATAGAGACGCTA	540
MpL3OH-PM2 Unigene0052571	ACGTGCTCCATCATCTGCAGGCGCGGCTTCGGGAGCGTGCATCGGGACAAACCGCGAGCTGGTGGGCTGGTCAAGGACCGCTCAGCATC	630
	ACGTGCTCCATCATCTGCAGGCGCGGCTTCGGGAGCGTGCATCGGGACAAACCGCGAGCTGGTGGGCTGGTCAAGGACCGCTCAGCATC	630
MpL3OH-PM2 Unigene0052571	GCCTCGGGTTCGAGCTCCGCGACATGTTCCCTCTCCAGCTCTCAACCTCTCTGCTGAAACAAGAGCAAGCTCTGGAGGATCGCG	720
	GCCTCGGGTTCGAGCTCCGCGACATGTTCCCTCTCCAGCTCTCAACCTCTCTGCTGAAACAAGAGCAAGCTCTGGAGGATCGCG	720
MpL3OH-PM2 Unigene0052571	CGCCGCTCGACACCATCTCGAGGCCATCGTGCAGCAGCACAAGCTCAAGAAGAGCGCGGAGTTCGGCGCGCAGGACATCATCGAGTTC	810
	CGCCGCTCGACACCATCTCGAGGCCATCGTGCAGCAGCACAAGCTCAAGAAGAGCGCGGAGTTCGGCGCGCAGGACATCATCGAGTTC	810
MpL3OH-PM2 Unigene0052571	CTCTTCAGGATCGAGAAGGACCCAGATCAAAGTCCCATCACCACCAACTCCATCAAAGCTTCATCTCGAGACCTTCCTCAGCAGGG	900
	CTCTTCAGGATCGAGAAGGACCCAGATCAAAGTCCCATCACCACCAACTCCATCAAAGCTTCATCTCGAGACCTTCCTCAGCAGGG	900
MpL3OH-PM2 Unigene0052571	ACTGAGACATCTCAACCAACCCATCGGGTCTGCCGAGCTGATGAGGAAACCGGAGTGCATGGCGAAAGCGAGGCGGAGGTGAGA	990
	ACTGAGACATCTCAACCAACCCATCGGGTCTGCCGAGCTGATGAGGAAACCGGAGTGCATGGCGAAAGCGAGGCGGAGGTGAGA	990
MpL3OH-PM2 Unigene0052571	CGCGCATGAAGCGAAGACGAAATGGGACGTGGTGAAGCTCAAGAGCTTAAGTACATGAAATCGGTGGTGAAGGACAGTGAAGATG	1080
	CGCGCATGAAGCGAAGACGAAATGGGACGTGGTGAAGCTCAAGAGCTTAAGTACATGAAATCGGTGGTGAAGGACAGTGAAGATG	1080
MpL3OH-PM2 Unigene0052571	CACCCCTCCGATCCCGTGTATCCCGAGATCATGCAGAGAAGAATGCGTGGTAAACGGGTATACGATTCGGAACAAGGCCAGAAATCATGATC	1170
	CACCCCTCCGATCCCGTGTATCCCGAGATCATGCAGAGAAGAATGCGTGGTAAACGGGTATACGATTCGGAACAAGGCCAGAAATCATGATC	1170
MpL3OH-PM2 Unigene0052571	AACGTCGTGTCATGGGACGAAATCTCTCTACTGGGAAAACCCGATACCTTTTGGCCGAAGGTTTGACGAGTTTCAAAGGATTTTC	1260
	AACGTCGTGTCATGGGACGAAATCTCTCTACTGGGAAAACCCGATACCTTTTGGCCGAAGGTTTGACGAGTTTCAAAGGATTTTC	1260
MpL3OH-PM2 Unigene0052571	ATGGAAATGATTTGAGTGTGTCGCGTTCGGAGCGGGAAAGAATTCGCCCGGCTGAACTTCGGTTCGGAAACGCTGAGGTTCCA	1350
	ATGGAAATGATTTGAGTGTGTCGCGTTCGGAGCGGGAAAGAATTCGCCCGGCTGAACTTCGGTTCGGAAACGCTGAGGTTCCA	1350
MpL3OH-PM2 Unigene0052571	TTGGGCGAGCTTCTTTACCACTTCGACTCGAAGTGGCGGAAGCTTGAAGAACTTCTGATATGGACATGCTGAGGCGGAAGGCTTACC	1440
	TTGGGCGAGCTTCTTTACCACTTCGACTCGAAGTGGCGGAAGCTTGAAGAACTTCTGATATGGACATGCTGAGGCGGAAGGCTTACC	1440
MpL3OH-PM2 Unigene0052571	GGAATACAAAGAACAATCTTCTTCTGTCCACACCCCTACGATCTCTGCAATC	1496
	GGAATACAAAGAACAATCTTCTTCTGTCCACACCCCTACGATCTCTGCAATC	1496

L3OH amino acid sequences alignment

MpL3OH-PM2 Unigene0052571	MELLQLWSALITLVVTVTISLLINOWRKKPKPKCKFPFGPKLPLIGHLLHLWGKLPQHALASVAKEYGPAHVQLGEVPSVLSREATK	90
	MELLQLWSALITLVVTVTISLLINOWRKKPKPKCKFPFGPKLPLIGHLLHLWGKLPQHALASVAKEYGPAHVQLGEVPSVLSREATK	90
MpL3OH-PM2 Unigene0052571	EAMKLVDPACANRFESIGTRIMWYDNEDIIFSPYSEHWROMRKCIVSELLSSRNVRSPGFIQDEVSRLLRHLRSSAGAAVDMTERIETL	180
	EAMKLVDPACANRFESIGTRIMWYDNEDIIFSPYSEHWROMRKCIVSELLSSRNVRSPGFIQDEVSRLLRHLRSSAGAAVDMTERIETL	180
MpL3OH-PM2 Unigene0052571	TCSITCRAAFGVSIRDNAELVGLVKDALSMASGFELADMPFSSKLLNLLCWNKSLWRMRGRVDTILEAVDEHRRKSGEFGGEDIIDV	270
	TCSITCRAAFGVSIRDNAELVGLVKDALSMASGFELADMPFSSKLLNLLCWNKSLWRMRGRVDTILEAVDEHRRKSGEFGGEDIIDV	270
MpL3OH-PM2 Unigene0052571	LFRMQLDQLKVPITTNSIKAFIFDTPSAGTETSSTTTLWLVAELMRNPAVMKQAEVRAALIKETNWDVDDVQELKYMKSVMKETMRM	360
	LFRMQLDQLKVPITTNSIKAFIFDTPSAGTETSSTTTLWLVAELMRNPAVMKQAEVRAALIKETNWDVDDVQELKYMKSVMKETMRM	360
MpL3OH-PM2 Unigene0052571	HPPILPIPRSCREECVNGYTI PNKARIMINWMSGRNPLYWEKDTFWPERFTVSKDFMGNDFEFVPPGAGRRIICPLNFGLANVEV	450
	HPPILPIPRSCREECVNGYTI PNKARIMINWMSGRNPLYWEKDTFWPERFTVSKDFMGNDFEFVPPGAGRRIICPLNFGLANVEV	450
MpL3OH-PM2 Unigene0052571	LAQLLVHFDWKLABGMKPSMDMSBAEGLTGRKNNLLLVPTPYDPS	497
	LAQLLVHFDWKLABGMKPSMDMSBAEGLTGRKNNLLLVPTPYDPS	497

iPD nucleotide sequences alignment

MpiPD
Unigene0033747
90
90

MpiPD
Unigene0033747
180
180

MpiPD
Unigene0033747
270
270

MpiPD
Unigene0033747
360
360

MpiPD
Unigene0033747
450
450

MpiPD
Unigene0033747
540
540

MpiPD
Unigene0033747
630
630

MpiPD
Unigene0033747
720
720

MpiPD
Unigene0033747
797
797

iPD amino acid sequences alignment

MpiPD
Unigene0033747
90
90

MpiPD
Unigene0033747
180
180

MpiPD
Unigene0033747
264
264

iPR nucleotide sequences alignment

MpiPR
Unigene0033916
90
90

MpiPR
Unigene0033916
180
180

MpiPR
Unigene0033916
270
270

MpiPR
Unigene0033916
360
360

MpiPR
Unigene0033916
450
450

MpiPR
Unigene0033916
540
540

MpiPR
Unigene0033916
630
630

MpiPR
Unigene0033916
720
720

MpiPR
Unigene0033916
810
810

MpiPR
Unigene0033916
900
900

MpiPR
Unigene0033916
944
944

iPR amino acid sequences alignment

MpiPR
Unigene0033916
90
90

MpiPR
Unigene0033916
180
180

MpiPR
Unigene0033916
270
270

MpiPR
Unigene0033916
313
313

MFS nucleotide sequences alignment

MpMFS Unigene0030907	ATGGC...GCTCTCTAGTATTTTCTCTCTCTCTTAATCTTCTGGCGTCCCTTTCCTAATACGAAAGCTCCAGTCTTT...CTCTCAAGA ATGGC...GCTCTCTAGTATTTTCTCTCTCTCTTAATCTTCTGGCGTCCCTTTCCTAATACGAAAGCTCCAGTCTTTCTCTCTCAAGA	87 90
MpMFS Unigene0030907	AAGAGGC...GCCCGCGTCTCCATTAAGGCTTCCGGTGTAGCGGCATTTCCACTGTATCGGACCCCTCTCCACCGCTCTCTCACTCC AAGAGGC...GCCCGCGTCTCCATTAAGGCTTCCGGTGTAGCGGCATTTCCACTGTATCGGACCCCTCTCCACCGCTCTCTCACTCC	174 180
MpMFS Unigene0030907	TTATCCAAAGCGCTACGCGGAGTGTACTACTCCATTTCCGAGCGCTCCGTCCTAGTGGCTCTCTCAGCGCGCGCGCTGAGATC TTATCCAAAGCGCTACGCGGAGTGTACTACTCCATTTCCGAGCGCTCCGTCCTAGTGGCTCTCTCAGCGCGCGCGCTGAGATC	264 270
MpMFS Unigene0030907	ATGARGAACCAAGACTGATCTTCCGAGGAGCGCGAGGCTGAGCACTTCCGACGGCTCTGTACAGCGCAAGCGCTGGCTTCCGCG ATGARGAACCAAGACTGATCTTCCGAGGAGCGCGAGGCTGAGCACTTCCGACGGCTCTGTACAGCGCTCTGTACAGCGCAAGCGCTGGCTTCCGCG	354 360
MpMFS Unigene0030907	CCTACGCGCAGCACTGGCGACCGCGGAGCATGTGCTGTCCAGCTGCTCAGCGCTAAGAGGGTCCAGTGTCTCCCGGATTCGA CCTACGCGCAGCACTGGCGACCGCGGAGCATGTGCTGTCCAGCTGCTCAGCGCTAAGAGGGTCCAGTGTCTCCCGGATTCGA	444 450
MpMFS Unigene0030907	GAAGAGGAACCTGGCGATGATTGAGAAGATCAGCGCATCCAGCCGACCGGCTGTAACCTGAGCGAGATGTCATGGCGTGAAG GAAGAGGAACCTGGCGATGATTGAGAAGATCAGCGCATCCAGCCGACCGGCTGTAACCTGAGCGAGATGTCATGGCGTGAAG	534 537
MpMFS Unigene0030907	AACGCGTAATTCACAGGCGCGGTTAGGGCGGAAGCCGACGGCGGAGATGATTTAAATCGGATCTGATCAAGCTTATCAAGCTCTTC AACGCGTAATTCACAGGCGCGGTTAGGGCGGAAGCCGACGGCGGAGATGATTTAAATCGGATCTGATCAAGCTTATCAAGCTCTTC	624 627
MpMFS Unigene0030907	CGA...GTTTCAACTGGGGATTACGTTCCATGGCTCTTTGGATTAACCGGATTAATGGCGTGGATCGAGAAGTGGAAAAGTCTTTGGA CGA...GTTTCAACTGGGGATTACGTTCCATGGCTCTTTGGATTAACCGGATTAATGGCGTGGATCGAGAAGTGGAAAAGTCTTTGGA	714 717
MpMFS Unigene0030907	AAGTTGGATGGATCATAGAGGGTATTCTTCGAATAATATAGAAAGAAAGCTGGTCTATGAAACGAAATTCGTAGACAGCTTGCCT AAGTTGGATGGATCATAGAGGGTATTCTTCGAATAATATAGAAAGAAAGCTGGTCTATGAAACGAAATTCGTAGACAGCTTGCCT	804 807
MpMFS Unigene0030907	CAGTTTCAGAGAGAGTAAAGATACTACCCCGTCGAGGATGACGTAATCAAAGCTCTAATCTCGACATGCTTTCGCCGGAACCGAT CAGTTTCAGAGAGAGTAAAGATACTACCCCGTCGAGGATGACGTAATCAAAGCTCTAATCTCGACATGCTTTCGCCGGAACCGAT	894 897
MpMFS Unigene0030907	ACGACTTTCGCGCTCTAGAGTGGACGATGGCGGAGCTCATAAAGCCGCGACCCCTAAAACCTTCGAGAACGAGGTGCGAGAAGTT ACGACTTTCGCGCTCTAGAGTGGACGATGGCGGAGCTCATAAAGCCGCGACCCCTAAAACCTTCGAGAACGAGGTGCGAGAAGTT	984 987
MpMFS Unigene0030907	TCTAGAAAACAAGCTGGATTAACGAGGATGACCTGGACAGATGCCATCTCTGAAAGCAGTATCCAGGATTTACGCTTACATCCCA TCTAGAAAACAAGCTGGATTAACGAGGATGACCTGGACAGATGCCATCTCTGAAAGCAGTATCCAGGATTTACGCTTACATCCCA	1074 1077
MpMFS Unigene0030907	CCTTTCGAAATCTGCTCCCTCGAGAATTGACTCAAGACCCCAATATGCTGGCTACGACATCCCACTGGCACCTCGTGTGTGGTCAAC CCTTTCGAAATCTGCTCCCTCGAGAATTGACTCAAGACCCCAATATGCTGGCTACGACATCCCACTGGCACCTCGTGTGTGGTCAAC	1164 1167
MpMFS Unigene0030907	AACTGGGCCATATCGAGAGACCCCTCGTTGTGGGAAAATCCCGAAGAATTTCTGTCAGAAAGGTTCTCTCGAGACGAGCATAGACTATAAA AACTGGGCCATATCGAGAGACCCCTCGTTGTGGGAAAATCCCGAAGAATTTCTGTCAGAAAGGTTCTCTCGAGACGAGCATAGACTATAAA	1254 1257
MpMFS Unigene0030907	GCG...TGCATTTTGGATGCTTCCGTTCCGGTCCGCGCAAGAGGGTCCCCCGGATCACGTTTCCGATGCTTTTATACGAGCTTGCACTA GCG...TGCATTTTGGATGCTTCCGTTCCGGTCCGCGCAAGAGGGTCCCCCGGATCACGTTTCCGATGCTTTTATACGAGCTTGCACTA	1344 1347
MpMFS Unigene0030907	TCCAACTCTTAAACGAGTTCGATTTGAGATTGGCTAAATGGAGATGAGCGAGGATTTGGACA...TGACTGAAGCTCTGATTTGTAGTCT TCCAACTCTTAAACGAGTTCGATTTGAGATTGGCTAAATGGAGATGAGCGAGGATTTGGACA.....TGACTGAAGCTCTGATTTGTAGTCT	1434 1411
MpMFS Unigene0030907	CATAAGAAGTCTCCITTTGCTTGTGCTTCTACTCCACGCTCAATCTTG	1481 1411

MFS amino acid sequences alignment

MpMFS Unigene0030907	MAALLVFFSVSLILLAVLFPHKRSLSLSS...RRRPPSHLRLPVIGHHLICSLHRSFHSLSKRYGEVMLLHFGSAPVLVASSAAAAREI MAALLVFFSVSLILLAVLFPHKRSLSLSPSRKRRLPPSHLRLPVIGHHLICSLHRSFHSLSKRYGEVMLLHFGSAPVLVASSAAAAREI	88 90
MpMFS Unigene0030907	MKNQDIFASRPRLSIDRLIVSGKVAFAFVYGEHWRARSMDLQLLSAKRVQSFGRIRREETSAMIEKIRRSQFSLVNLSSEMFALMT MKNQDIFASRPRLSIDRLIVSGKVAFAFVYGEHWRARSMDLQLLSAKRVQSFGRIRREETSAMIEKIRRSQFSLVNLSSEMFALMT	178 179
MpMFS Unigene0030907	NGVHRAALGRKDGGLSMLHLLKRLVHLLGSEFNVGDYVFWLAWINRIRINGVDAEVEKVKLDESEEGILRKYRKRKVGDDENFVDTLL NGVHRAALGRKDGGLSMLHLLKRLVHLLGSEFNVGDYVFWLAWINRIRINGVDAEVEKVKLDESEEGILRKYRKRKVGDDENFVDTLL	268 269
MpMFS Unigene0030907	QFORESKDTFVVEDDVIKALILNVAACIDTTSVLEWTMAELINRPTLTKLQNEVREVSRRKGGITEDDVDKMPYLKAVSPEILRLHF QFORESKDTFVVEDDVIKALILNVAACIDTTSVLEWTMAELINRPTLTKLQNEVREVSRRKGGITEDDVDKMPYLKAVSPEILRLHF	358 359
MpMFS Unigene0030907	PEASLLPRELTQDANMLGVDPRGIVLVNNAISRDPSSLWENPEEPRPERFLETSIDYKGFHPEMLPFGSGRRGCPGTFAMLSVLELAL PEASLLPRELTQDANMLGVDPRGIVLVNNAISRDPSSLWENPEEPRPERFLETSIDYKGFHPEMLPFGSGRRGCPGTFAMLSVLELAL	448 449
MpMFS Unigene0030907	SKLVNEFDRLKNGDRLEDLIMTEAPGVVHKKSPLLVLATPRQ SKLVNEFDRLKNGDRLEDL.....	492 470

PR nucleotide sequences alignment

MpPR
Unigene0047772
ATGGTGAATGAACAAGCAAAATGTAAGTCAACAACACTAGCAATTAAGGTTCTTAATAAAGATCCGACTTCGGTTGAGAAGCTTCCACGATCTGC
90
ATGGTGAATGAACAAGCAAAATGTAAGTCAACAACACTAGCAATTAAGGTTCTTAATAAAGATCCGACTTCGGTTGAGAAGCTTCCACGATCTGC
90

MpPR
Unigene0047772
ATGGAGATCCCAATGGCTGCAACGGTGGCAATTTGGTCAAGAAGCTGTACTTGTCCGTCATCTTATCTCATCTTCGACATGGGAAAA
180
ATGGAGATCCCAATGGCTGCAACGGTGGCAATTTGGTCAAGAAGCTGTACTTGTCCGTCATCTTATCTCATCTTCGACATGGGAAAA
180

MpPR
Unigene0047772
CTCGATATCCCAAGTTGATTCACATCTTCCCTGGCTCTACTATTTAGCTATGGAGTGTCAAAGTATTGGATTGACGCATCCGAGT
270
CTCGATATCCCAAGTTGATTCACATCTTCCCTGGCTCTACTATTTAGCTATGGAGTGTCAAAGTATTGGATTGACGCATCCGAGT
270

MpPR
Unigene0047772
TACGAGAAGGCGAAGCTGATTTGGGGTCAACAAGCTGGATGGGAGGAATATACCTTATCCAAAATCCATATAATTTGTTTAAATCCAA
360
TACGAGAAGGCGAAGCTGATTTGGGGTCAACAAGCTGGATGGGAGGAATATACCTTATCCAAAATCCATATAATTTGTTTAAATCCAA
360

MpPR
Unigene0047772
GACAAAAGATGTGCCTTTATCCTACTATGTTGGGATCTAGGAATGCCTGGGATGACAGCATATGCAGGATTTTTTGAGATTGCTCTCCG
450
GACAAAAGATGTGCCTTTATCCTACTATGTTGGGATCTAGGAATGCCTGGGATGACAGCATATGCAGGATTTTTTGAGATTGCTCTCCG
450

MpPR
Unigene0047772
AAAAAAGCGAAACTGTGTTTGAACGGCTGCAGCAGGATCTGTGGCCAGCTGTGGTCAAGATGTTGGGTGCTATGTT
540
AAAAAAGCGAAACTGTGTTTGAACGGCTGCAGCAGGATCTGTGGCCAGCTGTGGTCAAGATGTTGGGTGCTATGTT
540

MpPR
Unigene0047772
GTTGGAAGTCCAGGGACAAAGAGAGGTTGATCTTTTGAAGAACAATTTGGTTCGATGATCAATTAATTAAGAAGAGAGTGA
630
GTTGGAAGTCCAGGGACAAAGAGAGGTTGATCTTTTGAAGAACAATTTGGTTCGATGATCAATTAATTAAGAAGAGAGTGA
630

MpPR
Unigene0047772
TATGATACGCTTTGAAGAGGCACTTCCCGAAGGAATGATATATACCTCGATATGTTGGAGGGAAGATGCTTGAAGCTGTGATCAAC
720
TATGATACGCTTTGAAGAGGCACTTCCCGAAGGAATGATATATACCTCGATATGTTGGAGGGAAGATGCTTGAAGCTGTGATCAAC
720

MpPR
Unigene0047772
AACATGAGAGTCCACGGCCGATCCGGTATGTGGGATGCTCCAGTATGAGCCTGAAGCAGCCGAAAGCCTCCACAACCTTGCTTAAG
810
AACATGAGAGTCCACGGCCGATCCGGTATGTGGGATGCTCCAGTATGAGCCTGAAGCAGCCGAAAGCCTCCACAACCTTGCTTAAG
810

MpPR
Unigene0047772
CTAAATCCCAAAACAAATTCGTAAGCAAGGTTTGTGTTGTTGATTACTATCATCTCTACCCAAAGTTCCTTGAGATGGTTCGCGCCGCC
900
CTAAATCCCAAAACAAATTCGTAAGCAAGGTTTGTGTTGTTGATTACTATCATCTCTACCCAAAGTTCCTTGAGATGGTTCGCGCCGCC
900

MpPR
Unigene0047772
ATCAAGGAAGGAAAAGTGAATACGTCGAAGACATATCTGAAGCCCTTGAGAGCCGCTAGCCCTAGCCCTCTCTGGGGGTGAATGTCGTCGT
990
ATCAAGGAAGGAAAAGTGAATACGTCGAAGACATATCTGAAGCCCTTGAGAGCCGCTAGCCCTAGCCCTCTCTGGGGGTGAATGTCGTCGT
990

MpPR
Unigene0047772
AACCTTGGCAATCAATTTGTTGGCGTTTCTCGGAGTA
1028
AACCTTGGCAATCAATTTGTTGGCGTTTCTCGGAGTA
1028

PR amino acid sequences alignment

MpPR
Unigene0047772
MVMNKOIVLNNYVNGSLKESDIALRTSTICMEIIEGNGALIVKNLYLNVNPLYLLRMGKLDIPQFDSLPGSTIVSYGVSKVLDSTHPS
90
MVMNKOIVLNNYVNGSLKESDIALRTSTICMEIIEGNGALIVKNLYLNVNPLYLLRMGKLDIPQFDSLPGSTIVSYGVSKVLDSTHPS
90

MpPR
Unigene0047772
YEKGEIINGSQAGWEEYTLIQNPYLFKIQDKDVPLSYVGLLMPGMTAYAGFFELCSPKKGETVVFVTAAGSVGQLVGFQAKMFGCVV
180
YEKGEIINGSQAGWEEYTLIQNPYLFKIQDKDVPLSYVGLLMPGMTAYAGFFELCSPKKGETVVFVTAAGSVGQLVGFQAKMFGCVV
180

MpPR
Unigene0047772
VGSAGSKEKVDLLKNGFGFDFAFYKVESDYDTALKRHPFEGIDLYFDNVGGKMLEAVINNMVHGRIVAGCMVSYSLKQPEGVHNLK
270
VGSAGSKEKVDLLKNGFGFDFAFYKVESDYDTALKRHPFEGIDLYFDNVGGKMLEAVINNMVHGRIVAGCMVSYSLKQPEGVHNLK
270

MpPR
Unigene0047772
LIPKQIRMQGFVVDYVHLYPKFLEWVLEIKBGKVIIVEDISEGLESPSALLGVVGRNIGNOVVAVSR
341
LIPKQIRMQGFVVDYVHLYPKFLEWVLEIKBGKVIIVEDISEGLESPSALLGVVGRNIGNOVVAVSR
341

MR nucleotide sequences alignment

MpMR	ATGGCAGATACCTTTACGCAAGGTATGCTTTGCTTTACCTGTGCAAAACAAGGAATCGGGTTCGAGATATCGAGGCAGTTAGCTTCGAAA	90
Unigene0041050	ATGGCAGATACCTTTACGCAAGGTATGCTTTGCTTTACCTGTGCAAAACAAGGAATCGGGTTCGAGATATCGAGGCAGTTAGCTTCGAAA	90
MpMR	GGAATGAAGGTGATTTTAGCTTCAAGAACCAGAGAAGAGGCATCGAAGCTCGAGAAAGGCTACTTAAGGATTCGAGATCAAAATTTCTGAT	180
Unigene0041050	GGAATGAAGGTGATTTTAGCTTCAAGAACCAGAGAAGAGGCATCGAAGCTCGAGAAAGGCTACTTAAGGATTCGAGATCAAAATTTCTGAT	180
MpMR	GACGATGTGTTTTTCATCAACTGATGTTGATGACCTGCTAGCGCTGTGCTGTGCTCACTTCATCGAAACCAAAATTCGGGAGGCTT	270
Unigene0041050	GACGATGTGTTTTTCATCAACTGATGTTGATGACCTGCTAGCGCTGTGCTGTGCTCACTTCATCGAAACCAAAATTCGGGAGGCTT	270
MpMR	GATATTCGGTGAATAATCGGGATTTACTGGAGTAGCGATAGAGGGAGATATTCAGTCTATCAAGAGTGTCTGAGGCAAAACATTAAT	360
Unigene0041050	GATATTCGGTGAATAATCGGGATTTACTGGAGTAGCGATAGAGGGAGATATTCAGTCTATCAAGAGTGTCTGAGGCAAAACATTAAT	360
MpMR	GCAGCTCAGCTGGACAGGCATCCATTCCATCCCAAACTCTGGTAGGCTATGACACATTGGAGGGTTCAAAAGAGTGTATAGAA	450
Unigene0041050	GCAGCTCAGCTGGACAGGCATCCATTCCATCCCAAACTCTGGTAGGCTATGACACATTGGAGGGTTCAAAAGAGTGTATAGAA	450
MpMR	ACAAACTACTATGGCAAAAAGAATAACAGAAACCTTAATTCCTCTCCTGCAAAAATCTGATTCACCAACAATTGTCAATGTCTCTCC	540
Unigene0041050	ACAAACTACTATGGCAAAAAGAATAACAGAAACCTTAATTCCTCTCCTGCAAAAATCTGATTCACCAACAATTGTCAATGTCTCTCC	540
MpMR	ACCTCTCCTACTTTACTGCTCCAGCCTAATGAATGGCCAAAAGGAGTCTTTAGCAGCA.....CAGCTGAATGAAGCAAGGTGGAG	624
Unigene0041050	ACCTCTCCTACTTTACTGCTCCAGCCTAATGAATGGCCAAAAGGAGTCTTTAGCAGCA.....CAGCTGAATGAAGCAAGGTGGAG	630
MpMR	GAAGTTTTCGATGAATTTCTCAAGGATTTCTNTGATGTTAAATGCAACAAAACCACTGGCTCTCTAACCTTGCAGCCTACAAGCTATCG	714
Unigene0041050	GAAGTTTTCGATGAATTTCTCAAGGATTTCTNTGATGTTAAATGCAACAAAACCACTGGCTCTCTAACCTTGCAGCCTACAAGCTATCG	720
MpMR	AAAGCTCGCTGTTAATGCTATACTCGGATCATAGCGGAAAGTACCCGAGTTTCTGCATAAATTCAGTGTGCTCGTPTTGTGTAGAAC	804
Unigene0041050	AAAGCTCGCTGTTAATGCTATACTCGGATCATAGCGGAAAGTACCCGAGTTTCTGCATAAATTCAGTGTGCTCGTPTTGTGTAGAAC	810
MpMR	GATATTTGCTACAATCTTGGAGTACTAAGTGAAGCTGAAGGTGCTGAAGCTCCGGTGAAGCTGCCTTTTGTGCCCATGGCGGGCCCTCG	894
Unigene0041050	GATATTTGCTACAATCTTGGAGTACTAAGTGAAGCTGAAGGTGCTGAAGCTCCGGTGAAGCTGCCTTTTGTGCCCATGGCGGGCCCTCG	900
MpMR	GCCTCCTTTCTCTCGAGAGGAAGCCTTGTCTTGTACTA	935
Unigene0041050	GCCTCCTTTCTCTCGAGAGGAAGCCTTGTCTTGTACTA	941

MR amino acid sequences alignment

MpMR	MADTFIQRYALVTGANKGIGFEICRQLASKGMKVIILASNEKRGTEARERLLKESRSTSDDDVPHOLDVADPPASAVVAHFIEYKFGRL	90
Unigene0041050	MADTFIQRYALVTGANKGIGFEICRQLASKGMKVIILASNEKRGTEARERLLKESRSTSDDDVPHOLDVADPPASAVVAHFIEYKFGRL	90
MpMR	DLLVNNAGFTGVAEGDISVYQCLEANILAACGGAPPHPRTHGRLIETLEGSKBCIETNYGTRITETLLPLLKSDSPTIVNVSS	180
Unigene0041050	DLLVNNAGFTGVAEGDISVYQCLEANILAACGGAPPHPRTHGRLIETLEGSKBCIETNYGTRITETLLPLLKSDSPTIVNVSS	180
MpMR	TFSTILLQPNWAKGVFSS...SLNEGRVEEVLHEBKDFIDGKQQNHWPPIAAVYKSKAAVNAYTRLIARKYPSFCINSVCPGFVRT	268
Unigene0041050	TFSTILLQPNWAKGVFSS...SLNEGRVEEVLHEBKDFIDGKQQNHWPPIAAVYKSKAAVNAYTRLIARKYPSFCINSVCPGFVRT	270
MpMR	DICYNLGVLSEARGAEPVKLALLP...GGPSGSFFSREALS	310
Unigene0041050	DICYNLGVLSEARGAEPVKLALLP...GGPSGSFFSREALS	312

Supplementary Figure 6 Alignment of nucleotide and amino acid sequences of 9 menthol biosynthetic genes from *M. piperita* and *M. canadensis*.