

GPPS-I nucleotide sequences alignment

MpGPPS-1 Unigene0045757	ATGAGTCTCTGTTAATCCTGTGCGAAATGGCCTCAGACATCGGCGTTAGATGTTACGGCGGCGCGGAGCGGAGATCCAGATCC ATGAGTCTCTGTTAATCCTGTGCGAAATGGCCTCAGACATCGGCGTTAGATGTTACGGCGGCGCGGAGCGGAGATCCAGATCC	90 90
MpGPPS-1 Unigene0045757	ACTGTCTTTTCATGTCATCCACTTCGCGTGAATGCGCTTTCTCTCTACTTCTCATCCCGCTCAAGAGTCTCGCCACTTTTTCGGTT ACTGCTTTTCATGTCATCCACTTCGCGCTGAATGCGCTTTCTCTCTACTTCTCAAGCCCTTCAAGAGTCTCGCCACTTTTTCGGTT	180 180
MpGPPS-1 Unigene0045757	TCTGCGATTTATACCAAGAGCGCAGCGAAATTAGGCTTAAGATCGGCGCTTTCGACTTCGCGCGCGTTCGATTTTCGACGGATACATG TCTGCGATTTATACCAAGAGCGCAGCGAAATTAGGCTTAAGATCGGCGCTTTCGACTTCGCGCGCGTTCGATTTTCGACGGATACATG	270 270
MpGPPS-1 Unigene0045757	CTCCGGAAGCGCAAAATCCGTGAACAAGGCGTTGGAAGCGCGGTGAGATGAAGGAGCGCGCTGAAGATCCACGAGTCCATGCGGTACTCC CTCCGGAAGCGCAAAATCCGTGAACAAGGCGTTGGAAGCGCGGTGAGATGAAGGAGCGCGCTGAAGATCCACGAGTCCATGCGGTACTCC	360 360
MpGPPS-1 Unigene0045757	CTCTCGCCGCGCGCAAGAGAGTGCCTCATCTGTGCAATCGCGCTCGGAGCTCGTTCGCGCGCGACGAGTCAACGCGGATGCGCGCG CTCTCGCCGCGCGCGCAAGAGAGTGCCTCATCTGTGCAATCGCGCTCGGAGCTCGTTCGCGCGCGACGAGTCAACGCGGATGCGCGCG	450 450
MpGPPS-1 Unigene0045757	GCCTGCGCGCTCGAGATGATCCACAGATGTGCTGATGACACGACGACCTCCATGCATGGACAACGACGACCTCCGCGCGCGCAAGCCG GCCTGCGCGCTCGAGATGATCCACAGATGTGCTGATGACACGACGACCTCCATGCATGGACAACGACGACCTCCGCGCGCGCAAGCCG	540 540
MpGPPS-1 Unigene0045757	ACGAACCACTATGCTTCGCGGAGAGCTGGCGGTCTCTCGCGCGGACGCTCTCTCTCTCGCGTTCGAGCAGTGGCGCGCGCGGAC ACGAACCACTATGCTTCGCGGAGAGCTGGCGGTCTCTCGCGCGGACGCTCTCTCTCTCGCGTTCGAGCAGTGGCGCGCGCGGACG	630 630
MpGPPS-1 Unigene0045757	AAAGCGCGCGCGCGGAGCGGATGCTGAGGCTCTCGCGAGCTGGCTGTCTGATCGGCTCGGAGGCGCTGTGCGCGCGCGAGCTGTG AAGCGCGCGCGCGGAGCGGATGCTGAGGCTCTCGCGAGCTGGCTGTCTGATCGGCTCGGAGGCGCTGTGCGCGCGCGAGCTGTG	720 720
MpGPPS-1 Unigene0045757	GACATCTGCTCGGAGGGATGGCGGAGGTGCGCTGGACCACTCGAGTTCATCCACCACCACAAGACGCGCGCGCTGCTGACGGCTTCG GACATCTGCTCGGAGGGATGGCGGAGGTGCGCTGGACCACTCGAGTTCATCCACCACCACAAGACGCGCGCGCTGCTGACGGCTTCG	810 810
MpGPPS-1 Unigene0045757	GTGTTTGGGGGCGATTTTGGCGCGCGGAAGGAGGAGGAGGTGGCGAGCTGAGAAATTCGCGAATTGCATCGGATTGCTGTTTCAG GTGTTTGGGGGCGATTTTGGCGCGCGGAAGGAGGAGGAGGTGGCGAGCTGAGAAATTCGCGAATTGCATCGGATTGCTGTTTCAG	900 900
MpGPPS-1 Unigene0045757	GTGTTGAGCGTATCTTGAATGTGACGAAATCGTCAAGGAATTGGGGAAGACGCGCGGGAAGGATCTGTGCGCGGAATAACACACATAT GTGTTGAGCGTATCTTGAATGTGACGAAATCGTCAAGGAATTGGGGAAGACGCGCGGGAAGGATCTGTGCGCGGAATAACACACATAT	990 990
MpGPPS-1 Unigene0045757	CCGAGCTATAGCTGTGGAGAATTCGAAGGAATTCGCGATCGTTGAGGAGGAGGCGGAGCAGCTCTCCATTTCATCTTCAT CCGAGCTATAGCTGTGGAGAATTCGAAGGAATTCGCGATCGTTGAGGAGGAGGCGGAGCAGCTCTCCATTTCATCTTCAT	1080 1080
MpGPPS-1 Unigene0045757	AGGGCAGCTCCATTGATGCTCTCGCCAAATTAATGTGCTTAAGGACAAATTG AGGGCAGCTCCATTGATGCTCTCGCCAAATTAATGTGCTTAAGGACAAATTG	1133 1133

GPPS-I nucleotide sequences alignment

MpGPPS-1 Unigene0045757	MSLVLNLPVAKWPQTIGVSDVHGGRRRRSRSTLPSHPLRTEMPPSLYFSSLLKAFHFSVSAVYTKESSEIRKDPAPSSPAFDGDM MSLVLNLPVAKWPQTIGVSDVHGGRRRRSRSTLPSHPLRAKLPPSLYFSSLRGSFSPVSAVYTKESSEIRADDPSSPAFDGDM	90 90
MpGPPS-1 Unigene0045757	LRKAKSVNKALEAAVOMKEPLKIHESMRYSLLAGGKRVRLCIAACELVGGDESTAMPAACAVEMIHTMSLMHDDLPCMDNDLLRRGKP LRKAKSVNKALEAAVOMKEPLKIHESMRYSLLAGGKRVRLCIAACELVGGDESTAMPAACAVEMIHTMSLMHDDLPCMDNDLLRRGKP	180 180
MpGPPS-1 Unigene0045757	TNHRVFGESAVLAGDALLSPAFPHVAATRGAFTERIVRVLGELAVSIGSEGLVAGQVVDLCSEGMAEVGLSHLRIHHHKTAALLQGS TNHRVFGESAVLAGDALLSPAFPHVAATRGAFTERIVRVLGELAVSIGSEGLVAGQVVDLCSEGMAEVGLSHLRIHHHKTAALLQGS	270 270
MpGPPS-1 Unigene0045757	VVLGAILGGGEEFVAURLKRFANCIGLLPQVDDILDVTKSSKELGKTAGKDLVADKTTYPKLIGVEKSKEPADRIKREANBQLLHPFH VVLGAILGGGEEFVAURLKRFANCIGLLPQVDDILDVTKSSKELGKTAGKDLVADKTTYPKLIGVEKSKEPADRIKREANBQLLHPFH	360 360
MpGPPS-1 Unigene0045757	RAAPLIALANYIAYRD RAAPLIALANYIAYRD	376 376

GPPS-s nucleotide sequences alignment

MpGPPS-s Unigene0038587	ATGGCCATTAACTCTCCCATATCAACTCCAAAACATGTTTCCCTCTCAAAAACAGATCTGATCTCAGCCGTTCTTCTTCCGCGCGTTGC ATGGCCATTAACTCTCCCATATCAACTCCAAAACATGTTTCCCTCTCAAAAACAGATCTGATCTCAGCCGTTCTTCTTCCGCGCGTTGC	90 90
MpGPPS-s Unigene0038587	ATGCCAACTGCCGCGCTGCCGCTTCCCCACTATGCCACGCGCCCAAAAGTCAGCCGTATGGGCGCCCATCGCGCCGACATAGAG ATGCCAACTGCCGCGCTGCCGCTTCCCCACTATGCCACGCGCCCAAAAGTCAGCCGTATGGGCGCCCATCGCGCGCCGACATAGAG	180 180
MpGPPS-s Unigene0038587	AGATACTGAAGAAATCCATCGAATAAGSCCGCCGAGACAGTTTTCGGGCCCATGCACCACCTCACCTTCGCCGCCCCAGCCACCGCC AGATACTGAAGAAATCCATCGAATAAGSCCGCCGAGACAGTTTTCGGGCCCATGCACCACCTCACCTTCGCCGCCCCAGCCACCGCC	270 270
MpGPPS-s Unigene0038587	GCTCTCCCTCATATGCTTGGCGGGAGTGGAGCTCGTCGGCGCGGACCGAAGCCATGGCAGCCGCGGGCGATCCATCTCGTCCAC GCTCTCCCTCATATGCTTGGCGGGAGTGGAGCTCGTCGGCGCGGACCGAAGCCATGGCAGCCGCGGGCGATCCATCTCGTCCAC	360 360
MpGPPS-s Unigene0038587	GCGGCAGCCTACGTCCACGCACTCCTCCCTTAACCGACGGGTGGAGGCCATCCAAAGCCCGCAATCCAGCACAAGTACGGCCCGAAC GCGGCAGCCTACGTCCACGCACTCCTCCCTTAACCGACGGGTGGAGGCCATCCAAAGCCCGCAATCCAGCACAAGTACGGCCCGAAC	450 450
MpGPPS-s Unigene0038587	GTGAGCTCCTCACCGGAGACGGGATTGTCCCGTTCGGGTTTGAGTTGCTGGCCGGTCAGTGGACCCGGCCCGAACAGACGACCCGGAT GTGAGCTCCTCACCGGAGACGGGATTGTCCCGTTCGGGTTTGAGTTGCTGGCCGGTCAGTGGACCCGGCCCGAACAGACGACCCGGAT	540 540
MpGPPS-s Unigene0038587	AGGATCTGAGAGTTATAATAGAGATCAGTCGGGCCCGCGCGCCCGAGGGAAATGATAAGCGGGTGCATAGGGAAGAAATTTGTTGAT AGGATCTGAGAGTTATAATAGAGATCAGTCGGGCCCGCGCGCCCGAGGGAAATGATAAGCGGGTGCATAGGGAAGAAATTTGTTGAT	630 630
MpGPPS-s Unigene0038587	GGAATACGAGTTTAGACTTCATTGAATATGTGTCAAGAAAAAATACGGCGAGATGCATGCTTGGCGCGCGGCTTGTGAGCCATATTG GGAATACGAGTTTAGACTTCATTGAATATGTGTCAAGAAAAAATACGGCGAGATGCATGCTTGGCGCGCGGCTTGTGAGCCATATTG	720 720
MpGPPS-s Unigene0038587	GCGCGCGCAACCGAGCAGGAGATTCAAGAGCTGAGGAATTTGGGGCTTTATCAAGGAACCTCAGAGGAATGATGGAATGAAAAATTC GCGCGCGCAACCGAGCAGGAGATTCAAGAGCTGAGGAATTTGGGGCTTTATCAAGGAACCTCAGAGGAATGATGGAATGAAAAATTC	810 810
MpGPPS-s Unigene0038587	CATGAATTAATTGATGAGAATATAATTGAAAAATTGAAAGAATTGGCTCTCGAGGAGTTGGGAGGCTTCACGGGAAGAACGCTGAGCTG CATGAATTAATTGATGAGAATATAATTGAAAAATTGAAAGAATTGGCTCTCGAGGAGTTGGGAGGCTTCACGGGAAGAACGCTGAGCTG	900 900
MpGPPS-s Unigene0038587	ATGTCGAGCCTTGTAGCCGAGCCGAGCCTTTACCGGCTTA ATGTCGAGCCTTGTAGCCGAGCCGAGCCTTTACCGGCTTA	941 941

GPPS-s amino acid sequences alignment

MpGPPS-s Unigene0038587	MAINLSHINSKTCFPLKTRSDLRSSSSRCMPTAAAFPTTATAAOSOPYWAAISADIDRYLKKSITRPPETVFGPMHHLTFAAPATA MAINLSHINSKTCFPLKTRSDLRSSSSRCMPTAAAFPTTATAAOSOPYWAAISADIDRYLKKSITRPPETVFGPMHHLTFAAPATA	90 90
MpGPPS-s Unigene0038587	ASNLCLAAACELVGGDRSQAMAAAAATHLVHAAAYVHEHLPLTDGSRFVSKPAIQHKYGPNVELLTGDGIVPFGFELLAGSVDPARTDDPD ASNLCLAAACELVGGDRSQAMAAAAATHLVHAAAYVHEHLPLTDGSRFVSKPAIQHKYGPNVELLTGDGIVPFGFELLAGSVDPARTDDPD	180 180
MpGPPS-s Unigene0038587	RILRVIIETSRAGGPFGMISGLHREBEIVDGTSLDFIEYVCKKKYGEHMHACGAACGAILGGABEEIQKLRFNGLYQGTLRGMMEMKNS RILRVIIETSRAGGPFGMISGLHREBEIVDGTSLDFIEYVCKKKYGEHMHACGAACGAILGGABEEIQKLRFNGLYQGTLRGMMEMKNS	270 270
MpGPPS-s Unigene0038587	HEIDENIIQKLKELALEELGGFHGKNAELMSSILVAEPSLYV HEIDENIIQKLKELALEELGGFHGKNAELMSSILVAEPSLYV	312 312

## LS nucleotide sequences alignment

MpLS Unigene0018537	ATGGCTCTCAGTGTTTAGTGTGCAATGCAAAATCGCAATTCCTACGACGCTAACGACCTATCTTCAACCCCTCACACTTGAATTCCTCT ATGGCTCTCAGTGTTTAGTGTGCAATGCAAAATCGCAATTCCTACGACGCTAACGACCTATCTTCAACCCCTCACACTTGAATTCCTCT	90 90
MpLS Unigene0018537	CCTAAATTGTCTCTTAACACTAAGGGTACTAGTGGCTCTCGCTCCGTGTGTCTTCTGCTCCTCGCAACTACTACCGAAGAGCGATCC CCTAAATTGTCTCTTAACACTAAGGGTACTAGTGGCTCTCGCTCCGTGTGTCTTCTGCTCCTCGCAACTACTACCGAAGAGCGATCC	180 180
MpLS Unigene0018537	GGAACCTACAAACCTTCTCGTGGGATGTGACTTTATCCAAACGCTCCAGTGATTATAGGACGAGAGCATGCGAGAAGGGCTTCT GGAACCTACAAACCTTCTCGTGGGATGTGACTTTATCCAAACGCTCCAGTGATTATAGGACGAGAGCATGCGAGAAGGGCTTCT	270 270
MpLS Unigene0018537	GAGCTGGTCACTTTGGTGAAGATGGAATTGGAGAAAGAAACGATCAAAATCGACAGCTTGAATTGATTGATGACTTGCAGAGGATGGGG GAGCTGGTCACTTTGGTGAAGATGGAATTGGAGAAAGAAACGATCAAAATCGACAGCTTGAATTGATTGATGACTTGCAGAGGATGGGG	360 360
MpLS Unigene0018537	CTGTCCGATCATTTCCAGAAACGAGTTCAAAGAAATCTTGTCTCTGTATATCTCGACCATCTCTATTACAGAAATCTCTGATCCAAAGAA CTGTCCGATCATTTCCAGAAACGAGTTCAAAGAAATCTTGTCTCTGTATATCTCGACCATCTCTATTACAGAAATCTCTGATCCAAAGAA	450 450
MpLS Unigene0018537	GAAAGGAGTCTATACTCCACATCTCTGCATTTAGGCTCCTTCGAGAACATGGGTTTCAAGTTGCTCAAGAGGATTTCCAGAGTTTCAAG GAAAGGAGTCTATACTCCACATCTCTGCATTTAGGCTCCTTCGAGAACATGGGTTTCAAGTTGCTCAAGAGGATTTCCAGAGTTTCAAG	540 540
MpLS Unigene0018537	AACGAGGAGGGTGAGTTCAAAAGAAAGCCTTAGCGACGACACGACGAGGATGTGTCAACTGTACGAAAGCTTTCTTTCTGTGTACGGAAGGC AACGAGGAGGGTGAGTTCAAAAGAAAGCCTTAGCGACGACACGACGAGGATGTGTCAACTGTACGAAAGCTTTCTTTCTGTGTACGGAAGGC	630 627
MpLS Unigene0018537	GAAACGACGCTCGACTCAGCGAGAGAAATTCGCCACAAATTTCTCGAAGAAAGAGTGAATGAGGGTGGTGGTGTATGAAACCTTTTAAACA GAAACGACGCTCGACTCAGCGAGAGAAATTCGCCACAAATTTCTCGAAGAAAGAGTGAATGAGGGTGGTGGTGTATGAAACCTTTTAAACA	720 717
MpLS Unigene0018537	AGAATCGCATATCTTTTAGAATAATCCCACTTCATTGGAGAGATTAAAGGCCAAATGCACCTGTGTGGATTCATTCGTATAGGAAGAGGCC AGAATCGCATATCTTTTAGAATAATCCCACTTCATTGGAGAGATTAAAGGCCAAATGCACCTGTGTGGATTCATTCGTATAGGAAGAGGCC	810 807
MpLS Unigene0018537	AACATGAATCCAGTAGTGTGGACCTTGCCATACTCGACTTAAATATTGTTCAAGCTCATTTTCAACAGAACTCAAAGAAATCTTCTCGG AACATGAATCCAGTAGTGTGGACCTTGCCATACTCGACTTAAATATTGTTCAAGCTCATTTTCAACAGAACTCAAAGAAATCTTCTCGG	900 897
MpLS Unigene0018537	TGGTGGAGAAATACTGGGTTTGTGTGAGAAGCTGCCCTTCGCAAGGGTAGACTGTGTGAATGCTACTTTTGGAAATCTGGGATCATCGAG TGGTGGAGAAATACTGGGTTTGTGTGAGAAGCTGCCCTTCGCAAGGGTAGACTGTGTGAATGCTACTTTTGGAAATCTGGGATCATCGAG	990 987
MpLS Unigene0018537	CCAGCTCAGCATGCAAGTGCAGAGTAATGATGGGCAAGTCAACGCTCTGATTACGGTGATAGATGATATTTATGATGTCTATGTGTACC CCAGCTCAGCATGCAAGTGCAGAGTAATGATGGGCAAGTCAACGCTCTGATTACGGTGATAGATGATATTTATGATGTCTATGTGTACC	1080 1077
MpLS Unigene0018537	TTAGAAAGAACTGGAACAATTTCACAGACCTCATTOGGAGATGGGATATAGACTCAATCGACCAACTTCCCGATTACATGCAACTGTGCTTT TTAGAAAGAACTGGAACAATTTCACAGACCTCATTOGGAGATGGGATATAGACTCAATCGACCAACTTCCCGATTACATGCAACTGTGCTTT	1170 1167
MpLS Unigene0018537	CTCGCACTCAACAACCTTCGTGATGTACATCTGACGATGTTATGAAGAGAAAGGCGTCAACGTTATACCTTACTCTCCGCAATCGTGG CTCGCACTCAACAACCTTCGTGATGTACATCTGACGATGTTATGAAGAGAAAGGCGTCAACGTTATACCTTACTCTCCGCAATCGTGG	1260 1257
MpLS Unigene0018537	GTTGATTTGGCGGATAAGTAAATGTGTAGAGGACCGTGTCTTCAAGGCGCACAAACCAAGTTTGGAGAGTATTTGGAAGAACTCATGG GTTGATTTGGCGGATAAGTAAATGTGTAGAGGACCGTGTCTTCAAGGCGCACAAACCAAGTTTGGAGAGTATTTGGAAGAACTCATGG	1350 1347
MpLS Unigene0018537	ATGTGATTAAGTGGGCGCTGATGTTGACACATATTTTCGAGTAAGGATTCATTCACAAAGAGAGAGTGTGACAGTTTGTACAAAG CATGTGATTAAGTGGGCGCTGATGTTGACACATATTTTCGAGTAAGGATTCATTCACAAAGAGAGAGTGTGACAGTTTGTACAAAG	1440 1437
MpLS Unigene0018537	TACACAGATTTAGTTCGTTGGTCACTCTCTGTTTTCGCACTTGTCTGATGATTGGGAACCTCGSTGGAAGAGGTGAGCAGAGGCGATG TACACAGATTTAGTTCGTTGGTCACTCTCTGTTTTCGCACTTGTCTGATGATTGGGAACCTCGSTGGAAGAGGTGAGCAGAGGCGATG	1530 1527
MpLS Unigene0018537	CCGAAATCACTTCAGTGTACATGATGACTACAATGCTTCGGAGGCGGAGGCGCGAAGCACGTGAAATGGCTGATACCGAGAGTGTGG CCGAAATCACTTCAGTGTACATGATGACTACAATGCTTCGGAGGCGGAGGCGCGAAGCACGTGAAATGGCTGATACCGAGAGTGTGG	1620 1617
MpLS Unigene0018537	AAGAAGATGAATGCAAGAGGTTGCGAAGGATTCTCCATTGGCAAGATTTTATAGGATGTGCAGTTGATTTGGAAGGATGGCGCAG AAGAAGATGAATGCAAGAGGTTGCGAAGGATTCTCCATTGGCAAGATTTTATAGGATGTGCAGTTGATTTGGAAGGATGGCGCAG	1710 1707
MpLS Unigene0018537	TTGATGTACCATTAATGGAGATGGGCTTGGCACACAACATCTTATAATACATCAACAAATGACCGCAACTTATTTCAGGCCCTTTGCATG TTGATGTACCATTAATGGAGATGGGCTTGGCACACAACATCTTATAATACATCAACAAATGACCGCAACTTATTTCAGGCCCTTTGCATG	1799 1796

## LS amino acid sequences alignment

MpLS Unigene0018537	MALIVFSGAMQWIPSLTLYLPQSHLNSSPKLLSNTKGTSRSLRVSCSSQLTERRSGNYNPSRWVDVFIQTLHSDYKDEKHARRAS MALIVFSGAMQWIPSLTLYLPQSHLNSSPKLLSNTKGTSRSLRVSCSSQLTERRSGNYNPSRWVDVFIQTLHSDYKDEKHARRAS	90 90
MpLS Unigene0018537	ELVLVKMELEKETDQIROLELIDDLQRMGLSDHFQNEFKELSSVYLDHYYKNPDPKEERDLYSTSLAFRLREHGQVQAEVYVFGPK ELVLVKMELEKETDQIROLELIDDLQRMGLSDHFQNEFKELSSVYLDHYYKNPDPKEERDLYSTSLAFRLREHGQVQAEVYVFGPK	180 180
MpLS Unigene0018537	NESEFKESLSDDTRGLDLYEASFLLTBGETTLESAREEFATKFLERVNEGGDENLLTRIAYSLEIPLHWRIKRPNAPVWIDSYRKRP NESEFKESLSDDTRGLDLYEASFLLTBGETTLESAREEFATKFLERVNEGGDENLLTRIAYSLEIPLHWRIKRPNAPVWIDSYRKRP	270 269
MpLS Unigene0018537	NMNPVVLDAIILDNIQVAHRCSELKESFRWRNTGFVEKLFPARDRLVECFWNTGIIIEPRQHASARIMMKVNALITVDDIYDVYGT NMNPVVLDAIILDNIQVAHRCSELKESFRWRNTGFVEKLFPARDRLVECFWNTGIIIEPRQHASARIMMKVNALITVDDIYDVYGT	360 359
MpLS Unigene0018537	LEELFETDLIRRWIDSIDQLPDYMQLCFLAINFVLETSYDVMEKEGVNIPVLRQSWVDLADKYMVEARWIFYGGHKPSLEEYLENSW LEELFETDLIRRWIDSIDQLPDYMQLCFLAINFVLETSYDVMEKEGVNIPVLRQSWVDLADKYMVEARWIFYGGHKPSLEEYLENSW	450 449
MpLS Unigene0018537	MSISGFCMLTHIFFRVDSFTKETVDSLYKYHDLVRWSSFVLRLADDLGTVEEVSRGVDVPKSLQCYMSDYNAEABARKHKVWKLIAEVW MSISGFCMLTHIFFRVDSFTKETVDSLYKYHDLVRWSSFVLRLADDLGTVEEVSRGVDVPKSLQCYMSDYNAEABARKHKVWKLIAEVW	540 539
MpLS Unigene0018537	RKMNAERVSKDSPFGKDFIGCAVDLGRMAQLMYHNGDGHGTQHPILIHQQMTALFEFF RKMNAERVSKDSPFGKDFIGCAVDLGRMAQLMYHNGDGHGTQHPILIHQQMTALFEFF	598 597

L3OH nucleotide sequences alignment

MpL3OH-PM2 Unigene0052571	ATGGAGCTCCTCCAGCTTTGGTGGCGCTTATAATCCTCGTGTAACTACGTCATATCTCTCTAATCAACCAATGGCGAAAACCGAAA ATGGAGCTCCTCCAGCTTTGGTGGCGCTTATAATCCTCGTGTAACTACGTCATATCTCTCTAATCAACCAATGGCGAAAACCGAAA	90 90
MpL3OH-PM2 Unigene0052571	CCCCAAGGAAGTTCCCCCGGGCCCGCGAAGCTGCCGTGATCGGGACCTCCACCTCTGTGGGGGAAGCTGCCGAGCACGCGCTG CCCCAAGGAAGTTCCCCCGGGCCCGCGAAGCTGCCGTGATCGGGACCTCCACCTCTGTGGGGGAAGCTGCCGAGCACGCGCTG	180 180
MpL3OH-PM2 Unigene0052571	GCCAGCGTGGCAAGGAGTACGCGCCCGTGGCCACGTCAGCTGGGTGAGGTGTCTCCGTCGTCCTTTGTGTCGGGAGGGCGACGAAG GCCAGCGTGGCAAGGAGTACGCGCCCGTGGCCACGTCAGCTGGGTGAGGTGTCTCCGTCGTCCTTTGTGTCGGGAGGGCGACGAAG	270 270
MpL3OH-PM2 Unigene0052571	GAGGCGATGAAGCTGGTACACCGCGGTGGCGAACCCTTCGAGAGCATCGGAGCAGGATCATGTGTGACGACACGAGGACATCATC GAGGCGATGAAGCTGGTACACCGCGGTGGCGAACCCTTCGAGAGCATCGGAGCAGGATCATGTGTGACGACACGAGGACATCATC	360 360
MpL3OH-PM2 Unigene0052571	TTACAGCCCTACAGCGAGCACTGGCGCCAGATGCGCAAGTCTGGGTCTCCGAGCTCTCTCTCTCCCGCAAGCTCCGCTCTCTCGGCTTC TTACAGCCCTACAGCGAGCACTGGCGCCAGATGCGCAAGTCTGGGTCTCCGAGCTCTCTCTCTCCCGCAAGCTCCGCTCTCTCGGCTTC	450 450
MpL3OH-PM2 Unigene0052571	ATCCGGCAGGACGAGGTCTCCGCTCCTCCGCCACCTCCGCTCTCGGACGGGCGCCGCTGGACATGACGAGGAGATAGAGACGCTG ATCCGGCAGGACGAGGTCTCCGCTCCTCCGCCACCTCCGCTCTCGGACGGGCGCCGCTGGACATGACGAGGAGATAGAGACGCTA	540 540
MpL3OH-PM2 Unigene0052571	ACGTGCTCCATCATCTCGAGGGCGCGGTTCGGGAGCGTGATCAGGGACAACCGCGAGCTGGTGGGGCTGTCAAGGACCGCTCAGCATG ACGTGCTCCATCATCTCGAGGGCGCGGTTCGGGAGCGTGATCAGGGACAACCGCGAGCTGGTGGGGCTGTCAAGGACCGCTCAGCATG	630 630
MpL3OH-PM2 Unigene0052571	GCCTCGGGGTTGAGCTCGCGGACATGTTCCTCTCCTCAAGCTCCTCAAGCTCCTGCTGGAACAAGAGCAAGCTCTGGAGGATCGCG GCCTCGGGGTTGAGCTCGCGGACATGTTCCTCTCCTCAAGCTCCTCAAGCTCCTGCTGGAACAAGAGCAAGCTCTGGAGGATCGCG	720 720
MpL3OH-PM2 Unigene0052571	CGCGCGTTCGACACCATCTCGAGGCCATGTCGACGAGCAACAAGTCAAGAAGAGCGCGGAGTTCCGCGCGCAGGACATCATCGAGCTC CGCGCGTTCGACACCATCTCGAGGCCATGTCGACGAGCAACAAGTCAAGAAGAGCGCGGAGTTCCGCGCGCAGGACATCATCGAGCTC	810 810
MpL3OH-PM2 Unigene0052571	CTCTTCAGGATGCAAGGACATCCAGATCAAAGTCCCCATCACCACCAACTCCATCAAAGCCTTCATCTTCGAGACCTTCTCAGCAGGG CTCTTCAGGATGCAAGGACATCCAGATCAAAGTCCCCATCACCACCAACTCCATCAAAGCCTTCATCTTCGAGACCTTCTCAGCAGGG	900 900
MpL3OH-PM2 Unigene0052571	ACTGAGACATCTCAACCAACCACTATGGGTGCTGGCGAGCTGATGAGGAACCGGCACTGATGGCGAAGTGCAGGCGGAGGTGAGA ACTGAGACATCTCAACCAACCACTATGGGTGCTGGCGAGCTGATGAGGAACCGGCACTGATGGCGAAGTGCAGGCGGAGGTGAGA	990 990
MpL3OH-PM2 Unigene0052571	CGCGCATCTGAAGTGAAGACGAATGGGAGCTGGTACCTGCAAGAGCTTAAATACATGAAATCGGTGGTGAAGGACGATGAGGATG CGCGCATCTGAAGTGAAGACGAATGGGAGCTGGTACCTGCAAGAGCTTAAATACATGAAATCGGTGGTGAAGGACGATGAGGATG	1080 1080
MpL3OH-PM2 Unigene0052571	CACCTCCGATCCCGTTGATCCCGAGATCATGCAGAGAAGAATGGTGGTTAACGGGTATACGATTCGGAACAAGGCCAGAAATCATGATC CACCTCCGATCCCGTTGATCCCGAGATCATGCAGAGAAGAATGGTGGTTAACGGGTATACGATTCGGAACAAGGCCAGAAATCATGATC	1170 1170
MpL3OH-PM2 Unigene0052571	AACGTCGTGTCATGGCAGGAATCTCTCTACTGGGAAAAACCGGACCTTTTGGCCGAAAGGTTTGACGAGTTTCAAAGGATTTTC AACGTCGTGTCATGGCAGGAATCTCTCTACTGGGAAAAACCGGACCTTTTGGCCGAAAGGTTTGACGAGTTTCAAAGGATTTTC	1260 1260
MpL3OH-PM2 Unigene0052571	ATGGGAAATGATTTGAGTTCTGTCGGTTCGGAGCGGGAAGAAGATCTGCCCGGCTTGAACCTTCGGGTTGGCAACGTTGAGGTTCCA ATGGGAAATGATTTGAGTTCTGTCGGTTCGGAGCGGGAAGAAGATCTGCCCGGCTTGAACCTTCGGGTTGGCAACGTTGAGGTTCCA	1350 1350
MpL3OH-PM2 Unigene0052571	TTGGGCGAGCTTCTTTACCACTTCGACTGGAAGTGGCGGAAGCATGGAACCTTCTGATATGACATGTCTGAGCGGAAGGCTTACG TTGGGCGAGCTTCTTTACCACTTCGACTGGAAGTGGCGGAAGCATGGAACCTTCTGATATGACATGTCTGAGCGGAAGGCTTACG	1440 1440
MpL3OH-PM2 Unigene0052571	GGAATACAAAGAACAACTCTCTCTTGTTCACACACCCCTACGATCTCTGATG GGAATACAAAGAACAACTCTCTCTTGTTCACACACCCCTACGATCTCTGATG	1496 1496

L3OH amino acid sequences alignment

MpL3OH-PM2 Unigene0052571	MELLQLWSALITLVVTPISLLINQWRKPKPKCKFPFGPKPLPLIGHLHLWGKLPQHALASVAKEYGPAHVQLGEVPSVWLSREATK MELLQLWSALITLVVTPISLLINQWRKPKPKCKFPFGPKPLPLIGHLHLWGKLPQHALASVAKEYGPAHVQLGEVPSVWLSREATK	90 90
MpL3OH-PM2 Unigene0052571	EAMKLVDPAKANRFESIGTRIMWYDNEIDIIFSPYSEHWRQMRKICVSELLSSRNVRSPGFIHQDEVSRLLRLRSSAGAAVDMTERIETL EAMKLVDPAKANRFESIGTRIMWYDNEIDIIFSPYSEHWRQMRKICVSELLSSRNVRSPGFIHQDEVSRLLRLRSSAGAAVDMTERIETL	180 180
MpL3OH-PM2 Unigene0052571	TCSITCRAAFGVSIRDNAELVGLVKDALSMASGFEADMPSSKLLNLLCNKSKLWRMRVRVDTILEAIVDEHKKSGEFGGEDIIDV TCSITCRAAFGVSIRDNAELVGLVKDALSMASGFEADMPSSKLLNLLCNKSKLWRMRVRVDTILEAIVDEHKKSGEFGGEDIIDV	270 270
MpL3OH-PM2 Unigene0052571	LFRMCKLQIKVPIITNSIKAFIFDTPSAGTETSSTTTLWLAEMLMRNPVMAVQAEVRAALKKTNWQVDDVQELKYMKSVMKETMRM LFRMCKLQIKVPIITNSIKAFIFDTPSAGTETSSTTTLWLAEMLMRNPVMAVQAEVRAALKKTNWQVDDVQELKYMKSVMKETMRM	360 360
MpL3OH-PM2 Unigene0052571	HPPIPLIPRSCREECVNGYTIIPNKARIMINVWSMGRNPLYWEKDTFWPERFTVSKDFMGNDPEFVPPGAGRRIICPLNFGLANVEVF HPPIPLIPRSCREECVNGYTIIPNKARIMINVWSMGRNPLYWEKDTFWPERFTVSKDFMGNDPEFVPPGAGRRIICPLNFGLANVEVF	450 450
MpL3OH-PM2 Unigene0052571	LAQLLYHFDWKLAEGMKPSNDMMSAEGLTGIRKNNLLLVPTPYDPS LAQLLYHFDWKLAEGMKPSNDMMSAEGLTGIRKNNLLLVPTPYDPS	497 497

iPD nucleotide sequences alignment

MpiPD Unigene0033747	ATGGCAACGGTGAAGAAGCTCGCAGGCAAGGTAGCCATCGTAACCGGCGGGCCAGCGGCATCGGGCAGGTACACGGCCGCCCTCTTCGCC ATGGCAACGGTGAAGAAGCTCGCAGGCAAGGTAGCCATCGTAACCGGCGGGCCAGCGGCATCGGGCAGGTACACGGCCGCCCTCTTCGCC	90 90
MpiPD Unigene0033747	GAGCGCGCGCCCGCGCGGTGGTGTGATCGCGACATGCAGCCCGAGAAGGGCGGTACCGTGGCGGAATCCATCGCGCGCGCGGTGCAGC GAGCGCGCGCCCGCGCGGTGGTGTGATCGCGACATGCAGCCCGAGAAGGGCGGTACCGTGGCGGAATCCATCGCGCGCGCGGTGCAGC	180 180
MpiPD Unigene0033747	TACGTCCACTGCGACATCACCGACGAGCAACAGGTCAAGTCCGTGCTGGATTGGACCGCCGCCACCTACGGCGCGGTGCAGCTGATGTTTC TACGTCCACTGCGACATCACCGACGAGCAACAGGTCAAGTCCGTGCTGGATTGGACCGCCGCCACCTACGGCGCGGTGCAGCTGATGTTTC	270 270
MpiPD Unigene0033747	TGCACGCTGGCACCGCCAGCGCCACCGCTCAGACCGTCTCTGGACCTGGACCTGGCGCAGTTCGACCGCGTATGCGCTTCAACGCGCGT TGCACGCTGGCACCGCCAGCGCCACCGCTCAGACCGTCTCTGGACCTGGACCTGGCGCAGTTCGACCGCGTATGCGCTTCAACGCGCGT	360 360
MpiPD Unigene0033747	GGCACGCGCGCGTGGTGAAGCAGCGCGCGCTAAGATGGTGGAGCTGGGGAGGGCGGCGCTATCATCTGCACCGCCAGCGCGACCGTC GGCACGCGCGCGTGGTGAAGCAGCGCGCGCTAAGATGGTGGAGCTGGGGAGGGCGGCGCTATCATCTGCACCGCCAGCGCGACCGTC	450 450
MpiPD Unigene0033747	CAACACGCGCGGCCCAACTTGACGGACTACATCATGTGGAAGTGGGGGTCTGGGGCTGGTGGCGTGGCGAGTTTGCAGCTCGGGGTG CAACACGCGCGGCCCAACTTGACGGACTACATCATGTGGAAGTGGGGGTCTGGGGCTGGTGGCGTGGCGAGTTTGCAGCTCGGGGTG	540 540
MpiPD Unigene0033747	CACGGGATTAGGGTTAACAGCGTGTGCGCGACGGCGCTGCGCCACGCGCTCACCGCGACGATCGGGCTCCCGACGGCCCGGATGTGGAG CACGGGATTAGGGTTAACAGCGTGTGCGCGACGGCGCTGCGCCACGCGCTCACCGCGACGATCGGGCTCCCGACGGCCCGGATGTGGAG	630 630
MpiPD Unigene0033747	AGCTTCTATGGGCAGGTACCGACCTTGAAAGGGGTGGCGATCACGGCGGAGCACGTGGCGAGGCGGTGGCTTTCTGGCTTCGGATGAG AGCTTCTATGGGCAGGTACCGACCTTGAAAGGGGTGGCGATCACGGCGGAGCACGTGGCGAGGCGGTGGCTTTCTGGCTTCGGATGAG	720 720
MpiPD Unigene0033747	GCGGCGTTCGTACCGGCCATGATTGGGGGTGGATGGTGGACTGCAGTGTTTACCAATTGCTGGCGGTGGCCAAAGTG GCGGCGTTCGTACCGGCCATGATTGGGGGTGGATGGTGGACTGCAGTGTTTACCAATTGCTGGCGGTGGCCAAAGTG	797 797

iPD amino acid sequences alignment

MpiPD Unigene0033747	MAIVKKLAGKVAIVTGGASGIGEVITARLFAERGARAVVIADMOPEKGGTVAESIGGRCSYVHCDITDEQVRSVVDWTAATYGGVDVME MAIVKKLAGKVAIVTGGASGIGEVITARLFAERGARAVVIADMOPEKGGTVAESIGGRCSYVHCDITDEQVRSVVDWTAATYGGVDVME	90 90
MpiPD Unigene0033747	CNAGTASATAQTVLDLDAQPDRVMRVNARGTAACVKQAARKMVELGRGGAIICTASATVHHAGPNLTDYIMSKCGVLGLVRSASLQLGV CNAGTASATAQTVLDLDAQPDRVMRVNARGTAACVKQAARKMVELGRGGAIICTASATVHHAGPNLTDYIMSKCGVLGLVRSASLQLGV	180 180
MpiPD Unigene0033747	HGIRVNSVSPTALATPLTATIGLRTAADVESFYGVQVTSILKGVAITAEHVAAEVAFLASDEAAAFVTGHDLAVDGGLQCLPFVAVA HGIRVNSVSPTALATPLTATIGLRTAADVESFYGVQVTSILKGVAITAEHVAAEVAFLASDEAAAFVTGHDLAVDGGLQCLPFVAVA	264 264

iPR nucleotide sequences alignment

MpiPR	ATGGCAAGTACAGAGGTATGCATTGGTGACGGGAGCAAAAGAGGAATCGGGTTCGAAATCTGCAGGCAGTTG	90
Unigene0033916	ATGGCAAGTACAGAGGTATGCATTGGTGACGGGAGCAAAAGAGGAATCGGGTTCGAAATCTGCAGGCAGTTG	90
MpiPR	ATAGTATATTTTAACATGAGAAATGAAAAGAGAGGCTTCGAAGCTCGACAAAGCTGCTGAAGGACTTGAATGTTCTGAAAATCGTTT	180
Unigene0033916	ATAGTATATTTTAACATGAGAAATGAAAAGAGAGGCTTCGAAGCTCGACAAAGCTGCTGAAGGACTTGAATGTTCTGAAAATCGTTT	180
MpiPR	GTTTTTCATCACTGATGTACGATGTAGCTAGCGTTCGCTGTTGGTCTTATCAAATCTAATTCGGAAGCTGATATCTTG	270
Unigene0033916	GTTTTTCATCACTGATGTACGATGTAGCTAGCGTTCGCTGTTGGTCTTATCAAATCTAATTCGGAAGCTGATATCTTG	270
MpiPR	GTGAATATTCAGGAGTTAGCGGATAGAGATGGTTGGAGATGTTTCTGTGTCAAGAGTATATTTAGGCTGACTTCAAAGCCCTTCAA	360
Unigene0033916	GTGAATATTCAGGAGTTAGCGGATAGAGATGGTTGGAGATGTTTCTGTGTCAAGAGTATATTTAGGCTGACTTCAAAGCCCTTCAA	360
MpiPR	GCACCTCGAAGCTGGTGCAAGGAAGAGCGCCCAATTAAAGCCAAAGCAATGGAGAAATGATCGAAAAATTCGAAGGAGCCAAAGATTGC	450
Unigene0033916	GCACCTCGAAGCTGGTGCAAGGAAGAGCGCCCAATTAAAGCCAAAGCAATGGAGAAATGATCGAAAAATTCGAAGGAGCCAAAGATTGC	450
MpiPR	GTTCTTACAAACTACTACGGTCCAAAGAGACTAACACAAGCCCTCATTCCTCTCTTACAACTATCTCCTTCACCGAGAATCGTCAAGCTC	540
Unigene0033916	GTTCTTACAAACTACTACGGTCCAAAGAGACTAACACAAGCCCTCATTCCTCTCTTACAACTATCTCCTTCACCGAGAATCGTCAAGCTC	540
MpiPR	TCCCTCCTCTTCGGGAGTTTACTTGTCTGTGTGAACGAATGGGCAAGGGAGTCTGGGCGACGAGGATGCTGACGAAGAGAGAGTGC	630
Unigene0033916	TCCCTCCTCTTCGGGAGTTTACTTGTCTGTGTGAACGAATGGGCAAGGGAGTCTGGGCGACGAGGATGCTGACGAAGAGAGAGTGC	630
MpiPR	GAAGAGTCTGGAGGTTTCTTCAAGATATAAAGAGGTTAAGCTTGAAGAAACCAATGGCTCCACATTTTGGGCGGAAAGAGTCT	720
Unigene0033916	GAAGAGTCTGGAGGTTTCTTCAAGATATAAAGAGGTTAAGCTTGAAGAAACCAATGGCTCCACATTTTGGGCGGAAAGAGTCT	720
MpiPR	TGGAAGCGCGCTTGAACGCTTACACTAAGATTCGGCGAAGAAGTACCCGAGTTTCCGCATAAATGCATATGCCCGGTTATGCGAAA	810
Unigene0033916	TGGAAGCGCGCTTGAACGCTTACACTAAGATTCGGCGAAGAAGTACCCGAGTTTCCGCATAAATGCATATGCCCGGTTATGCGAAA	810
MpiPR	ACCGACATTACCTTCCATGCGGGCTGATGAGTGTGCTGGAAGCTGCTCAAGTTCGGGTGAAGCTGGCTCTGCTGCTGATGCGGGGCC	900
Unigene0033916	ACCGACATTACCTTCCATGCGGGCTGATGAGTGTGCTGGAAGCTGCTCAAGTTCGGGTGAAGCTGGCTCTGCTGCTGATGCGGGGCC	900
MpiPR	TCCGGTGTCTTCTCCCTCGAGACAAAGCTTTGSCCTTCTATTATTA	944
Unigene0033916	TCCGGTGTCTTCTCCCTCGAGACAAAGCTTTGSCCTTCTATTATTA	944

iPR amino acid sequences alignment

MpiPR	MANVORYALVTGANKGIGFEICRQLAEKGIIVILTSNEKRGTAPRRLLLKELNVSARLVPFOLDVITLASVAAVAFIKSRFGKLDIL	90
Unigene0033916	MANVORYALVTGANKGIGFEICRQLAEKGIIVILTSNEKRGTAPRRLLLKELNVSARLVPFOLDVITLASVAAVAFIKSRFGKLDIL	90
MpiPR	VNNAGVSGVMVGDVSVFNEYIEADENALQALEAGAKEEPPFKPRANGEMIEKFEGAKDCVVTNYYGPKRLTQALIPLLQLSPSPRIVNV	180
Unigene0033916	VNNAGVSGVMVGDVSVFNEYIEADENALQALEAGAKEEPPFKPRANGEMIEKFEGAKDCVVTNYYGPKRLTQALIPLLQLSPSPRIVNV	180
MpiPR	SSSFGSLLLLWNEWAGVLGDEDSUTEERVDEVVEVFLKDIKEGKLEESQWPPHFAAERVSKAALNAYTKIAAKKYPSPFINAICPGYAK	270
Unigene0033916	SSSFGSLLLLWNEWAGVLGDEDSUTEERVDEVVEVFLKDIKEGKLEESQWPPHFAAERVSKAALNAYTKIAAKKYPSPFINAICPGYAK	270
MpiPR	TDITFHAGPLSVSAAQVPVKLALLPDGGPSGCTFPRDKALAL	313
Unigene0033916	TDITFHAGPLSVSAAQVPVKLALLPDGGPSGCTFPRDKALAL	313

## MFS nucleotide sequences alignment

MpMFS Unigene0030907	ATGGCAGCTCTTCTAGTATTTTCTCTCTCTCTTTAAATCTTCTGGCGTCTCTTTCCATAACGAAAGTCCAGTCTTT...CCTCAAGA ATGGCAGCTCTTCTAGTATTTTCTCTCTCTCTTTAAATCTTCTGGCGTCTCTTTCCATAACGAAAGTCCAGTCTTTCTCTCTCAAGA	87 90
MpMFS Unigene0030907	AAGAGGCT...GCGCCGCTCTCCATTAAGGCTTCGGGTGATCGGCCATTTCACACTGATCGGAACCCCTCTCCACCGCTCTCTACCTCC AAGAGGCTGCTGCGCCGCTCTCCATTAAGGCTTCGGGTGATCGGCCATTTCACACTGATCGGAACCCCTCTCCACCGCTCTCTACCTCC	174 180
MpMFS Unigene0030907	TTATCCAAAGCGCTACGCGAGGTGATGCTACTCCATTTCGCGAGCGCTCGCTGCTAGTGGCTCTCTCAGCGCGCGCGCGCTGAGATC TTATCCAAAGCGCTACGCGAGGTGATGCTACTCCATTTCGCGAGCGCTCGCTGCTAGTGGCTCTCTCAGCGCGCGCGCGCTGAGATC	264 270
MpMFS Unigene0030907	ATGAAGAACAAGACATGATCTTCGCGAGCGAGGCGAGGCTGAGCATCTTCGACAGGCTCTGTACAGCTGCAAGCGCTGGCTTCGCGC ATGAAGAACAAGACATGATCTTCGCGAGCGAGGCGAGGCTGAGCATCTTCGACAGGCTCTGTACAGCTGCAAGCGCTGGCTTCGCGC	354 360
MpMFS Unigene0030907	CCCTACCGCGAGCACTGGCGCTACCGCGGAGCATGTGCTGTCTGACAGTCTCTACGCTAAGAGGGTCCAGTGGTTCGCGGATTCGA GCTTACCGCGAGCACTGGCGCTACCGCGGAGCATGTGCTGTCTGACAGTCTCTACGCTAAGAGGGTCCAGTGGTTCGCGGATTCGA	444 450
MpMFS Unigene0030907	GAAGAGGAACGTCGGCTATGATTGAGAAGATCAGGCGATCGACGCCACGAGGTCGTGAACCTTGAGCGAGATGTTATGGCGCTGAGC GAAGAGGAACGTCGGCTATGATTGAGAAGATCAGGCGATCGACGCCCT...CGTCTGTGAACCTTGAGCGAGATGTTATGGCGCTGAGC	534 537
MpMFS Unigene0030907	AACGCGTAACTTCACAGGCGCGCTGTTAGGCGGAAAGCGACGCGCGGAGATGATTAAATCGGATCTGATTAAGCTTATCAAGCTCTTG AACGCGTAACTTCACAGGCGCGCTGTTAGGCGGAAAGCGACGCGCGGAGATGATTAAATCGGATCTGATTAAGCTTATCAAGCTCTTG	624 627
MpMFS Unigene0030907	GGAATTTCAACCTGGGGATTACGTTCCATGGCTCTTTTGGATTAACCGGATTAATGGCGTCTGATCGAGAAGTGGAAAAAGTCTTTAGA GGAATTTCAACCTGGGGATTACGTTCCATGGCTCTTTTGGATTAACCGGATTAATGGCGTCTGATCGAGAAGTGGAAAAAGTCTTTAGA	714 717
MpMFS Unigene0030907	AAGTTGGATGGATCATAGAGGGTATTTCTTCGAATAATATAGAAAGGAAGCTGGTCTATGAAACGAATTTCTGAGACAGCTTGCTT AAGTTGGATGGATCATAGAGGGTATTTCTTCGAATAATATAGAAAGGAAGCTGGTCTATGAAACGAATTTCTGAGACAGCTTGCTT	804 807
MpMFS Unigene0030907	CAGTTTCAGAGAGAGTAAAGATACTACCCCGTCGAGGATGACGTAATCAAAGCTCTAATCTTCGACATGCTTTTSCCGCGAATCGAT CAGTTTCAGAGAGAGTAAAGATACTACCCCGTCGAGGATGACGTAATCAAAGCTCTAATCTTCGACATGCTTTTSCCGCGAATCGAT	894 897
MpMFS Unigene0030907	ACGAGCTTCGCGCTCTAGAGTGGACGATGGCGGAGCTCATAAATAACCGCGTACCCCTAAAAACTTTCGAGAAGCAGGTGCGAGAAGTT ACGAGCTTCGCGCTCTAGAGTGGACGATGGCGGAGCTCATAAATAACCGCGTACCCCTAAAAACTTTCGAGAAGCAGGTGCGAGAAGTT	984 987
MpMFS Unigene0030907	TCTAGAAACAAGCTGGGATTACGAGGATGACGTGGACAAGATGCCATCTCTGAAAGCAGTATCCATGAGATTCTACGCTTACATCCA TCTAGAAACAAGCTGGGATTACGAGGATGACGTGGACAAGATGCCATCTCTGAAAGCAGTATCCATGAGATTCTACGCTTACATCCA	1074 1077
MpMFS Unigene0030907	CTTTTCGCAATCTGCTCCCTTCGAGAATTGACTCAAGACGCCAATATGCTCGGCTACGACATCCCACTGGCACCTCTGTTGTTGGTCAAC CTTTTCGCAATCTGCTCCCTTCGAGAATTGACTCAAGACGCCAATATGCTCGGCTACGACATCCCACTGGCACCTCTGTTGTTGGTCAAC	1164 1167
MpMFS Unigene0030907	AACTGGGCGATATCGAGAGACCCCTCGTTGTGGGAAAAATCCCGAAGAATTTCGTCAGAAAGGTTCTCTCGAGACGAGCATAGACTATAAA AACTGGGCGATATCGAGAGACCCCTCGTTGTGGGAAAAATCCCGAAGAATTTCGTCAGAAAGGTTCTCTCGAGACGAGCATAGACTATAAA	1254 1257
MpMFS Unigene0030907	GGCTTCGATTTTGAGATGCTTCCGTTCCGGTCCGGTCCGAAGAGGTCGCCCGGATTCACAGTTTTCGATGCTTTTATACGAGCTTGCACTA GGCTTCGATTTTGAGATGCTTCCGTTCCGGTCCGGTCCGAAGAGGTCGCCCGGATTCACAGTTTTCGATGCTTTTATACGAGCTTGCACTA	1344 1347
MpMFS Unigene0030907	TCCAGCTCTTAAACGAGTTGATTTTGAGATTGGTAAATGGAGATAGAGCGAGGATTTGGACATGACTGAAGCTCTCGATTTTGTAGTC TCCAGCTCTTAAACGAGTTGATTTTGAGATTGGTAAATGGAGATAGAGCGAGGATTTGGACATGACTGAAGCTCTCGATTTTGTAGTC	1434 1411
MpMFS Unigene0030907	CATAAGAAGTCTCCCTTGCTTTGCTGTGCTACTCCACGCTCAATCTTG .....	1481 1411

## MFS amino acid sequences alignment

MpMFS Unigene0030907	MAALLVFFPSLLILLAVLFHKRSSSS...RMRPPSHRLPVIGHHLICSLHRSFTSLSKRYGEVMLLHFGSAPVLVASSAAAAAREI MAALLVFFPSLLILLAVLFHKRSSSLIPSRKRPPSHRLPVIGHHLICSLHRSFTSLSKRYGEVMLLHFGSAPVLVASSAAAAAREI	88 90
MpMFS Unigene0030907	MKNQDIFASRPRLSIDRLVYSGKVAFAPYGEHWRARSMCVLQLLSAKRVQSFRRIREETSAMIEKIRRSMTIVNLSEMFMAIT MKNQDIFASRPRLSIDRLVYSGKVAFAPYGEHWRARSMCVLQLLSAKRVQSFRRIREETSAMIEKIRRSMTIVNLSEMFMAIT	178 179
MpMFS Unigene0030907	NGVHRAALGRKDCGGDDENRDLRVIMLLGSFNVGDYVPWLSWINRINGVDAEVEKVGKLDSEEGILRKYRRKVGDDENFVDTL NGVHRAALGRKDCGGDSEMTLNRDLRVIMLLGSFNVGDYVPWLSWINRINGVDAEVEKVGKLDSEEGILRKYRRKVGDDENFVDTL	268 269
MpMFS Unigene0030907	QFQRESKDTLPVEDDVIKALILNVPAGCTDTTSVLEWTMAELINRPRTLKTLQNEVREVS RNKGGITEDDVDMKPYLKAVSMPIILRLH QFQRESKDTLPVEDDVIKALILNVPAGCTDTTSVLEWTMAELINRPRTLKTLQNEVREVS RNKGGITEDDVDMKPYLKAVSMPIILRLH	358 359
MpMFS Unigene0030907	PFALLPRELTQDANMLGYDPRGTVLVNNWAISRDPSSLWENPEEPRPERFLETSIDYKGMHPEMLPFGSGRRGCPGTFAMSLVELAL PFALLPRELTQDANMLGYDPRGTVLVNNWAISRDPSSLWENPEEPRPERFLETSIDYKGMHPEMLPFGSGRRGCPGTFAMSLVELAL	448 449
MpMFS Unigene0030907	SKLVNEFDRLANGDRVEDLI... SKLVNEFDRLANGDRVEDLI.....	492 470

PR nucleotide sequences alignment

MpPR	ATGGTGATGAACAAGCAAAATTGTACTCAACAACACTACGCTTAAGGGTTCCTAAAGCAATCCGACTTCGGTTGAGAACTTCCACGATCTGC	90
Unigene0047772	ATGGTGATGAACAAGCAAAATTGTACTCAACAACACTACGCTTAAGGGTTCCTAAAGCAATCCGACTTCGGTTGAGAACTTCCACGATCTGC	90
MpPR	ATGGAGATCCCATATGGCTGCAACGGTGCCGTTTGGTCAAGAACTTGTAAGTTCGCTCAATCCTTATCTCATCTCTCGCATGGGAAAA	180
Unigene0047772	ATGGAGATCCCATATGGCTGCAACGGTGCCGTTTGGTCAAGAACTTGTAAGTTCGCTCAATCCTTATCTCATCTCTCGCATGGGAAAA	180
MpPR	CTCGATATCCCAAGTCTTGATTCACCTTCCTCGCTCTACTATGTTAGCTATGGAGTGTCAAAAGTATTGGATTGACGCATCCGAGT	270
Unigene0047772	CTCGATATCCCAAGTCTTGATTCACCTTCCTCGCTCTACTATGTTAGCTATGGAGTGTCAAAAGTATTGGATTGACGCATCCGAGT	270
MpPR	TACGAGAAGGCGAACTGATTTGGGGTCACAAGCTGGATGGGAGGAATATACCTTATCCAAAATCCATATAATTGTTTAAATCCAA	360
Unigene0047772	TACGAGAAGGCGAACTGATTTGGGGTCACAAGCTGGATGGGAGGAATATACCTTATCCAAAATCCATATAATTGTTTAAATCCAA	360
MpPR	GACAAAAGATGTGCTTTATCTACTATGTTGGGATCTAGGAATGCCTGGGATGACAGCATATGCAGGATTTTTTGAGATTTCCTCTCCG	450
Unigene0047772	GACAAAAGATGTGCTTTATCTACTATGTTGGGATCTAGGAATGCCTGGGATGACAGCATATGCAGGATTTTTTGAGATTTCCTCTCCG	450
MpPR	AAAAAAGCGAAACTGTGTTTGTAAACGGCTGCAGCAGGATCTGTGGCCAGCTTGTGGTCAGTTTGCAAGATGTTTGGTTCGTATGTT	540
Unigene0047772	AAAAAAGCGAAACTGTGTTTGTAAACGGCTGCAGCAGGATCTGTGGCCAGCTTGTGGTCAGTTTGCAAGATGTTTGGTTCGTATGTT	540
MpPR	GTTGGAATGCCGGGACAAAGAGAAGTTGATCTTTTGAAGAACAAATTTGGTTCGATGATGCATTTAATTATAAAGAGAGATGAT	630
Unigene0047772	GTTGGAATGCCGGGACAAAGAGAAGTTGATCTTTTGAAGAACAAATTTGGTTCGATGATGCATTTAATTATAAAGAGAGATGAT	630
MpPR	TATGATATGCTTTTGAAGAGGCACCTTCCCGAAGGAATGATATATACTTCGATATGTTGGAGGGAAGATGCTTGAAGCTGTGATCAAC	720
Unigene0047772	TATGATATGCTTTTGAAGAGGCACCTTCCCGAAGGAATGATATATACTTCGATATGTTGGAGGGAAGATGCTTGAAGCTGTGATCAAC	720
MpPR	AACATGAGAGTCCACGGCCGCATCGCGGTATGTGGGATGCTCTCCAGTAAAGCCTGAAGCAGCCGAAGCGCTCCACAACCTTGCTTAAAG	810
Unigene0047772	AACATGAGAGTCCACGGCCGCATCGCGGTATGTGGGATGCTCTCCAGTAAAGCCTGAAGCAGCCGAAGCGCTCCACAACCTTGCTTAAAG	810
MpPR	CTAAATCCCAAGCAAAATTCGTATGCAAGGGTTTGTGTTGTTGATTACTATCATCTCTACCCAAAGTTCCTTGAGATGGTTCGCGCGCC	900
Unigene0047772	CTAAATCCCAAGCAAAATTCGTATGCAAGGGTTTGTGTTGTTGATTACTATCATCTCTACCCAAAGTTCCTTGAGATGGTTCGCGCGCC	900
MpPR	ATCAAGGAGGAAAAGTGAATACGTGGAAGACATATCTGAAGGCCCTTGAGAGCGCCCTAGCCTCTCTTGGGGGTGATGTCGGTTCGT	990
Unigene0047772	ATCAAGGAGGAAAAGTGAATACGTGGAAGACATATCTGAAGGCCCTTGAGAGCGCCCTAGCCTCTCTTGGGGGTGATGTCGGTTCGT	990
MpPR	AACCTTGGCAATCAATGTTGTTGCCGTTTCTCGGAGTA	1028
Unigene0047772	AACCTTGGCAATCAATGTTGTTGCCGTTTCTCGGAGTA	1028

PR amino acid sequences alignment

MpPR	MVMNKQIVLNNYVNGSLKESDLALRTSTICMEIFEGCNGAHLVKNLYLSVNPYLILRMGKLDIPOFDSILPGSTIVSYGVSKVLDSHPS	90
Unigene0047772	MVMNKQIVLNNYVNGSLKESDLALRTSTICMEIFEGCNGAHLVKNLYLSVNPYLILRMGKLDIPOFDSILPGSTIVSYGVSKVLDSHPS	90
MpPR	YEKGELIWGSQAGWEEYTLIQNPYNLFKIQDKDVPLSYVVGILLMPGMTAYAGFFEICSPKKGETVFVTTAAAGSVGQLVGQFAKMFQCYV	180
Unigene0047772	YEKGELIWGSQAGWEEYTLIQNPYNLFKIQDKDVPLSYVVGILLMPGMTAYAGFFEICSPKKGETVFVTTAAAGSVGQLVGQFAKMFQCYV	180
MpPR	VGSAGSKEKVDLLKNKFGFDDAFNYKBEESDYDTALKRHPFBGIDIFYDNVGGKMLEAVINNMRVHGR IAVCGMV SQYSLKQPEGVHNLK	270
Unigene0047772	VGSAGSKEKVDLLKNKFGFDDAFNYKBEESDYDTALKRHPFBGIDIFYDNVGGKMLEAVINNMRVHGR IAVCGMV SQYSLKQPEGVHNLK	270
MpPR	LPKQIRMQGFVVVDYVHLYPKFLEWVLPKIKBGKVTIVEDISBGLSAPSALLGVVGRNHCNQVVAVSR	341
Unigene0047772	LPKQIRMQGFVVVDYVHLYPKFLEWVLPKIKBGKVTIVEDISBGLSAPSALLGVVGRNHCNQVVAVSR	341

MR nucleotide sequences alignment

MpMR Unigene0041050	ATGGCAGATACCTTTACGCAAGGTATGCTTTCCTTACCGTGC AAAACAAAGGAATCGGGTTCGAGATATCGAGGCAGTTAGCTTCGAAA ATGGCAGATACCTTTACGCAAGGTATGCTTTCCTTACCGTGC AAAACAAAGGAATCGGGTTCGAGATATCGAGGCAGTTAGCTTCGAAA	90 90
MpMR Unigene0041050	GGAAATGAAGGTGATTTTAGCTTCAAGAAACGAGAAGAGAGGCATCGAAGCTCGAGAAAGGCTACTTAAGGATCGAGATCAATTTCTGAT GGAAATGAAGGTGATTTTAGCTTCAAGAAACGAGAAGAGAGGCATCGAAGCTCGAGAAAGGCTACTTAAGGATCGAGATCAATTTCTGAT	180 180
MpMR Unigene0041050	GACGATGTGTTTTTCATCAACTGATGTGCTGACCCCTGCTAGGCGCTGTGCTGTGCTCAGTTCATCGAAACCAAAATCGGGAGGCTT GACGATGTGTTTTTCATCAACTGATGTGCTGACCCCTGCTAGGCGCTGTGCTGTGCTCAGTTCATCGAAACCAAAATCGGGAGGCTT	270 270
MpMR Unigene0041050	GATATTCGTGTAATAATCGCGGATTTACTGGAGTAGCGATAGAGGGAGATATTTCAGTGTATCAAGAGTGTCTGAGGCAAAACATTATT GATATTCGTGTAATAATCGCGGATTTACTGGAGTAGCGATAGAGGGAGATATTTCAGTGTATCAAGAGTGTCTGAGGCAAAACATTATT	360 360
MpMR Unigene0041050	GCAGCTCAGCGTGGACAGGCATCCATTCCATCCCAAACTACTGGTAGGCTCATTTGACACATTGGAGGGTTCAAAAGAGTGTATAGAA GCAGCTCAGCGTGGACAGGCATCCATTCCATCCCAAACTACTGGTAGGCTCATTTGACACATTGGAGGGTTCAAAAGAGTGTATAGAA	450 450
MpMR Unigene0041050	ACAAACTACTATGGCAAAAAGAATAACAGAAACCCCTAATTCCTCTCCTGCAAAAATCTGATTCCCAACAATTGTCAATGTCTCTCTCC ACAAACTACTATGGCAAAAAGAATAACAGAAACCCCTAATTCCTCTCCTGCAAAAATCTGATTCCCAACAATTGTCAATGTCTCTCTCC	540 540
MpMR Unigene0041050	ACCTCTCTGACTTTACTGCTCCAGCCTAATGAATGGC AAAAGGAGTCTTTAGCAGCA ..... CAGCTGAATGAAGCAAGGTGGAG ACCTCTCTGACTTTACTGCTCCAGCCTAATGAATGGC AAAAGGAGTCTTTAGCAGCTGAGACACACACTGAATGAAGCAAGGTGGAG	624 630
MpMR Unigene0041050	GAAGTTTTCATGAATTCTCAAGGATTTCATGATGTTAAATGCAACAAAACCACTGGCTCTCTAACCTTGCAGCCTACAAAAGTATCG GAAGTTTTCATGAATTCTCAAGGATTTCATGATGTTAAATGCAACAAAACCACTGGCTCTCTAACCTTGCAGCCTACAAAAGTATCG	714 720
MpMR Unigene0041050	AAAGCTCGCTGTTAATGCTATACCTCGGATCATAGCGCGAAAGTACCCGAGTTTCTGCATAAATTCAGTGTGCTCTGGTTTGTGTAGAACAA AAAGCTCGCTGTTAATGCTATACCTCGGATCATAGCGCGAAAGTACCCGAGTTTCTGCATAAATTCAGTGTGCTCTGGTTTGTGTAGAACAA	804 810
MpMR Unigene0041050	GATATTGTCTACAATCTTGGAGTACTAAGTGAAGCTGAAGGTGCTGAAGCTCCGGTGAAGCTGGCTTTTGTGCCCATGGCGGGCCCTCG GATATTGTCTACAATCTTGGAGTACTAAGTGAAGCTGAAGGTGCTGAAGCTCCGGTGAAGCTGGCTTTTGTGCCCATGGCGGGCCCTCG	894 900
MpMR Unigene0041050	GGCTCCTTCTCTCTCGAGAGGAAGCCTTGTCTTGTACTIA GGCTCCTTCTCTCTCGAGAGGAAGCCTTGTCTTGTACTIA	935 941

MR amino acid sequences alignment

MpMR Unigene0041050	MADTFTORVALITGANKGIGFEICRQLASKGMKVILASRNEKRGTEARERLLKESRSISDDDVPHOLDVDPASAVAVAHFIETKFGRL MADTFTORVALITGANKGIGFEICRQLASKGMKVILASRNEKRGTEARERLLKESRSISDDDVPHOLDVDPASAVAVAHFIETKFGRL	90 90
MpMR Unigene0041050	DILVNNAGFTGVAIEGDISVYQCEANIIAACGGAPPHPTSGRLIETLEGSKECIETNYYGTRITETLLIPLLKSDSPTIVNVSS DILVNNAGFTGVAIEGDISVYQCEANIIAACGGAPPHPTSGRLIETLEGSKECIETNYYGTRITETLLIPLLKSDSPTIVNVSS	180 180
MpMR Unigene0041050	TFSTILLQPNENAKGVFSSSLNLSKVVEVLHEHMDPIDGKLQQNHWPPIAAKYVSKAAVNAYTRIARKYPSFCINSVCPGEVRT TFSTILLQPNENAKGVFSSMDSLNLSKVVEVLHEHMDPIDGKLQQNHWPPIAAKYVSKAAVNAYTRIARKYPSFCINSVCPGEVRT	268 270
MpMR Unigene0041050	DICYNLGVLSAEGAEAPVKLALLPNSGPGSGFTSREALS DICYNLGVLSAEGAEAPVKLALLPNSGPGSGFTSREALS	310 312

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