

CLUSTAL O(1.2.4) multiple sequence alignment

BoMCM6_2	-----	0
BoMCM6_1	-----	0
AtMCM6	-----	0
BrMCM6	-----	0
ZmMCM6	-----	0
PsMCM6	-----	0
MCM6_Glyma09g05240	-----	0
MCM6_Glyma15g16570	-----	0
AtMCM2	MAGENS---DNEPSSPASPSSAGF-NTDQLPISTSQNS-----ENFSDEEEAAVDTQV	49
BoMCM2_1	MAGEDS---DNQPSS--PSSAGF-NTDQLPFCTSQNS-----ENFSDG-EAEVDPQV	45
BrMCM2_1	MAGEDS---DNQPSSPASPSSAGF-NTDQLPFSTSQNS-----ENFSDEEEAEVDPQV	49
BoMCM2_2	MAGEDS---DNQPSSPASPSSAGF-NTDQLPFSTSQNS-----ENISDE-EAEVDPQI	48
BrMCM2_2	MAGEDS---ENQPSSPASPSSAGF-NTDQLPFSTSQNS-----ENFSDE-EAEVDPQI	48
ZmMCM2	MDD--S---ENNAPS---TPGSPGF-STDRLPPNTTTSRGATDPSSYSDDDGEAEVDPHV	51
PsMCM2	MEPGIP---PSTPDSP-TSPSIGF-NTDQLPHTHTSR-----TSEDDEASVDPDI	45
MCM2_Glyma07g36680	-----MASDPESP-TSPSVGF-NTDQLPHTHTSR-----ASEDDEASVDPDI	40
MCM2_Glyma17g03920	MAPENP--STPDPESP-TSPSVGF-NTDQLPHTHTSH-----ASQDDEASVDPDI	46
ZmMCM5	-----	0
AtMCM5	-----	0
BoMCM5	-----	0
BrMCM5	-----	0
PsMCM5	-----	0
MCM5_Glyma13g22420	-----	0
MCM5_Glyma17g11220	-----	0
ZmMCM3	-----	0
AtMCM3	-----	0
BrMCM3_1	-----	0
BoMCM3	-----	0
BrMCM3_2	-----	0
MCM3_Glyma05g25980	-----	0
MCM3_Glyma08g08920	-----	0
PsMCM3	-----	0
AtMCM7	-----	0
BoMCM7_2	-----	0
BrMCM7_1	-----	0
BoMCM7_1	-----	0
BrMCM7_2	-----	0
ZmMCM7	-----	0
PsMCM7	-----	0
MCM7_Glyma03g37770	-----	0
MCM7_Glyma19g40370	-----	0
ZmMCM4	MASDGGGS-SPPPASSPYGRPSSPLAVTNSSPSQPT-----	35
AtMCM4	MASDSSLGNTNDGPPSPGENVSSPIENTYSSPAALH-----	36
BoMCM4	MASDSPPANTNDGPSSPGENASSPIGNTYSSPSLR-----	36
BrMCM4	MASDSPPANTNDGPSSPGENASSPIGNTYSSPSLR-----	36
MCM4_Glyma11g12110	MASDSSPPNFNNGPSSPDDSLSSPIGNTFSSPAS-----	34
MCM4_Glyma12g04320	MASDSSPLNFNNGPSSPDDSLSSPIGNTFSSPAS-----	34
PsMCM4	MASNSSPMDF--DPSSPDIPPSSPIPNTLSTPGR-----	32
BoMCM6_2	-----	0
BoMCM6_1	-----	0
AtMCM6	-----	0
BrMCM6	-----	0
ZmMCM6	-----	0
PsMCM6	-----	0
MCM6_Glyma09g05240	-----	0

MCM6_Glyma15g16570	-----	0
AtMCM2	IRDEPDE--AEDEEEEGEDLFNDTFMNDYRKMDENDQYESNGIDDSVDDERDLGQAML	106
BoMCM2_1	IRDEPED--EE--EEEGEDLFNDNFHQDYEKRDDQDQYESVGLDDSVVDDRGLGQIAL	100
BrMCM2_1	IRDEPED--E-----EEEGEDLFNDNFHQDYEKRDDQDQYESVGLDDSVVDNRGLGQIAL	106
BoMCM2_2	IRDEPEE--E--EEEDGEDLFNDNFLQDYGRDEQDQYESVGLDDSVDDDRDLGQIAL	102
BrMCM2_2	IRDEPEE---PEE--EEEDGEDLFNDNFLQDYGRDEQDQYESVGLDDSVDDDRDLGQIAL	104
ZmMCM2	LPDDDDPAAVAAPDEDEEGEDLFNDNYLDDYRRMDEHDQYESVGLDDSLIEDERNLDEIMA	111
PsMCM2	IRDEPE-----PEEDEDGEDLYNDNFLDYRRMDEADQFESVGLDDSVEDERDFDQIME	99
MCM2_Glyma07g36680	VRDEIE--EQPEE--EEDGEDLYNDNFLDDYKRMDEADQFESFGLDDSLIEDRDFDQIMQ	96
MCM2_Glyma17g03920	VRDDIE--EQPEEEEDGEDLYNDNFLDDYKRMDEADQFESFGLDDSLIEDRDFDQIMQ	103
ZmMCM5	-----	0
AtMCM5	-----	0
BoMCM5	-----	0
BrMCM5	-----	0
PsMCM5	-----	0
MCM5_Glyma13g22420	-----	0
MCM5_Glyma17g11220	-----	0
ZmMCM3	-----	0
AtMCM3	-----	0
BrMCM3_1	-----	0
BoMCM3	-----	0
BrMCM3_2	-----	0
MCM3_Glyma05g25980	-----	0
MCM3_Glyma08g08920	-----	0
PsMCM3	-----	0
AtMCM7	-----	0
BoMCM7_2	-----	0
BrMCM7_1	-----	0
BoMCM7_1	-----	0
BrMCM7_2	-----	0
ZmMCM7	-----	0
PsMCM7	-----	0
MCM7_Glyma03g37770	-----	0
MCM7_Glyma19g40370	-----	0
ZmMCM4	-----	35
AtMCM4	-----	36
BoMCM4	-----	36
BrMCM4	-----	36
MCM4_Glyma11g12110	-----	34
MCM4_Glyma12g04320	-----	34
PsMCM4	-----	32
BoMCM6_2	-----	0
BoMCM6_1	-----	0
AtMCM6	-----	0
BrMCM6	-----	0
ZmMCM6	-----	0
PsMCM6	-----	0
MCM6_Glyma09g05240	-----	0
MCM6_Glyma15g16570	-----	0
AtMCM2	DRRAADADLDARENRL--ANRKLPHLLHDN-DSDDWNYRPSKRSRRTTVPPRG-----N	156
BoMCM2_1	DRRAAEAVLDARESRL--ANRKLPHLLHDN-DSDDSNYRPSKRARAAVPPRG-----N	150
BrMCM2_1	DRRAAEAVLDARETRL--ANRKLPHLLHDN-DSDDSNYRPSKRARAAVPPRG-----N	156
BoMCM2_2	DRRAADAVLDARESRL--ANRKLPHLLHDNDSDDWNYRPSKRARAAVPPRD-----P	153
BrMCM2_2	DRRAADAVLDARESRL--ANRKLPHLLHDN-DSDEWNYRPSKRARAAVPPRG-----S	154
ZmMCM2	DRRAAEAVLDAREVRTGATADRKLPRLMLHDQDTDDDTNFRPKRHRASFRQPSGPRTPRS	171
PsMCM2	DRRAAEVELDTRDGRA--SNRTKLPQLLHDQDTDDDS-YRPSKRARADHRS---SVPPS	152
MCM2_Glyma07g36680	DRRAAEIELEARDGRA--SNRNKLPQLLHDQDTDDDN-HRSSKRARADFRP---SA-AS	148
MCM2_Glyma17g03920	DRRAAEVELEARDGRA--SNRNKLPQLLHDQDTDDDN-HRSSKRARADFRP---SV-AS	155
ZmMCM5	-----	0

BoMCM5	-----	0
BrMCM5	-----	0
PsMCM5	-----	0
MCM5_Glyma13g22420	-----	0
MCM5_Glyma17g11220	-----	0
ZmMCM3	-----	0
AtMCM3	-----	0
BrMCM3_1	-----	0
BoMCM3	-----	0
BrMCM3_2	-----	0
MCM3_Glyma05g25980	-----	0
MCM3_Glyma08g08920	-----	0
PsMCM3	-----	0
AtMCM7	-----	0
BoMCM7_2	-----	0
BrMCM7_1	-----	0
BoMCM7_1	-----	0
BrMCM7_2	-----	0
ZmMCM7	-----	0
PsMCM7	-----	0
MCM7_Glyma03g37770	-----	0
MCM7_Glyma19g40370	-----	0
ZmMCM4	RRSG-----GRRRRGSASPYASSPSLG-----GFE-----TPPHPGRRTPS-	71
AtMCM4	RRRR-----GRSSTPT-----QFA-----TPPPPSRLASS	62
BoMCM4	RRRR-----ARSSTPS-----QFA-----TPPP-PSRLGVP	61
BrMCM4	TRRR-----ARSSTPS-----QFA-----TPPP-PSRLGVP	61
MCM4_Glyma11g12110	-RRR-----RRSSTPS-----AFA-----TPSERRSRFASS	59
MCM4_Glyma12g04320	-RRR-----RRSSTPS-----AFA-----TPSERRSRFASS	59
PsMCM4	-RRR-----RQSTTPS-----AYG-----TPQPNRSRLASS	57
BoMCM6_2	-----	0
BoMCM6_1	-----	0
AtMCM6	-----	0
BrMCM6	-----	0
ZmMCM6	-----	0
PsMCM6	-----	0
MCM6_Glyma09g05240	-----	0
MCM6_Glyma15g16570	-----	0
AtMCM2	GGDPDGNPPS---SPGVS-----QPDISMTDQTDDYQEDDNDD	192
BoMCM2_1	GGDPDGNP-S---SPGTS-----LPDVSMTDQTDDYQED---D	182
BrMCM2_1	GRDPDGNP-S---SP-----LPDVSMTDQTDDYQED---D	185
BoMCM2_2	DGDPS-----S-----QPDVSMTDQTDDYQEDDNDD	180
BrMCM2_2	GGDPDGNP-S---SPGTS-----QPDVSMTDQTDDYQEDDNDD	189
ZmMCM2	DDDLGATPS---SPGRSHRG-----MSSGGDVPMTDQTDDDPYEDEFDE	213
PsMCM2	EDDLG-MNS---SPGRSQRG-----QHSRDDNPTTDQNEDDQYEDDFDD	193
MCM2_Glyma07g36680	DDDLG-MQS---SPGRSQRG-----HP-REDVLMTDQTEDDRDDDDFD-	187
MCM2_Glyma17g03920	DDDFDG-MQS---SPGRSQR-----HS-REDILMTDQTEDDRDDDDFD-	193
ZmMCM5	-----MSG-WDEGA-VFYSDQAQFPRG---G-----	21
AtMCM5	-----MSG-WDEGA-VYYS DQPQFP-----	18
BoMCM5	-----MSG-WDEGA-VYYS DQPQFP-----	18
BrMCM5	-----MSG-WDEGA-VYYS DQPQFP-----	18
PsMCM5	-----MSG-WDEGG-VYYS DQAHSWDD---G-----	21
MCM5_Glyma13g22420	-----MSG-WDEGA-VYYS DQALAGDD---G-----	21
MCM5_Glyma17g11220	-----MSG-WDEGA-VYYS DQALAGDD---G-----	21
ZmMCM3	-----	0
AtMCM3	-----	0
BrMCM3_1	-----	0
BoMCM3	-----	0
BrMCM3_2	-----	0

MCM3_Glyma05g25980	-----	0
MCM3_Glyma08g08920	-----	0
PsMCM3	-----	0
AtMCM7	-----	0
BoMCM7_2	-----	0
BrMCM7_1	-----	0
BoMCM7_1	-----	0
BrMCM7_2	-----	0
ZmMCM7	-----	0
PsMCM7	-----	0
MCM7_Glyma03g37770	-----	0
MCM7_Glyma19g40370	-----	0
ZmMCM4	GA-GAGAPR-----QPRQNSTGRFPPTPSTPMSTDDVPPSSSEAGDDET-----	113
AtMCM4	NS-TPPTSRPSAARSKGRNGHGGGGGGGGGDPGTPMSTDEPLPSSDDG-----	110
BoMCM4	SS-TPPTSRPSAARSN-----RPATPSHTDEPPSSDDG-----	94
BrMCM4	NS-TPPASRPSAARSN-----RPATPSHTDEPPSSDDG-----	94
MCM4_Glyma11g12110	DA-TPTAPRS-----RQRS---GGGRVPATSTSTTDDVPASSDG---G-----	95
MCM4_Glyma12g04320	DA-TPTAPRS-----RQRGGSGGGGHVPATPTSTTDDVPVSSDG---G-----	99
PsMCM4	DA-TPTPSRH-----RR-GGGIPSGRRVPATPTSTSDDIPMSSEG---G-----	96
BoMCM6_2	-----	0
BoMCM6_1	MEAFGGFV-----MDEQA-IQVENVFLEFLKSFRLDA-----NKPGLYY	38
AtMCM6	MEAFGGFV-----MDEQA-IQVENVFLEFLKSFRLDA-----NKPELYY	38
BrMCM6	MEAFGGFV-----MDEQA-IQVENVFLEFLKSFRLDA-----NKPELYY	38
ZmMCM6	MEAFGGFF-----VDEKA-ARVENIFLEFLKRFKESD-----GAGEPFY	38
PsMCM6	MEAFGGYL-----VDEKA-VRVENAFLDFLKSFRS-G-----QRNELYY	37
MCM6_Glyma09g05240	MEAYGGFM-----IDEKA-VRVENAFLDFLKSFKSSS-----HRNELYY	38
MCM6_Glyma15g16570	MEAYGGFM-----VDEKA-VRVENAFLDFLKSFKSSS-----QRNELYY	38
AtMCM2	EAEFEMYRIQGTLEWVVRDEVRRFIAKKFKDFLLTYVKPK-----NENGDI EY	241
BoMCM2_1	EAEFEMYRIQGSLEWVVRDEVRRFIAKKFRDFLLTYVKPN-----SENG--EY	229
BrMCM2_1	EAEFEMYRIQGSLEWVVRDEVRRFIAKKFRDFLLTYVKPN-----SENG--EY	232
BoMCM2_2	EAEFEMYRIQGSLEWVVRDEVRRFIAKKFRDFLLTFVKPN-----NENG--EY	227
BrMCM2_2	EAEFEMYRIQGSLEWVVRDEVRRFIAKKFRDFLLTYVKPN-----SENG--EY	236
ZmMCM2	EDEMNYRVQGTLEWVTRDEVRRFIAKKFKDFLLTYVHPK-----NDQGEFEY	262
PsMCM2	EAGYEMYRVQGTLEWVTRDEVRRFIARKFKDFLLTYVNPK-----NEHGDFEY	242
MCM2_Glyma07g36680	-DGYEMYHVQGTLEWVTRDEVRRFIARKFKDFLLTYVNPK-----NEHRDKEY	235
MCM2_Glyma17g03920	-DGYEMYHVQGTLEWVTRDEVRRFIARKFKDFLLTYLNPK-----NEHRDKEY	241
ZmMCM5	-PGGDP-A-----ADLTR-HSALRKFKFELRGFTGPT-----GDFPY	55
AtMCM5	---EAGDA-----ATISP-HAVLTKFKEFIRNFEIQ-----NCFPY	51
BoMCM5	---EAGDA-----ATVSP-HAVMTKFKEFIRTFEIQ-----NCFPY	51
BrMCM5	---EAGDA-----ATVSP-HAVMTKFKEFIRTFEIQ-----NCFPY	51
PsMCM5	-RGEA--E-----ATVSN-HTILQKFKEFIRNFETGN-----NVFPY	54
MCM5_Glyma13g22420	-SGARGE A-----GTDSN-HSLIQKFKEFIRNFETTN-----NVFPY	56
MCM5_Glyma17g11220	-AGARGE A-----GTDSN-HTLIQKFKEFIRNFETTN-----NVFPY	56
ZmMCM3	-----MEINE--EAMAAHKRAFDFLD-----QDVGKGVY	28
AtMCM3	-----MDVPE--ETRLRHKRDFIQFLD-----SMY	23
BrMCM3_1	-----MDVPE--ETRLRHKRDFIQFLE-----NIY	23
BoMCM3	-----MDVPE--ETRLRHKRDFIQFLE-----NIY	23
BrMCM3_2	-----MDVPE--ETRLRHKRDFIQFLE-----NIY	23
MCM3_Glyma05g25980	-----MDLSE--EVRAAHKREFSDFLD-----QDVGKGIY	28
MCM3_Glyma08g08920	-----MDLSE--EVRAAHKREFSDFLD-----QDVGKGIY	28
PsMCM3	-----	0
AtMCM7	-----MKD HDF-DGDKGLAKGFLENFADAN-----GRSKY	29
BoMCM7_2	-----MKEHDF-EADKALAKEFLANFTDAS-----GGSKY	29
BrMCM7_1	-----MKEHDF-EADKALAKEFLANFTYAS-----GGSKY	29
BoMCM7_1	-----MKEHDF-EADKAVAKEFLANFTDAN-----GRSKY	29
BrMCM7_2	-----MKEHDF-EADKAVAKEFLANFTDAN-----GRSKY	29
ZmMCM7	-----MKNPDF-AADKALAKDFLSNFTGPH-----GEPKY	29
PsMCM7	-----MNTKGVDF-ASDKVLASRFLSEFADAN-----GEAKY	31
MCM7_Glyma03g37770	-----MSAKNLNF-DADTALAKDFLSNFADAN-----GEAKY	31

MCM7_Glyma19g40370	-----MSTKDLNF-DADTALAKDFLSNFADAN-----GEAKY	31
ZmMCM4	-DGGGGVD-ATPVFVWGTNISV-QDVNAAILRFLRHFRDPRDAGR-----VDPVMDEGKY	165
AtMCM4	-EEDGGDD-TTPTFVWGTNISV-QDVKSAIEMFVKHFREARENS-----DDLRFREGKY	160
BoMCM4	-GEDGADD-ATPTFVWGTNISV-QDVKSAIEMFVKHFREAKESS-----DDLRFREGKY	144
BrMCM4	-GEDGADD-ATPTFVWGTNISV-QDVKSAIEMFVKHFREAKESS-----DDLRFREGKY	144
MCM4_Glyma11g12110	-DGFDMDD-ARPTFVWGTNISV-EDVNDAIKRFLRNFRDASSSQGGDNDGLHLHTEGKY	152
MCM4_Glyma12g04320	-DGFDMDD-ARPTFVWGTNISV-EDVNDAIKRFLRNFRDASSSQGGDDDDGLHLHTEGKY	156
PsMCM4	-DGYDMDD-AGPTYVWGTNISV-EDVNDAIQRFLKHFREQSTSQGDID---DLDTGKY	149
BoMCM6_2	-----	0
BoMCM6_1	EAEIEAIRGGES-TMMYIDFSHVMGFN-----DALQKAIADERYLRFEPYLRNACKRFVI	91
AtMCM6	EAEIEAIRGGES-TMMYIDFSHVMGFN-----DALQKAIADERYLRFEPYLRNACKRFVI	91
BrMCM6	EAEIEAIRGGES-TMMYIDFSHVMGFN-----DALQRAIADERYLRFEPYVRNACKRFVI	91
ZmMCM6	EAEMEVMRSRES-TTMYVDFAHVMRFN-----DVLQKAISEEYLRFEYLRNACKRFAL	91
PsMCM6	EAEIEVMRANES-NTMFIDFEHVIRFS-----DLLQKAISDEYLRFEYLRNACKRFVM	90
MCM6_Glyma09g05240	EAEIELMKSNDN-NTMFVDFDHVIRFS-----DLLQQTISDEYLRFEYLRNACKRRLVM	91
MCM6_Glyma15g16570	EAEIELMKSNDN-NTMFIDFDHVIRFS-----DLLQQTISDEYLRFEYLRNACKRFVM	91
AtMCM2	VRLINEMVSANK-CSLEIDYKEFIHVH-----PNIAIW-LADAPQPVLEVMEEVSEKVI	294
BoMCM2_1	VRLINEMVSANK-CSLEIDYKEFIHVH-----PNIAIW-LADAPQPVLEVMEEVSEKVI	282
BrMCM2_1	VRLINEMVSANK-CSLEIDYKEFIHVH-----PNIAIW-LADAPQPVLEVMEEVSEKVI	285
BoMCM2_2	VRLINEMVSANK-CSLEIDYKEFIHVH-----PNIAIW-LADAPQPVLEVMEEVSEKVI	280
BrMCM2_2	VRLINEMVSANK-CSLEIDYKEFIHVH-----PNIAIW-LADAPQPVLEVMEEVSEKVI	289
ZmMCM2	VRLINEMVLANK-CSLEIDYKQFIYIH-----PNIAIW-LADAPQSVLEVMEEVAKNVVF	315
PsMCM2	VRLINEMVSANK-CSLEIDYKQFIYVH-----PNIAIW-LADAPHSVLEVMEDVAKSVVF	295
MCM2_Glyma07g36680	VWLNEMVSASK-CSLEIDYKQFIYVH-----PNIAIW-LADAPQSVLEVMEDVTKSVVF	288
MCM2_Glyma17g03920	VWLNEMVSASK-CSLEIDYKQFIYVH-----PNIAIW-LADAPQSVLEVMEDVTKNVVF	294
ZmMCM5	R---ESLVHNR-DHVTVAIEDLDAFD-----AELSDK-IRKSPADYLPVFEKAAEVL	104
AtMCM5	R---EALLDNP-KRLVHLEDLLSFD-----SDLPSL-IRSAPADYLPVFEKAAEVL	100
BoMCM5	R---EALLDNP-KRLVHLEDLLSFD-----SDLPSL-IRSAPADYLPVFEKAAEVL	100
BrMCM5	R---EALLDNP-KRLVHLEDLLSFD-----SDLPSL-IRSAPADYLPVFEKAAEVL	100
PsMCM5	R---ESLLNNP-KFLVIDMEDLDSFD-----PDLPSK-LRSAPADYLPVFEKAAEVL	103
MCM5_Glyma13g22420	R---ESLLHNP-KFLVDMGDLDTFD-----SDLPSK-LRSNPADYLPVFEKAAEVL	105
MCM5_Glyma17g11220	R---ESLIHNP-KFLVDMGDLDTFD-----SELPK-LRSNPADYLPVFEKAAEVL	105
ZmMCM3	MQAVRDMVQNK-HRLIINISDIHHHF---REV---ASR-ILKNPNEYMQSFCDAAEATR	81
AtMCM3	MDEIKALVQNK-HRLIVNVDIHTHF---RESESSR-ILKNPIEYMQSFCDAAEATR	76
BrMCM3_1	MDEIKALVQNK-HRLIVNVDIHTHF---RESESSR-ILKNPIEYMQSFCDAAEATR	78
BoMCM3	MDEIKALVQNK-HRLIVNVDIHTHF---RESESSR-ILKNPIEYMQSFCDAAEATR	78
BrMCM3_2	MDEIKALVQNK-HRLIVNVDIHTHF---RESESSR-ILKNPIEYMQSFCDAAEATR	78
MCM3_Glyma05g25980	MDEIKTLINLKR-HRLIVNISDLHNF---R---DLGSR-ILRSPSEYMQPFCDAVTEATR	80
MCM3_Glyma08g08920	MDEIKTLINLKR-HRLIVNISDLHNF---R---DLGSR-ILRSPSEYMQPFCDAVTEATR	80
PsMCM3	-----MQSFCDAVTDAVR	13
AtMCM7	MEILQEVSNRKI-RAIQVDLDDLFNYKD---ESEFLGR-LTENTRRYVSIFSAVDELDP	85
BoMCM7_2	LEILQEVANRKS-RAIQVDLQDLINYGDFEFHEFMTR-LTENTRRYVSIFSSAIDELDP	87
BrMCM7_1	LEILQEVANRKT-RAIQVDLQDLINYGDFEFHEFMTR-LTENTRRYVSIFSSAIDELDP	87
BoMCM7_1	LEILQEVANRKV-RAIQIDLQDLINDKGFDDFHEFIGR-LTENTRRYVSIFSSAIDELDP	87
BrMCM7_2	LEILQEVANRKV-RAIQIDLQDLINDKGFDDFHEFIGR-LTENTRRYVSIFSSAIDELDP	87
ZmMCM7	LNILQDVANRKI-RAVQIELDDLFHYKDVD---EFLQR-VTENTRRYIGIFAEAMDELMP	85
PsMCM7	INILQDVANHKT-RSVEIDLDDLMNYKDL---EFLTR-VTENTRRYVIGIFADAIDELMP	87
MCM7_Glyma03g37770	MNILQDVANHKT-RAVQIDLEDLFNYKDL---EFLSR-VTDNTRRYIGIFSNAIDELMP	87
MCM7_Glyma19g40370	MNILQDVANHKT-RAVQIDLEDLFNYKDL---EFLSR-VTDNTRRYIGIFSNAIDELMP	87
ZmMCM4	MRAIHRILELEGESLDVDAHDFDHD---PDLYSK-MVRYPLEVLAIFDIV-----	213
AtMCM4	MVSIRKVIEWEG-EWIDVDAFVDFDYD---PDLYNK-MVRYPLEVLAIFDIV-----	207
BoMCM4	MASIRKVIEWEG-EWIDVDAYDFDYD---PDLYNK-MVRYPLEVLAIFDIV-----	191
BrMCM4	MASIRKVIEWEG-EWIDVDAYDFDYD---PDLYNK-MVRYPLEVLAIFDIV-----	191
MCM4_Glyma11g12110	EKLIRQVIEVEG-DSLVDVARDVDFHD---PDLYTK-MVRYPLEVLAIFDLV-----	199
MCM4_Glyma12g04320	EKLIRQVIDVEG-DSLVDVARDVDFHD---PDLYTK-MVRYPLEVLAIFDLV-----	203
PsMCM4	EKLIRQVIELEG-ESIDVDARDVDFHD---PDLYTK-MVRYPLEVLAIFDMV-----	196
BoMCM6_2	-----MNPE-----TPNKDINVSFYN	16

BoMCM6_1	EMN----PSFISDE-----TPNKDINVSFYN	113
AtMCM6	EMN----PSFISDD-----TPNKDINVSFYN	113
BrMCM6	EMN----PSFVSD-----TPNKDINVSFYN	113
ZmMCM6	EHRAGENRAPLISDD-----SPNKDINIAFYN	118
PsMCM6	ELK----PTFISDD-----NPNKDINVAFYN	112
MCM6_Glyma09g05240	DLK----PSIVSDD-----SPDKDINIAFYN	113
MCM6_Glyma15g16570	DLK----PSLVSDD-----SPDKDINIAFYN	113
AtMCM2	DLH----PNYKNI-----HTKIYVRVTN	313
BoMCM2_1	DLH----PNYKNI-----HQKIYVRVTN	301
BrMCM2_1	DLH----PNYKNI-----HQKIYVRVTN	304
BoMCM2_2	DLH----PNYKNI-----HQKIYVRVTN	299
BrMCM2_2	DLH----PNYKNI-----HQKIYVRVTN	308
ZmMCM2	DLH----KNYRNI-----HQKIYVRISN	334
PsMCM2	QLH----PNYKHI-----HQKIYVRITN	314
MCM2_Glyma07g36680	ELH----PNYRNI-----HQKIYVRITN	307
MCM2_Glyma17g03920	ELH----PNYRNI-----HQKIYVRITN	313
ZmMCM5	SLR----SKVAGET-----GEMEEPVTGVDVQIFLSS	131
AtMCM5	GLK----MREANEG-----GVMEEPLTRDVQILLTS	127
BoMCM5	GLR----MREANET-----GEMEEPTPSDVQILLTS	127
BrMCM5	GLR----MREANET-----GEMEEPTPSDVQILLTS	127
PsMCM5	NLK----TKVAGDT-----GVMEDAAPGDVQILLTS	130
MCM5_Glyma13g22420	NLK----TKVAGDT-----GDMEDQTPGDVQILLTS	132
MCM5_Glyma17g11220	NLK----TKVAGDT-----GDMEDQTPGDVQILLTS	132
ZmMCM3	NLD----PKFLKEGER-----VMV----GFSG----PF	102
AtMCM3	AID----PKYLKEGEL-----VLV----GFEG----YF	97
BrMCM3_1	NID----PKYLKEGEQ-----VLV----GFEG----HF	99
BoMCM3	NID----PKYLKEGEQ-----VLV----GFEG----HF	99
BrMCM3_2	NID----PKYLKEGEQ-----VLV----GFEG----HF	99
MCM3_Glyma05g25980	AID----PKYLKEGEQ-----VLV----GFEG----PF	101
MCM3_Glyma08g08920	AID----PKYLKEGEQ-----VLV----GFEG----PF	101
PsMCM3	AID----PKYLKEGEH-----VLV----GLEG----PF	34
AtMCM7	EPT----EAFP-DDDHDILMTQRADDGTD-NPDVSDPHQQIPSEIKRYYEVYFK--APS	136
BoMCM7_2	EPT----EAFP-DDDHDILMTQRADDGTD-NADVSDPRQQIPSEIKRFYEVYFK--APS	138
BrMCM7_1	EPT----EAFP-DDDHDILMTQRADDGTD-NADVSDPRQQIPSEIKRFYEVYFK--APS	138
BoMCM7_1	EPT----EAFP-DDDHDILMTQRADGAD-NADVSDPRQQIPSEIKRFYEVYFK--APS	138
BrMCM7_2	EPT----EAFP-DDDHDILMTQRADDGAD-NADVSDPRQQIPSEIKRFYEVYFK--APS	138
ZmMCM7	EPT----EAYTVDEDDQDILMTQRVDEGADGGADGTDPLQKMPPEIKRFFEVYIK--AFS	138
PsMCM7	EPT----EAFI-DDDHDILMTQRSDEGTE-GADGSDPHQKMPSEIKRFFEVYVK--ASS	138
MCM7_Glyma03g37770	EPT----EDFT-DDDHDILMTQRSDEGVE-GTDGSDPRQKMPPEIKRYYELYIK--ASS	138
MCM7_Glyma19g40370	EPT----EDFT-DDDHDILMTQRSDEGAE-GTDGSDPRQKMPAEIKRYYELYIK--ASS	138
ZmMCM4	-----LMDLVARIEPLFEKHIQTRIYN	235
AtMCM4	-----LMDIVSTINRLFVKHVQVRIFN	229
BoMCM4	-----LMDIVSSIDRLFVKHVQVRIFN	213
BrMCM4	-----LMDIVSSIDRLFVKHVQVRIFN	213
MCM4_Glyma11g12110	-----LMNMVSELKPMFEKHIQTRIFN	221
MCM4_Glyma12g04320	-----LMNMVSELKPMFEKHIQTRIFN	225
PsMCM4	-----LMNMVTRMKPMFEKHVQTRIFN	218
BoMCM6_2	LPFTKRLRELTTAIEIGKLVSVTGVVTRTSEVRPELLYGTFKCLDCGSVIKNVEQQ--FKY	74
BoMCM6_1	LPFTKRLRELTTSIEIGKLVSVTGVVTRTSEVRPELLYGTFKCLDCGSVIKNVEQQ--FKY	171
AtMCM6	LPFTKRLRELTTAIEIGKLVSVTGVVTRTSEVRPELLYGTFKCLDCGSVIKNVEQQ--FKY	171
BrMCM6	LPFTKRLRELTTSIEIGKLVSVTGVVTRTSEVRPELLYGTFKCLDCGSVIKNVEQQ--FKY	171
ZmMCM6	IPMLKKLRELGTAEIGKLTVMGVVTRTSEVRPELLQGTFFKCLDCGNVKNVEQQ--FKY	176
PsMCM6	IPIVKRLRELATSEIGRLVSVTGVVTRTSEVRPELLQGTFFKCLECGGVKNVEQQ--FKY	170
MCM6_Glyma09g05240	MPIVKRLRELGTSEIGRLVSVTGVVTRTSEVRPELLQGTFFKCLECGGVKNVEQQ--FKY	171
MCM6_Glyma15g16570	MPIVKRLRELGTSEIGRLVSVTGVVTRTSEVRPELLHGTFFKCLECGGVKNVEQQ--FKY	171
AtMCM2	LPVNDQIRNIRQIHLNMTMIRIGGVVTRRSVFPQLQOVKYDCNKCGAVLGPFFQNS-YSE	372
BoMCM2_1	LPVNDQIRNIRQIHLNMTMIRIGGVVTRRSVFPQLQOVKYDCNKCGAILGPFFQNS-YSE	360
BrMCM2_1	LPVNDQIRNIRQIHLNMTMIRIGGVVTRRSVFPQLQOVKYDCNKCGAILGPFFQNS-YSE	363
BoMCM2_2	LPVNDQIRNIRQIHLNMTMIRIGGVVTRRSVFPQLQOVKYDCNKCGAVLGPFFQNS-YSE	358

BrMCM2_2	LPVNDQIRNIRQIHLNTMIRIGGVVTRRSGVFPQLQQVKYDCNKCGAVLGPFFQNS-YSE	367
ZmMCM2	LPVYDQIRNIRQIHLNTMIRIGGVVTRRSGVFPQLQQVKYDCNKCGTILGPFFQNS-YTE	393
PsMCM2	LPVYDQIRNIRQIHLNTMIRIGGVVTRRSGVFPQLQQVKYDCNKCGAILGPFFQNS-YSE	373
MCM2_Glyma07g36680	LPVYDQIRNIRQIHLNTMIRIGGVVTRRSGVFPQLQQVKYDCNKCGAILGPFFQNS-YSE	366
MCM2_Glyma17g03920	LPVYDQIRNIRQIHLNTMIRIGGVVTRRSGVFPQLQQVKYDCNKCGAILGPFFQNS-YSE	372
ZmMCM5	KENCLSMRSVGDYMSKLVKIAGIAIAASRVKAKATHVTLICKNCRSVRTPVCRPGLGGA	191
AtMCM5	REDPVMRLLGAQYISKLVKISGISIAASRVKAKATYVFLVCKNCKKTRVPCRPGLGGA	187
BoMCM5	REDPVMRLLGAQYISKLVKISGISIAASRVKAKATYVFLVCKNCKKTRVPCRPGLGGA	187
BrMCM5	REDPVMRLLGAQYISKLVKISGISIAASRVKAKATYVFLVCKNCKKTRVPCRPGLGGA	187
PsMCM5	KEDLSMRSLGAQYISKLVKIAGITIAASRTKAKATYVTLICKNCKKQVPCRPGLGGA	190
MCM5_Glyma13g22420	KEDPVMRSLGAQYISKLVKIAGITIAASRTKAKATYVTLICKNCKKQVPCRPGLGGA	192
MCM5_Glyma17g11220	KEDPVMRSLGAQYISKLVKIAGITIAASRTKAKATYVTLICKNCKKQVPCRPGLGGA	192
ZmMCM3	GFHRVTPRDLMSFFIGTMVCEGIVTKCSLVRPKVVKSVHFPCVTDGFLSREYRD-ITSF	161
AtMCM3	VSRVTPRELLSDFIGSMVCEGIVTKCSLVRPKVVKSVHFPCSTGEFTNRDYRD-ITSH	156
BrMCM3_1	VSRVTPRELLSEFIGSLVCEGIVTKCSLVRPKVVKSVHFPCSTGEFTNREYRD-ITSH	158
BoMCM3	VSRVTPRELLSEFIGSLVCEGIVTKCSLVRPKVVKSVHFPCSTGEFTNREYRD-ITSH	158
BrMCM3_2	VSRVTPRELLSEFIGSLVCEGIVTKCSLVRPKVVKSVHFPCSTGEFTNREYRD-ITSH	158
MCM3_Glyma05g25980	VSRVTPRDLLSQFIGSMVCEGIVTKCSLVRPKVVKSVHFCPTTGSFTSREYRD-ITSN	160
MCM3_Glyma08g08920	VSRVTPRELLSEFIGSMVCEGIVTKCSLVRPKVVKSVHFCPTTGSFTSREYRD-ITSN	160
PsMCM3	VSRVTPRDLLSEFIGSMVCEGIIITKCSLVRPKVVKSVHFCPTTGSFTSRDYRD-ITSN	93
AtMCM7	KGRPSTIREVKASHIGQLVRIISGIVTRCSDVKPLMAVAVYTCEDCGHEIYQEVTS-RV-F	194
BoMCM7_2	KGRPSTIREVKASHIGQLVRIAGIVTRCSDVKPLMAVAVYTCEDCGHEIYQEVTS-RV-F	196
BrMCM7_1	KGRPSTIREVKASHIGQLVRIAGIVTRCSDVKPLMAVAVYTCEDCGHEIYQEVTS-RV-F	196
BoMCM7_1	KGRPSTIREVKASHIGQLVRIAGIVTRCSDVKPLMAVAVYTCEDCGHEIYQEVTS-RV-F	196
BrMCM7_2	KGRPSTIREVKASHIGQLVRIAGIVTRCSDVKPLMAVAVYTCEDC-----VTS-RV-F	189
ZmMCM7	KVTPLTIRQVKASNIGQLVKISGIVTRCSDVKPLMQVAVYTCCECGFEIYQEVTA-RV-F	196
PsMCM7	KGRPFTIREVKASNIGQLVRLAGIVTRCSDVKPLMQVAVYTCEDCGFEIYQEVTA-RI-F	196
MCM7_Glyma03g37770	KGRPSTIREVKASNIGQLVRIISGIVIRCSADVPLMKVAVYTCEDCGFEIYQEVTA-RV-F	196
MCM7_Glyma19g40370	KGRPSTIREVKALNIGQLVRIISGIVTRCSDVKPLMKVAVYTCEDCGFEIYQEVTA-RV-F	196
ZmMCM4	LKSSICLRNLPNSDIEKMVSIKGMIIIRSSSIPEIREAVFRCLVCGYFSDPIIVD-RGKI	294
AtMCM4	LRTSTSMRNLNPSDIEKMISLKGMIIRSSSIPEIREAVFRCLVCGYFSDPIIVD-RGKI	288
BoMCM4	LRSSTSMRNLNPSDIEKMISLKGMIIRSSSIPEIREAVFRCLVCGYFSDPIIVD-RGKI	272
BrMCM4	LRSSTSMRNLNPSDIEKMISLKGMIIRSSSIPEIREAVFRCLVCGYFSDPIIVD-RGKI	272
MCM4_Glyma11g12110	LRNSTSMRNLNPSDIERMVSLKGMVIRSSSIPEIREAIFRCLVCGFCSEPPVPE-RGRI	280
MCM4_Glyma12g04320	LRTSTSMRNLNPSDIERMVSLKGMVIRSSSIPEIREAIFRCLVCGFCSEPPVPE-RGRI	284
PsMCM4	LKTSTSMRNLNPSDVERMISMKGMIIRSSSIPEIREAIFRCLVCGYCSDPVLVE-RGRI	277

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BoMCM6_2	TQP-----TICVSPTCLNR----ARWALLRQESKFADWQRVRMQETSKEIPAGSLPRSL	124
BoMCM6_1	TQP-----TICVSPTCLNR----ARWALLRQESKFADWQRVRMQETSKEIPAGSLPRSL	221
AtMCM6	TQP-----TICVSPTCLNR----ARWALLRQESKFADWQRVRMQETSKEIPAGSLPRSL	221
BrMCM6	TQP-----TICVSPTCLNR----ARWALLRQESKFADWQRVRMQETSKEIPAGSLPRSL	221
ZmMCM6	TEP-----IICVNATCQNR----TKWALLRQESKFADWQRVRMQETSKEIPAGSLPRSL	226
PsMCM6	TEP-----TICPNATCNR----TRWALLRQESKFADWQRVRMQETSKEIPAGSLPRSL	220
MCM6_Glyma09g05240	TEP-----TICTNATCSNR----TRWVLLRQESKFADWQRVRMQETSKEIPAGSLPRSL	221
MCM6_Glyma15g16570	TEP-----TICANATCSNR----TRWVLLRQESKFADWQRVRMQETSKEIPAGSLPRSL	221
AtMCM2	V-----KVGSCSECQSK----GPFVNVVEQTIYRNYQKLTIQESPGTVPAGRLPRHK	420
BoMCM2_1	V-----KVGSCSECQSK----GPFVNVVEQTIYRNYQKLTIQESPGTVPAGRLPRHK	408
BrMCM2_1	V-----KVGSCSECQSK----GPFVNVVEQTIYRNYQKLTIQESPGTVPAGRLPRHK	411
BoMCM2_2	V-----KVGSCSECQSK----GPFVNVVEQTIYRNYQKLTIQESPGTVPAGRLPRHK	406
BrMCM2_2	V-----KVGSCSECQSK----GPFVNVVEQTIYRNYQKLTIQESPGTVPAGRLPRHK	415
ZmMCM2	V-----KVGSCPECQSK----GPFVNVVEQTIYRNYQKLTQLQESPGIVPAGRLPRYK	441
PsMCM2	V-----KVGSCPECQSK----GPFVNVVEQTIYRNFQKLTQLQESPGIVPAGRLPRYK	421
MCM2_Glyma07g36680	V-----KVGSCPECQSK----GPFVNVVEQTIYRNFQKLTQLQESPGIVPAGRLPRYK	414
MCM2_Glyma17g03920	V-----KVGSCPECQSK----GPFVNVVEQTIYRNFQKLTQLQESPGIVPAGRLPRYK	420
ZmMCM5	IVPRSCDHVPQPGEEPCLD-----PWIAVPDKSKYVDLQTLKLQENPEDVPTGELPRNV	246
AtMCM5	IVPRSCDNIPQPGEEPCLD-----PWMVVPDRSQYVDQTLKLQENPEDVPTGELPRNM	242
BoMCM5	IVPRSCDHVPQPGEEPCLD-----PWMVVPDRSQYVDQTLKLQENPEDVPTGELPRNM	242
BrMCM5	IVPRSCDHVPQPGEEPCLD-----PWMVVPDRSQYVDQTLKLQENPEDVPTGELPRNM	242
PsMCM5	VVPRSCDHVPQPGEEPCLD-----PWLIVPDKSKYVDQTLKLQENPEDVPTGELPRNL	245
MCM5_Glyma13g22420	IVPRSCDHVPQPGEEPCLD-----PWLIVPDKSKYVDQTLKLQENPEDVPTGELPRNL	247

MCM5_Glyma17g11220	I V P R S C D H V P Q P G E E P C I D ----- P W L V V P D K S R Y V D Q Q T L K M Q E N P E D V P T G E L P R N L	247
ZmMCM3	V G L ----- P T G S -- V Y P T R D D N G N L L V T E Y G M C E Y K D H Q T L S I Q E V P E N A A P G Q L P R T V	213
AtMCM3	A G L ----- P T G S -- V Y P T R D D K G N L L V T E Y G L C K Y K D H Q T L S I Q E V P E N A A P G Q L P R S V	208
BrMCM3_1	A G L ----- P T G S -- V Y P T R D D N G N L L V T E Y G L C K Y K D H Q T M S I Q E V P E N A A P G Q L P R S V	210
BoMCM3	A G L ----- P T G S -- V Y P T R D D N G N L L V T E Y G L C K Y K D H Q T L S I Q E V P E N A A P G Q L P R S V	210
BrMCM3_2	A G L ----- P T G S -- V Y P T R D D N G N L L V T E Y G L C K Y K D H Q T L S I Q E V P E N A A P G Q L P R S V	210
MCM3_Glyma05g25980	L G L ----- P T G S -- V Y P T R D E N G N L L V T E F G L C K Y K D H Q T L S I Q E V P E N S A P G Q L P R T V	212
MCM3_Glyma08g08920	L G L ----- P T G S -- V Y P T R D E N G N L L V T E F G L C K Y K D H Q T L S I Q E V P E N S A P G Q L P R T V	212
PsMCM3	L G L ----- P T G S -- V Y P T R D E N G N L L V T E Y G L C K Y K D H Q T L S M Q E V P E N S A P G Q L P R T V	145
AtMCM7	M P L ----- F K C P S S R C R L N - S K A G N P I L Q L R A S K F L K F Q E A K M Q E L A E H V P K G H I P R S M	247
BoMCM7_2	M P L ----- F K C P S S R C R V N - S K A G N P I L Q L R A S K F L K F Q E A K M Q E L A E H V P K G H I P R S M	249
BrMCM7_1	M P L ----- F K C P S S R C R V N - S K A G N P I L Q L R A S K F L K F Q E A K M Q E L A E H V P K G H I P R S M	249
BoMCM7_1	M P L ----- F K C P S S R C R V N - S K A G N P I L Q L R A S K F L K F Q E A K M Q E L A E H V P K G H I P R S M	249
BrMCM7_2	M P L ----- F K C P S S R C R V N - G K S G N P I L Q L R A S K F L K F Q E A K M Q E L A E H V P K G H I P R S M	242
ZmMCM7	M P L ----- I E C P S Q R C K L N - K A K G N L I L Q L R A S K F L K F Q E V K L Q E L A E H V P K G H I P R A L	249
PsMCM7	M P L ----- F E C P S R R C V M N - K N K G N V I L Q L R A S K F L R F Q E A K I Q E L A E H V P K G H I P R T M	249
MCM7_Glyma03g37770	M P L ----- F E C P S K R C D T N - R R K G N V I L Q L R A S K F L R F Q E A K I Q E L A E H V P K G H I P R T M	249
MCM7_Glyma19g40370	M P L ----- F E C P S K R C D T N - R R K G N V I L Q H R A S K F L R F Q E A K I Q E L A E H V P K G H I P R T M	249
ZmMCM4	T E P ----- H I C Q K E Q C K A T ----- N S M T L V H N R C R F S D K L I I K L Q E T P D E I P E G G T P H T V	344
AtMCM4	S E P ----- P T C L K Q E C M T K ----- N S M T L V H N R C R F A D K Q I V R L Q E T P D E I P E G G T P H T V	338
BoMCM4	S E P ----- P T C L K Q E C L A K ----- N S M T L V H N R C R F A D K Q I V R L Q E T P D E I P E G G T P H T V	322
BrMCM4	S E P ----- P T C L K Q E C L A K ----- N S M T L V H N R C R F A D K Q I V R L Q E T P D E I P E G G T P H T V	322
MCM4_Glyma11g12110	T E P ----- T I C L K E E C Q S R ----- N S M T L V H N R C R F A D K Q I V R V Q E T P D E I P E G G T P H T V	330
MCM4_Glyma12g04320	T E P ----- T I C L R E E C Q S R ----- N S M A L V H N R C R F A D K Q I V R V Q E T P D E I P E G G T P H T V	334
PsMCM4	A E P ----- T V C L R E E C Q S R ----- N S M T L V H N R C K F T D K Q I V R L Q E T P D E I P E G G T P H T V	327

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BoMCM6_2	D V I L R H E I V E Q A R A G D T V I F T G A V I V L P D I S A M A S P G E R A E C R R D S S Q Q K S S T A G H E G F K	184
BoMCM6_1	D V I L R H E I V E Q A R A G D T V I F T G T V V V I P D I S A L A A P G E R A E C R R D S S Q Q K S S T A G H E G V K	281
AtMCM6	D V I L R H E I V E Q A R A G D T V I F T G T V V V I P D I S A L A A P G E R A E C R R D S S Q Q K S S T A G H E G V Q	281
BrMCM6	D V I L R H E I V E Q A R A G D T V I F T G T V V V I P D I S A L A A P G E R A E C R R D S S Q Q K S S T A G H E G V K	281
ZmMCM6	D V I L R H E I V E K A R A G D T V I F T G T V V A V P D V M A L T S P G E R A E C R R E A P Q R K N G - G V Q E G V K	285
PsMCM6	D V I L R H E I V E H A R A G D T V I F T G T V I V I P D I L A L A S P G E R S E C R R E A S Q R K G S S S G N E G V R	280
MCM6_Glyma09g05240	D V I L R H E I V E Q A R A G D T V I F T G T V V A I P D I M A L A S P G E R S E C R R D A S Q R K G S T A G N E G V S	281
MCM6_Glyma15g16570	D I I L R H E I V E H A R A G D T V I F T G T V V V I P D I M A L A S P G E R S E C R R D A S Q R K G S T A G N E G V S	281
AtMCM2	E V I L L N D L I D C A R P G E E I E V T G I Y T N N F D L S L N -- T ----- K N G F	458
BoMCM2_1	E V I L L N D L I D C A R P G E E I E V T G I Y T N N F D L S L N -- T ----- K N G F	446
BrMCM2_1	E V I L L N D L I D C A R P G E E I E V T G I Y T N N F D L S L N -- T ----- K N G F	449
BoMCM2_2	E V I L L N D L I D C A R P G E E I E V T G I Y T N N F D L S L N -- T ----- K N G F	444
BrMCM2_2	E V I L L N D L I D C A R P G E E I E V T G I Y T N N F D L S L N -- T ----- K N G F	453
ZmMCM2	E V I L L N D L I D C A R P G E E I E V T G I Y T N N F D L S L N -- T ----- K N G F	479
PsMCM2	E V I L L N D L I D C A R P G E E I E V T G I Y T N N F D L S L N -- T ----- K N G F	459
MCM2_Glyma07g36680	E V I L L N D L I D C A R P G E E I E V T G V Y T N N F D L S L N -- T ----- K N G F	452
MCM2_Glyma17g03920	E V I L L N D L I D C A R P G E E I E V T G V Y T N N F D L S L N -- T ----- K N G F	458
ZmMCM5	L L S V D R H L V Q T I V P G T R L T V V G I Y S V Y Q A S T -- T Q ----- K G A V	283
AtMCM5	L L S V D R H L V Q T I V P G T R L T V M G I Y S I F Q A S S S S N S H ----- K G A V	282
BoMCM5	L L S V D R H L V Q L I V P G T R L T V M G I Y S I F Q A S S S S N S H ----- K G A V	282
BrMCM5	L L S V D R H L V Q L I V P G T R L T V M G I Y S I F Q A S S S S N S H ----- K G A V	282
PsMCM5	L L S V D R H L V Q T V V P G P R L T I V G I Y S I F Q A S N S S T S N ----- K G A V	285
MCM5_Glyma13g22420	L L S V D R H L V Q T V V P G S R L T I M G I F S I Y Q A S N S N T S H ----- K G A V	287
MCM5_Glyma17g11220	L L S L D R H L V Q T V V P G S R L T I M G I F S I Y Q A S N S N T S N ----- K G A V	287
ZmMCM3	D V I V E D D L V D C K P G D R V S I V G V Y K A L P G K ----- S K ----- G S V S	249
AtMCM3	D V I A E D D L V D S C K P G D R V S V F G I Y K A L P G K ---- S K ----- G S V N	244
BrMCM3_1	D V I A E D D L V D S C K P G D R V A V V G I Y K A L P G K ---- S K ----- G S V N	246
BoMCM3	D V I A E D D L V D S C K P G D R V A I V G I Y K A L P G K ---- S K ----- G S V N	246
BrMCM3_2	D V I A E D D L V D S C K P G D R V A I V G I Y K A L P G K ---- S K ----- G S V N	246
MCM3_Glyma05g25980	D V I A E D D L V D S C K P G D R V A I V G I Y K A L A G K ---- S K ----- G S V N	248
MCM3_Glyma08g08920	D V I A E D D L V D S C K P G D R V A I V G I Y K A L A G K ---- S K ----- G S V N	248
PsMCM3	D V I A E D D L V D S C K P G D R V A I V G I Y K A L P G K ---- S K ----- G S V N	181
AtMCM7	T V H L R G E L T R K V S P G D V V E F S G I F L P I P Y T G F K -- A ----- L R A G	285
BoMCM7_2	T V H L R G E L T R K V A P G D V V E F S G I F L P I P Y T G F K -- A ----- L R A G	287

BrMCM7_1	TVHLRGELTRKVAPGDVVEFSGIFLPIPYTGFK--A-----LRAG	287
BoMCM7_1	TVHLRGELTRKVAPGDVVEFSGIFLPIPYTGFK--A-----LRAG	287
BrMCM7_2	TVHLRGELTRKVAPGDVVEFSGIFLPIPYTGFK--A-----LRAG	280
ZmMCM7	TVHLRGELTRKVAPGDVVEMSGIFLPMPIYGF--A-----MRAG	287
PsMCM7	TVHLRGELTRKVAPGDVVELSGIFLPIPYVGF--A-----MRAG	287
MCM7_Glyma03g37770	TVHLRGELTRKVAPGDVVEFSGIFLPIPYTGFR--A-----MRAG	287
MCM7_Glyma19g40370	TVHLRGELTRKVAPGDVVELSGIFLPIPYTGFR--A-----MRAG	287
ZmMCM4	SVLMHDKLVDAGKPGDRVEITGIYRAMSIRIGP-TQ-----RTVK	383
AtMCM4	SLLLHDKLVDNGKPGDRIEVTGIYRAMTVRVGP-AH-----RTVK	377
BoMCM4	SLLLHDKLVDNGKPGDRIEVTGIYRAMTVRVGP-AH-----RT--	359
BrMCM4	SLLLHDKLVDNGKPGDRIEVTGIYRAMTVRVGP-AH-----RT--	359
MCM4_Glyma11g12110	SLLMHDKLVDNAKPGDRVEVTGIYRAMSVRIGP-TQ-----RTVK	369
MCM4_Glyma12g04320	SLLMHDKLVDNAKPGDRVEVTGIYRAMSVRIGP-TQ-----RTVK	373
PsMCM4	SLLMHDKLVDGKPGDRVEVTGIYRAMSVRIGP-TQ-----RSVK	366

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BoMCM6_2	GLKALGVRDLSYRLSFIANSVQIADGSRNTD---TRHRQNDSNEDDQQQFTGEELEYEIQL	241
BoMCM6_1	GLKALGVRDLSYRLAFIANSVQIADGSRNTD---MRNRQNDSNEDDQQQFTGEELEDEIQQ	338
AtMCM6	GLKALGVRDLSYRLAFIANSVQIADGSRNTD---MRNRQNDSNEDDQQQFTAEELEDEIQQ	338
BrMCM6	GLKALGVRDLSYRLAFIANSVQIADGSRNTD---MRNRQNDSNEDDQQQFTGEELEDEIQQ	338
ZmMCM6	GLKSLGVRDLSYRLAFVANSVQVADGRREVD---IRERDTGDGDSERQKFTEEEEDEVVR	342
PsMCM6	GLRALGVRDLSYRLAFIANSVQICDGRREID---IRNRKKDSEED-DLLFSQQELDEEVR	336
MCM6_Glyma09g05240	GLKALGVRDLSYRLAFIANSVQICDGRREID---IRNRKKDADDD-NQQFTDQELLEEIKR	337
MCM6_Glyma15g16570	GLKALGVRDLNYRLAFIANSQAICDGRREID---IRNRKKDVED-NQQFTDQELLEEIKR	337
AtMCM2	P-----VFATVVEANYVTK-----KQDLFSAYKLTQEDKTOIEE	492
BoMCM2_1	P-----VFATVVEANYVTK-----KQDLFSAYKLTQEDKTOIEE	480
BrMCM2_1	P-----VFATVVEANYVTK-----KQDLFSAYKLTQEDKTOIEE	483
BoMCM2_2	P-----VFATVVEANYVTK-----KQDLFSAYKLTQEDKTOIEE	478
BrMCM2_2	P-----VFATVVEANYVTK-----KQDLFSAYKLTQEDKTOIEE	487
ZmMCM2	P-----VFATVVEANYVAK-----KQDLFSAYKLTDEDKAEIEK	513
PsMCM2	P-----VFSTVVEANYVTK-----KQDLFSAYKLTQEDKKEEIEEN	493
MCM2_Glyma07g36680	P-----VFATVVEANYVTK-----KQDLFSAYKLTQEDIEEIEEN	486
MCM2_Glyma17g03920	P-----VFATVVEANYVTK-----KQDLFSAYKLTQEDIEEIEEN	492
ZmMCM5	G-----VKQPYIRVVGLEQS-----RDNNSNGPSNFTLDEEMEFKE	319
AtMCM5	A-----IRQPYIRVVGLEDT-----NEASSRGPANFTPDDEEEFVK	318
BoMCM5	A-----IRQPYIRVVGLEDT-----NEASSRGPANFTPDDEEEFVK	318
BrMCM5	A-----IRQPYIRVVGLEDT-----NEASSRGPANFTPDDEEEFVK	318
PsMCM5	A-----VRQPYIRVVGIEDA-----NEAKSRGPTSFTEEEIEEFVK	321
MCM5_Glyma13g22420	A-----IRQPYIRVVGIEET-----NETNSRGPAAFTQDEIEEFVK	323
MCM5_Glyma17g11220	A-----IRQPYIRVVGIEET-----NETNSRGPAAFTQDEIEEFVK	323
ZmMCM3	G-----VFRTVLIANNVSL-----LNKEANAPVYTREDLKRME	283
AtMCM3	G-----VFRTILIANNIAL-----LNKEANAPIYTKQDLDNIKN	278
BrMCM3_1	G-----VFRTILIANNISL-----LNKEANAPIYTPRDLQEIKK	280
BoMCM3	G-----VFRTILIANNISL-----LNKEANAPIYTPRDLQEIKK	280
BrMCM3_2	G-----VFRTILIANNISL-----LNKEANAPIYTPRDLQEIKK	280
MCM3_Glyma05g25980	G-----VFRTVLIANNVSL-----LNKEANAPIYSAEDVKSIKE	282
MCM3_Glyma08g08920	G-----VFRTVLIANNVSL-----LNKEANAPIYSAEDVKNIKE	282
PsMCM3	G-----VFRTVLIANNVAL-----LNKEANAPIYSTEDLKNIKK	215
AtMCM7	L-----VADTYLEATSVTH-----FKKKYEEYEFQKDEEEQIAR	319
BoMCM7_2	L-----VADTYLEATSVTH-----FKKKYEEYEFQKDEEEQIAR	321
BrMCM7_1	L-----VADTYLEATSVTH-----FKKKYEEYEFQKDEEEQIAR	321
BoMCM7_1	L-----VADTYLEATAVTH-----FKKKYEEYEFQKDEEEQIAR	321
BrMCM7_2	L-----VADTYLEATAVTH-----FKKKYEEYEFQKDEEEQIAR	314
ZmMCM7	L-----VADTYLEAMSVTH-----FKKKYEEYDLKGDEEQIDR	321
PsMCM7	L-----VADTYLEAMSVSH-----FKKKYEEYELRGDEEEQIKR	321
MCM7_Glyma03g37770	L-----VADTYLEAMSVMH-----FKKKYEEYEFRGDEEEQIAR	321
MCM7_Glyma19g40370	L-----VADTYLEAMSVTH-----FKKKYEEYEFRGDEEEQIAR	321
ZmMCM4	S-----IFKTYIDCLHIKKTDKSRLHVEDTMDIDNSNASKSTEEDFLSDKVEKLKE	434
AtMCM4	S-----VFKTYIDCLHIKSKLRMSAEDPMDVDNSLRRVDEDVELDEEKLRKFQE	428
BoMCM4	-----TYIDCLHIKSKTRMAAEDPMDVDNSLRRVDEDVELDEEKLRKFEE	406
BrMCM4	-----TYIDCLHIKSKTRMAAEDPMDVDNSLRRVDEDVELDEEKLRKFEE	406

MCM4_Glyma11g12110	S-----LFKTYIDCLHIKKTDKSRMLVEDAMDVDGQD--KNAEVLFDDEKVAQLKE	418
MCM4_Glyma12g04320	S-----LFKTYIDCLHIKKTDKSRMFVEDVMDVDGQD--RNAEVLFDDEKVAQLKE	422
PsMCM4	S-----LFKTYIDCLHIKKTSKSRMLVEDAMEADSGQGRNAEEVIFSEEKVAQLRE	417

BoMCM6_2	MKKTDPDYFNKLVGSMAPT VFRHQDIKRAILLMLLGGVHKT TT THEGINLRGDINVCIVGDP	301
BoMCM6_1	MRNTPDYFNKLVGSMAPT VFGHQDIKRAVLLMLLGGVHKT-THEGINLRGDINVCIVGDP	397
AtMCM6	MRNTPDYFNKLVGSMAPT VFGHQDIKRAVLLMLLGGVHKT-THEGINLRGDINVCIVGDP	397
BrMCM6	MRNTPDYFNKLVGSMAPT VFGHQDIKRAVLLMLLGGVHKT-THEGINLRGDINVCIVGDP	397
ZmMCM6	MRNTPDFFNKIVDSICTP VFGHQEIKRAVLLMLLGGVHKT-THEGINLRGDINVCIVGDP	401
PsMCM6	MRNTPDFFTKLVESVAPTIFGHQDIKRAILLMLLMSGVHKS-THEGISLRGDINVCIVGDP	395
MCM6_Glyma09g05240	MRSTPDFFTKLVESIAPT VFGHPDIKRAILLMLLGGVHKF-THEGINLRGDINVCVVGDP	396
MCM6_Glyma15g16570	MRSTPDFFTKLVESIAPT VFGHPDIKRAILLMLLGGVHKF-THEGINLRGDINVCVVGDP	396
AtMCM2	LSKDPRIVERIIKSIAPSIYGHEDIKTALALAMFGGQEK- IKGKHRLRGDINVLLLGDP	551
BoMCM2_1	LSKDPRIVERIIKSIAPSIYGHEDIKTALALAMFGGQEK- IKGKHRLRGDINVLLLGDP	539
BrMCM2_1	LSKDPRIVERIIKSIAPSIYGHEDIKTALALAMFGGQEK- IKGKHRLRGDINVLLLGDP	542
BoMCM2_2	LSKDPRIVERIIKSIAPSIYGHEDIKTALALAMFGGQEK- IKGKHRLRGDINVLLLGDP	537
BrMCM2_2	LSKDPRIVERIIKSIAPSIYGHEDIKTALALAMFGGQEK- IKGKHRLRGDINVLLLGDP	546
ZmMCM2	LSKDPRIGERIIKSIAPSIYGHEDIKTALALAMFGGQEK- VKGKHRLRGDINVLLLGDP	572
PsMCM2	LKDPRIGERIVKSIAPSIYGHDDIKTGIALAMFGGQEK- VEGKHRLRGDINVLLLGDP	552
MCM2_Glyma07g36680	LAKDPRIGERIVKSIAPSIYGHDDIKTAIALAIFGGQEK- VEGKHRLRGDINVLLLGDP	545
MCM2_Glyma17g03920	LAKDPRIGERIVKSIAPSIYGHDDIKTAIALAMFGGQEK- VEGKHRLRGDINVLLLGDP	551
ZmMCM5	FAQRPDYAKLCSMIGPSIYGHSDVKKAIACLLFGGSKKR-LPDGVRLRGDIHVLLLGDP	378
AtMCM5	FADSQDVYKNICTKIAPSIYGHEDVKRAAACLLFGGSRKS-LPDGVKLRGDINVLLLGDP	377
BoMCM5	FAGGQDVYSNICTKIAPSIYGHEDVKKAVACLLFGGSRKS-LPDGVKLRGDINVLLLGDP	377
BrMCM5	FAASQDVYSNICTKIAPSIYGHEDVKKAVACLLFGGSRKS-LPDGVKLRGDINVLLLGDP	377
PsMCM5	FASEPDAYKNICSKSIAPSIYGHEDVKKAVACLLFGGSRKH-LPDGVRLRGDINVLLLGDP	380
MCM5_Glyma13g22420	FASEPDAYKNICSMIAPSIYGHEDVKKAVACLLFGGSRKN-LPDGVRLRGDINVLLLGDP	382
MCM5_Glyma17g11220	FAAEPDAYKNICSMIAPSIYGHDDVKKAVACLLFGGSRKN-LPDGVRLRGDINVLLLGDP	382
ZmMCM3	ISRRNDTFDLLGNSLAPSIYGHLWIKKAVLLMLLGGVEKN-LKNGTHLRGDINMMVGD	342
AtMCM3	IARRDDAFDLLARSLAPSIYGHAWIKKAVLLMLLGGVEKN-LKNGTHLRGDINMMVGD	337
BrMCM3_1	IAARDDAFDLLSRSLAPSIYGHAWIKKAVILLMLLGGMEKN-LKNGTHLRGDINMMVGD	339
BoMCM3	IAARDDAFDLLSRSLAPSIYGHAWIKKAVILLMLLGGMEKN-LKNGTHLRGDINMMVGD	339
BrMCM3_2	IAARDDAFDLLSRSLAPSIYGHAWIKKAVILLMLLGGMEKN-LKNGTHLRGDINMMVGD	339
MCM3_Glyma05g25980	IAARDDAFDLLSNSLAPSIYGHSWIKKAVILLMLSGVEKN-LKNGTHLRGDINMMVGD	341
MCM3_Glyma08g08920	IAARDDAFDLLSNSLAPSIYGHSWIKKAVILLMLSGVEKN-LKNGTHLRGDINMMVGD	341
PsMCM3	IAERDDTFDLLGNSLAPSIYGHHSWIKKAVILLMLSGVEKN-LKNGTHLRGDINMMVGD	274
AtMCM7	LAEDGDIYNKLSRSLAPEIYGHEDIK KALLLLLVLGAPHRQ-LKDG MKIRGDVHICLMGDP	378
BoMCM7_2	LAEDGDIYNKLSRSLAPEIYGHEDIK KALLLLLVLGAPHRQ-LKDG MKIRGDVHICLMGDP	380
BrMCM7_1	LAEDGDIYNKLSRSLAPEIYGHEDIK KALLLLLVLGAPHRQ-LKDG MKIRGDVHICLMGDP	380
BoMCM7_1	LAEDGDIYNKLSRSLAPEIYGHEDIK KALLLLLVLGAPHRQ-LKDG MKIRGDVHICLMGDP	380
BrMCM7_2	LAEDGDIYNKLSRSLAPEIYGHEDIK KALLLLLVLGAPHRQ-LKDG MKIRGDVHICLMGDP	373
ZmMCM7	LAEDGDIYDKLARSLAPEIYGHEDVKKALLLLLVLGAPHRK-LADGMKIRGDLHICMMDP	380
PsMCM7	LAEDGDIYDKLARSLAPEIYGHEDIK KALLLLLVLGAPHRQ-LKDG MKIRGDLHICLMGDP	380
MCM7_Glyma03g37770	LAEDGDIYNKLARSLAPEIFGHDDIK KALLLLLVLGAPHRT-LKDG MKIRGDLHICLMGDP	380
MCM7_Glyma19g40370	LAEDGDIYNKLSRSLAPEIFGHDDIK KALLLLLVLGAPHRT-LNDGMKIRGDLHICLMGDP	380
ZmMCM4	LSKLPDIYERLRS LAPNIWELDDVKKGLLCQLFGGNPLK-LPSGASFRGDINILLVGD	493
AtMCM4	LSKQPDYERLRS LAPNIWELDDVKKGLLCQLFGGNPNL-LASGANFRGDINILLVGD	487
BoMCM4	LSKQPDYERLRS LAPNIWELDDVKKGLLCQLFGGNPNL-LASGANFRGDINILLVGD	465
BrMCM4	LSKQPDYERLRS LAPNIWELDDVKKGLLCQLFGGNPNL-LASGANFRGDINILLVGD	465
MCM4_Glyma11g12110	LSKRPDIYEILTKSMAPNIWELDDVKKGLLCQLFGGNALK-LASGANFRGDINILLVGD	477
MCM4_Glyma12g04320	LSKRPDIYEILTNSLAPNIWELDDVKKGLLCQLFGGNALK-LASGANFRGDINILLVGD	481
PsMCM4	LSKQPDYERLTKSLAPNIWELDDVKKGLLCQLFGGNALK-LATGASFRGDINILLVGD	476

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BoMCM6_2	SCAKSQFLKYTAGIVPRS VYTSKSSSAAGLTATVAKEPETGEFCIEAGALMLADNGICC	361
BoMCM6_1	SCAKSQFLKYTAGIVPRS VYTSKSSSAAGLTATVAKEPETGEFCIEAGALMLADNGICC	457
AtMCM6	SCAKSQFLKYTAGIVPRS VYTSKSSSAAGLTATVAKEPETGEFCIEAGALMLADNGICC	457
BrMCM6	SCAKSQFLKYTAGIVPRS VYTSKSSSAAGLTATVAKEPETGEFCIEAGALMLADNGICC	457
ZmMCM6	SCAKSQFLKYTAGIVPRS VYTSKSSSAAGLTATVAKEPETGEFCIEAGALMLADNGVCC	461
PsMCM6	SCAKSQFLKYTAGIVPRS VYTSKSSSAAGLTATVAKEPETGEFCIEAGALMLADNGICC	455

ZmMCM5	IDEFDKMRPEDRVAIHEAMEQQTISIAKAGITTVLNSRTSVLAAANPIAGRYDDLKTAQD	498
AtMCM5	IDEFDKMRPEDRVAIHEAMEQQTISIAKAGITTVLNSRTSVLAAANPPSGRYDDLKTAQD	497
BoMCM5	IDEFDKMRPEDRVAIHEAMEQQTISIAKAGITTVLNSRTSVLAAANPPSGRYDDLKTAQD	497
BrMCM5	IDEFDKMRPEDRVAIHEAMEQQTISIAKAGITTVLNSRTSVLAAANPPSGRYDDLKTAQD	497
PsMCM5	IDEFDKMRPEDRVAIHEAMEQQTISIAKAGITTVLNSRTSVLAAANPPSGRYDDLKTAQD	500
MCM5_Glyma13g22420	IDEFDKMRPEDRVAIHEAMEQQTISIAKAGITTVLNSRTSVLAAANPPSGRYDDLKTAQD	502
MCM5_Glyma17g11220	IDEFDKMRPEDRVAIHEAMEQQTISIAKAGITTVLNSRTSVLAAANPPSGRYDDLKTAQD	502
ZmMCM3	IDEFDKMNDQDRVAIHEVMEQQTVTIAKAGIHASLNARCSVIAAANPIYGTDRSLTPTK	462
AtMCM3	IDEFDKMNDQDRVAIHEVMEQQTVTIAKAGIHASLNARCSVIAAANPIYGTDRSLTPTK	457
BrMCM3_1	IDEFDKMNDQDRVAIHEVMEQQTVTIAKAGIHASLNARCSVIAAANPIYGTDRSLTPTK	459
BoMCM3	IDEFDKMNDQDRVAIHEVMEQQTVTIAKAGIHASLNARCSVIAAANPIYGTDRSLTPTK	459
BrMCM3_2	IDEFDKMNDQDRVAIHEVMEQQTVTIAKAGIHASLNARCSVIAAANPIYGTDRSLTPTK	459
MCM3_Glyma05g25980	IDEFDKMNDQDRVAIHEVMEQQTVTIAKAGIHASLNARCSVIAAANPIYGTDRSLTPTK	461
MCM3_Glyma08g08920	IDEFDKMNDQDRVAIHEVMEQQTVTIAKAGIHASLNARCSVIAAANPIYGTDRSLTPTK	461
PsMCM3	IDEFDKMNDQDRVAIHEVMEQQTVTIAKAGIHASLNARCSVIAAANPIYGTDRSLTPTK	394
AtMCM7	IDEFDKMDESDRTAIHEVMEQQTVSIAKAGITTSLNARTAVLAAANPAWGRYDLRRTPAE	498
BoMCM7_2	IDEFDKMDESDRTAIHEVMEQQTVSIAKAGITTSLNARTAVLAAANPAWGRYDLRRTPAE	500
BrMCM7_1	IDEFDKMDESDRTAIHEVMEQQTVSIAKAGITTSLNARTAVLAAANPAWGRYDLRRTPAE	500
BoMCM7_1	IDEFDKMDESDRTAIHEVMEQQTVSIAKAGITTSLNARTAVLAAANPAWGRYDLRRTPAE	500
BrMCM7_2	IDEFDKMDESDRTAIHEVMEQQTVSIAKAGITTSLNARTAVLAAANPAWGRYDLRRTPAE	493
ZmMCM7	IDEFDKMEESDRTAIHEVMEQQTVSIAKAGITTSLNARTAILAAANPAWGRYDMRRTPAE	500
PsMCM7	IDEFDKMEESDRTSIHEVMEQQTVSIAKAGITTSLNARTAVLAAANPAWGRYDLRRTPAE	500
MCM7_Glyma03g37770	IDEFDKMDESDRTAIHEVMEQQTVSIAKAGITTSLNARTAVLAAANPAWGRYDLRRTPAE	500
MCM7_Glyma19g40370	IDEFDKMDESDRTAIHEVMEQQTVSIAKAGITTSLNARTAVLAAANPAWGRYDLRRTPAE	500
ZmMCM4	IDEFDKMSDNARSMLHEVMEQQTVSIAKAGIIASLNARTSVLACANPESRYNPRLSVID	613
AtMCM4	IDEFDKMSDSARSMLHEVMEQQTVSIAKAGIIASLNARTSVLACANPSGSRYNPRLSVIE	607
BoMCM4	IDEFDKMSDSARSMLHEVMEQQTVSIAKAGIIASLNARTSVLACANPSGSRYNPRLSVIE	585
BrMCM4	IDEFDKMSDSARSMLHEVMEQQTVSIAKAGIIASLNARTSVLACANPSGSRYNPRLSVIE	585
MCM4_Glyma11g12110	IDEFDKMSDNARSMLHEVMEQQTVSIAKAGIIASLNARTSVLACANPSGSRYNPRLSVID	597
MCM4_Glyma12g04320	IDEFDKMSDNARSMLHEVMEQQTVSIAKAGIIASLNARTSVLACANPSGSRYNPRLSVID	601
PsMCM4	IDEFDKMSDNARSMLHEVMEQQTVSIAKAGIIASLNARTSVLACANPSGSRYNPRLSVID	596

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BoMCM6_2	NVNLPPAILSRFDLVYL-----	438
BoMCM6_1	NVNLPPAILSRFDLVYVMIDDPDELTDYHIAHHIVRVHQHEAA-----	561
AtMCM6	NVNLPPAILSRFDLVYVMIDDPDEVTDYHIAHHIVRVHQHEAA-----	561
BrMCM6	NVNLPPAILSRFDLVYVMIDDPDELTDYHIAHHIVRVHQHEAA-----	561
ZmMCM6	NVALPPAILSRFDLVYIMIDDPDENTDYHIAHHIVRVHQKREEA-----	565
PsMCM6	NVALPPAILSRFDLVYIMIDDPDDNTDYHIAHHIVRVHQKREDA-----	559
MCM6_Glyma09g05240	NVALPPAILSRFDLVYVMIDDPDDQTDYHIAHHIVRVHQKREGA-----	560
MCM6_Glyma15g16570	NVALPPAILSRFDLVYVMIDDPDDQTDYHIAHHIVRVHQKREGA-----	560
AtMCM2	NVELTDPILSRFDILCVVKDVVDVPTDEMLAEFVVNSHFKSQPK-GGKM-----	719
BoMCM2_1	NVELTDPILSRFDILCVVKDVVDVPTDEMLAEFVVNSHFKSQPK-GGKM-----	707
BrMCM2_1	NVELTDPILSRFDILCVVKDVVDVPTDDMLAEFVVNSHFKSQPK-GGKM-----	710
BoMCM2_2	NVELTDPILSRFDILCVVKDVVDVPTDEMLAEFVVNSHFKSQPK-GGKM-----	705
BrMCM2_2	NVELTDPILSRFDILCVVKDVGDVPTDEMLAEFVVNSHFKSQPK-GGKM-----	714
ZmMCM2	NVELTDPILSRFDILCVVKDVVDVPTDEMLARFVVDSSHARSQPK-GANL-----	740
PsMCM2	NVELTDPILSRFDILCVVKDVVDVPTDEMLAKFVVDSSHFKSQPK-GANN-----	720
MCM2_Glyma07g36680	NVELTDPILSRFDILCVVKDVVDVPTDEMLATFVVDSSHFKSQPK-GANQ-----	713
MCM2_Glyma17g03920	NVELTDPILSRFDILCVVKDVVDVPTDEMLATFVVDSSHFKSQPK-GAKQ-----	719
ZmMCM5	NIDLQTTILSRFDLIFIVKDIRMYDQDKRIASHIIRVHASGAAAS-----	543
AtMCM5	NIDLQTTILSRFDLIFIVKDIRKYSQDKEIASHIIRVHASANKFS-----	542
BoMCM5	NIDLQTTILSRFDLIFIVKDIRKYSQDKEIASHIIRVHASADKVT-----	542
BrMCM5	NIDLQTTILSRFDLIFIVKDIRKYSQDKEIASHIIRVHASADKVT-----	542
PsMCM5	NIDLQTTILSRFDLIFIVKDIRMYDQDKTIAASHIIRVHASASATR-----	545
MCM5_Glyma13g22420	NIDLQTTILSRFDLIFIVKDIRMYDQDKTIANHIIRVHASAGGRM-----	547
MCM5_Glyma17g11220	NIDLQTTILSRFDLIFIVKDIRMYDQDKTIANHIIRVHASAGGRM-----	547
ZmMCM3	NIGLPDSLLSRFDLLFIVLDQMDPEIDRQISEHVARMHRYCT--DDGGARSLDKEGYAEE	520
AtMCM3	NIGLPDSLLSRFDLLFIVLDQMDAGIDSMISEHVLRMHRYKN--DRGEAGPDGSLPYARE	515
BrMCM3_1	NIGLPDSLLSRFDLLFIVLDQMDAGIDSMISEHVLRMHRYQN--DRGEAGPDGNLPYGRD	517
BoMCM3	NIGLPDSLLSRFDLLFIVLDQMDAGIDSMISEHVLRMHRYQN--DRGEAGPDGNLPYGRE	517

BrMCM3_2	NIGLPDSSLRSRFDLLFIVLDQMDAGIDSMISEHVLRMHRVYQN--DRGEAGPDGNLPYGRE	517
MCM3_Glyma05g25980	NIGLPDSSLRSRFDLLFIVLDQMDPDIDRRISEHVLRMHRFRSAVDGGEAVLHGSSRYGRE	521
MCM3_Glyma08g08920	NIGLPDSSLRSRFDLLFIVLDQMDPDIDRRISEHVLRMHRFRSAVDGGEAALDGSRRYGRE	521
PsMCM3	NIGLPDSSLRSRFDLLFIVLDQMDPDIDRQISEHVLRMHRFRSAIDGGEAAHDGSARYGKK	454
AtMCM7	NINLPPALLSRFDLLWLILDRADMDSLELAKHVLHVHQTQTESP-----	542
BoMCM7_2	NINLPPALLSRFDLLWLILDRADMDSLELAKHVLHVHQTQTESP-----	544
BrMCM7_1	NINLPPALLSRFDLLWLILDRADMDSLELAKHVLHVHQTQTESP-----	544
BoMCM7_1	NINLPPALLSRFDLLWLILDRADMDSLELAKHVLHVHQTQTESP-----	544
BrMCM7_2	NINLPPALLSRFDLLWLILDRADMDSLELAKHVLHVHQTQTESP-----	537
ZmMCM7	NINLPPALLSRFDLLWLILDRADMETDLEMARHVHVHVNLESPE-----	544
PsMCM7	NINLPPALLSRFDLLWLILDRADMNDLEMARHVVVVHVNKESPE-----	544
MCM7_Glyma03g37770	NINLPHALLSRFDLLWLILDRADMNDLEMARHVLYVHVNKESPE-----	544
MCM7_Glyma19g40370	NINLPHALLSRFDLLWLILDRADMNDLEMARHVVVVHVNKESPE-----	544
ZmMCM4	NIHLAPTLLSRFDLIYLILDKADEQTDRLAKHIVSLHFENPN-----	656
AtMCM4	NIHLPTLLSRFDLIYLILDKPDEQTDRLAKHIVALHFFENAE-----	650
BoMCM4	NIHLPTLLSRFDLIYLILDKPDEQTDRLAKHIVALHFFENAE-----	628
BrMCM4	NIHLPTLLSRFDLIYLILDKPDEQTDRLAKHIVALHFFENAE-----	628
MCM4_Glyma11g12110	NIHLPTLLSRFDLIYMLDKADEQTDRLAKHIVSLHFENPE-----	640
MCM4_Glyma12g04320	NIHLPTLLSRFDLIYLLDKAHEQTDRLAKHIVSLHFENPE-----	644
PsMCM4	NIHLPTLLSRFDLIYLLDKADEQTDRLAKHIVSLHFKDHE-----	639

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BoMCM6_2	-----SPEARKL	445
BoMCM6_1	-----LSPEFTTVQLKRYIAYAKT-LKPKLSPEARKL	592
AtMCM6	-----LSPEFTTVQLKRYIAYAKT-LKPKLSPEARKL	592
BrMCM6	-----LSPEFTTVQLKRYIAYAKT-LKPKLSPEARKL	592
ZmMCM6	-----LAPAFSTAQLKRYISFAKS-LKPQLSSEAKKV	596
PsMCM6	-----LAPTFTTAEKRYIAYAKT-LKPKLTS DARKL	590
MCM6_Glyma09g05240	-----LAPAFTTAEKRYIAYAKI-LKPKLSPDARKL	591
MCM6_Glyma15g16570	-----LAPAFTTAEKRYIAYAKT-LKPKLSPDARKL	591
AtMCM2	----EDSD---PEDGIQG---SSGSTDPEVLPQNLLKLYLTYSKLYVFPKLGELDAKK	767
BoMCM2_1	----DDSE---PQDDNHG---SSGSSDPEVLPQNLLRKYLTYSKLYVFPKLSEIDAKK	755
BrMCM2_1	----DDSE---PQDDNHG---SSGSSDPEVLPQNLLRKYLTYSKLYVFPKLSEIDAKK	758
BoMCM2_2	----DDSE---PQDVVQG---SSGSSDPEVLPQDLLRKYLTYSKLYVFPKLSEIDAKK	753
BrMCM2_2	----DDSE---PQDGVQG---SSGSSDPEVLPQNLLRKYLTYSKLYVFPKLSEIDAKK	762
ZmMCM2	----EDRVSTVDVDDPLA---AARQADPDVLSQDMLKKYITYAKLNVFPKIH DADLDK	791
PsMCM2	----DDKSVSESQ-D--A---SGMPTDPEILPQDLLKYSTYAKLNVFPRFNDVDLDK	768
MCM2_Glyma07g36680	----DDKSFSESQ-DVHA---SAMPADPEILPQQLLKKYITYAKLNI FPRLQDADMDK	763
MCM2_Glyma17g03920	----DDKSFSEFQ-DIHA---SAMPADPEILPQQLLKKYITYAKLNI FPRLQDADMDK	769
ZmMCM5	-----ST-NTEGSEGENWLKRYIEYCRATCKPRLSEKAAEM	578
AtMCM5	-----DENT--DSKEDNWLKRYIQYCRARCPRLSKDAAEN	576
BoMCM5	-----DENT--DSKEDNWLKRYIQYCRSRCPRLTEAAMK	576
BrMCM5	-----DENT--DSKEDNWLKRYIQYCRSRCPRLTEAAMK	576
PsMCM5	-----GENKTIISKEENWLKRYLKYCRTECHPRLSE TA AKL	581
MCM5_Glyma13g22420	-----GESRT--FKEENWLKRYLQYCR TQCHPRLSESATTL	581
MCM5_Glyma17g11220	-----GESRT--LKEENWLKRYLQYCR TQCHPRLSESATTL	581
ZmMCM3	DDGDANAAIFVKYDRMLHGQDRRRGKKSQDRLTVKFLKKYIHYAKNLIQ PRLTDEASDH	580
AtMCM3	DN--AESEMFVKYNQTLHGKK-KRGQT-HDKTLTIKFLKKYIHYAKHRI TP KLTDEASER	571
BrMCM3_1	DD--GESEFVKYNRMLHGK KKKR GQT-NEKTLTIKFLKKYIHYAKHRIQ PELTDEASER	574
BoMCM3	ED--GESEFVKYNRMLHGK KKKR GQT-NEKTLTIKFLKKYIHYAKHRIQ PELTDEASER	574
BrMCM3_2	ED--GESEFVKYNRMLHGK KKKR GQT-NEKTLTIKFLKKYIHYAKHRIQ PELTVEASER	574
MCM3_Glyma05g25980	DEADMSSVFVKYNRMLHGKKTGRGQK-R-DTLTIKFLK KFIHYAKHRIQ PELTDEASEN	579
MCM3_Glyma08g08920	DEADMSSVFVKYNRMLHGKKTGRGQK-R-DTLTIKFLK KFIHYAKHRIQ PELTDEASEN	579
PsMCM3	EEADTESSVFVKYNRMLHGKKTDRGRK-R-DTLTIKFLK KFIHYAKHRIQ PDLTDEASDQ	512
AtMCM7	-----ALGFEPLEPNILRAYISAARR-LSPYVPAELEEY	575
BoMCM7_2	-----ALGFEPLEPNILRAYISAARR-LSPYVPAELEEY	577
BrMCM7_1	-----ALGFEPLEPNILRAYISAARR-LSPYVPAELEEY	577
BoMCM7_1	-----ALGFEPLEPNILRAYISAARR-LSPYVPAELEEY	577
BrMCM7_2	-----ALGFDPLEPNILRAYISAARR-LSPYVPAELEEY	570
ZmMCM7	-----ALGFTPLEPSVLRAYISAARR-VIPSPRELEEY	577
PsMCM7	-----ALGFTPLEPSVLRAYISTARR-LSP TVPRELEEY	577

MCM7_Glyma03g37770 -----ALGFTPLEPSVLRAYISAARR-LSPSPVPRELEEY 577
MCM7_Glyma19g40370 -----ALGFTPLEPSVLRAYISAARR-LSPSPVPRELEEY 577
ZmMCM4 -----LEELEVLDTLQTLVSYISYARKYIQPQLSDEAAEE 690
AtMCM4 -----SAQEEAIDITTLTTYVSYARKNIHPKLSDEAAEE 684
BoMCM4 -----SAQEEALDITTLTSYVSYARKNIHPKLSDEAAEE 662
BrMCM4 -----SAQEEALDITTLTSYVSYARKNIHPKLSDEAAEE 662
MCM4_Glyma11g12110 -----NVEQDVLDISTLTDYVSYARKHIHPQLSDEAAEE 674
MCM4_Glyma12g04320 -----NVEQDVLDISTLTDYVSYARRHIHPQLSDEAAEE 678
PsMCM4 -----AMEQDVLDISTLTDYVSYARKHIHPQLSDEAADE 673

BoMCM6_2 LVDSYVDLRSGDTP---GTRVAYRMTV-----KPSHVLLAV 479
BoMCM6_1 LVESYVALRRGDTP---GTRVAYRMTVVRQLEALIRLSEAIARSHLETIVKPSHVLLAV 648
AtMCM6 LVESYVALRRGDTP---GTRVAYRMTVVRQLEALIRLSEAIARSHLETIVKPSHVLLAV 648
BrMCM6 LVESYVALRRGDTP---GTRVAYRMTVVRQLEALIRLSEAIARSHLETIVKPSHVLLAV 648
ZmMCM6 LVESYVTLRRGDSTP---GTRVAYRMTVVRQLEALIRLSEAIARSHLERVVLPAHVRLAV 652
PsMCM6 LVDSYVALRRADTNP---GSRVAYRMTVVRQLEALIRLSEAIARSHLDNQVQPRHVRLAV 646
MCM6_Glyma09g05240 LVDSYVALRRGDTP---GSRVAYRMTVVRQLEALIRLSEAIARSHLDNEVQPRHVRLAV 647
MCM6_Glyma15g16570 LVDSYVALRRGDTP---GSRVAYRMTVVRQLEALIRLSEAIARSHLDNEVQPRHVRLAV 647
AtMCM2 LETVYANLRRESMN-----GQGVSIATRHLSESMIRMSEAHARMHLRQVVTEDDVNMAI 820
BoMCM2_1 LETVYANLRRESMN-----GQGVSIATRHLSESMIRMSEANARMHLRQVVTEDDVNMAI 808
BrMCM2_1 LETVYANLRRESMN-----GQGVSIATRHLSESMIRMSEANARMHLRQVVTEDDVNMAI 811
BoMCM2_2 LETVYANLRRESMN-----GQGVSIATRHLSESMIRMSEAHARMHLRQVVTEDDVNMAI 806
BrMCM2_2 LETVYANLRRESMN-----GQGVSIATRHLSESMIRMSEAHARMHLRQVVTEDDVNMAI 815
ZmMCM2 ISHVYAE LRRESSH-----GQGVPIAVRHIESIIRMSEAHARMHLRSYVSQEDVDMAI 844
PsMCM2 LTHVYAE LRKESH-----GQGVPIAVRHIESMIRMSEAHARMHLRQHVTPEDVDMAI 821
MCM2_Glyma07g36680 LSHVYAE LRRESSH-----GQGVPIAVRHIESMIRMSEAHARMHLRQHVTPEDVDMAI 816
MCM2_Glyma17g03920 LSHVYAE LRRESSH-----GQGVPIAVRHIESMIRMSEAHARMHLRQHVTPEDVDMAI 822
ZmMCM5 LQNKYIEIRQKMRQQAHEGTGRAAAIPITVRQLEAIIRLSESLAKMRLTSVATPEHVEEAF 638
AtMCM5 LQRKYVTIRMDKRRRAHETGEAAPIPITVRQLEAIVRLSESLAKMRLSHEATPDDVDKAF 636
BoMCM5 LQQQYVKIREDMRRRAHETGEAAPIPITVRQLEAIVRLSESLAKMRLSHDATEDDVGKAF 636
BrMCM5 LQQQYVKIREDMRRRAHETGEAAPIPITVRQLEAIVRLSESLAKMRLSHDATEDDVGKAF 636
PsMCM5 LQNNYVKIRQDMRQQA NETGAAAIPITVRQLEAIVRLSESLAKMRLSHLATEENVQEA I 641
MCM5_Glyma13g22420 LQNHVVKIRQDMRQQA NETGAAAIPITVRQLEAIVRLSEALAKMRLSHLATEENVQEA V 641
MCM5_Glyma17g11220 LQNHVVKIRQDMRQQA NETGAAAIPITVRQLEAIVRLSEALAKMRLSHLATEENVQEA V 641
ZmMCM3 IAEYADLRNAGSDT---KT-GGTLPIPARTLETIIRLATAHAKMKLSEVTKADAEAA L 627
AtMCM3 IAEYADLRNAGSDT---KT-GGTLPIPARTLETIIRLATAHAKMKLSEVTKADAEAA L 630
BrMCM3_1 IAEYADLRNAGSDT---KT-GGTLPIPARTLETIIRLATAHAKMKLSEVTKADAEAA L 630
BoMCM3 IAEYADLRNAGSDT---KT-GGTLPIPARTLETIIRLATAHAKMKLSEVTKADAEAA L 630
BrMCM3_2 IAEYADLRNAGSDT---KT-GGTLPIPARTLETIIRLATAHAKMKLSEVTKADAEAA L 630
MCM3_Glyma05g25980 IATAYAE LRNASSNA---KT-GGTLPIPARTLETIIRLSTAHAKMKLSEVSKSDVEAA L 635
MCM3_Glyma08g08920 IATAYAE LRNASSNA---KT-GGTLPIPARTLETIIRLSTAHAKMKLSEVSKSDVEAA L 635
PsMCM3 IATAYAE LRNANSNA---KT-GGTLPIPARTLETIIRLSTAHAKMKLSEVSKSDVDAAL 568
AtMCM7 IATAYSSIRQEEAKS-----NTPHSYTTVRTLLSILRISAALARLRFSESVQSDVDEAL 630
BoMCM7_2 IATAYSSIRQEEAKS-----NTPHSYTTVRTLLSILRISAALARLRFSESVQSDVDEAL 632
BrMCM7_1 IATAYSSIRQEEAKS-----NTPHSYTTVRTLLSILRISAALARLRFSESVQSDVDEAL 632
BoMCM7_1 IATAYSSIRQEEAKS-----NTPHSYTTVRTLLSILRISAALARLRFSESVQSDVDEAL 632
BrMCM7_2 IATAYSSIRQEEAKS-----NTPHSYTTVRTLLSILRISAALARLRFSESVQSDVDEAL 625
ZmMCM7 IATAYSSIRQEEAKS-----NAPTSYTTIRTLLSILRISIALARLRFSETVAQSDVDEAL 632
PsMCM7 IASAYSSIRQEEAKS-----TTPHSYTTVRTLLSILRISAALARLRFSETVAQSDVDEAL 632
MCM7_Glyma03g37770 IATAYSSIRQEEARS-----NAPHSYTTVRTLLSILRISAALARLRFSETVAQSDVDEAL 632
MCM7_Glyma19g40370 IATAYSCIRQEEARS-----NAPHSYTTVRTLLSILRISAALARLRFSETVAQSDVDEAL 632
ZmMCM4 LTRGYVEMRKRGNP---GSRKKVITATPRQIESLIRLSEALARMRFSEVVEVRDVEEAF 747
AtMCM4 LTRGYVELRKAGKFA---GSSKKVITATPRQIESLIRLSEALARMRFSEVVEKHDVDEAF 741
BoMCM4 LTRGYVELRKAGKFA---GSSKKVITATPRQIESLIRLSEALARMRFSEVVEKHDVDEAF 719
BrMCM4 LTRGYVELRRAGKFA---GSSKKVITATPRQIESLIRLSEALARMRFSEVVEKDDVDEAF 719
MCM4_Glyma11g12110 LTRGYVEIRKRGNFP---GSSKKVITATPRQIESLIRLSEALARMRFSEVVEKHDVMEAF 731
MCM4_Glyma12g04320 LTRGYVEIRKRGNFP---GSSKKVITATPRQIESLIRLSEALARMRFSEVVEKHDVMEAF 735
PsMCM4 LITGYVKIRGRKFT---GSSKKVITATPRQIESLLRLSEALARIRFSEVVEKHDVLEAF 730

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BoMCM6_2	TLLKTSVISVESADVDLSEYQDANGDNIDDDVENTGNGDKEQQNGAA-----	528
BoMCM6_1	RLLKTSVISVESGDIDLSEYQDANGDNMDNADDAENPVNGDEDQQNGSA-----	697
AtMCM6	RLLKTSVISVESGDIDLSEYQDANGDNMDDTDDIENPVDGEEDQQNGAA-----	697
BrMCM6	RLLKTSVISVESGDIDLSEYQDANGDNMDNADDADNPANGDEDQQNGSA-----	697
ZmMCM6	KLLKTSIISVESSEVDLSEFQDAEDGTNVPSES-----DAGQPAEEDA-APQQG---	701
PsMCM6	KLLQTSIIRVESSEIDLSEFQDREEEAGSGDGNNNN-NDADGTN-----	691
MCM6_Glyma09g05240	KLLKTSIISVESSEIDLSEFQEENHDDGAGGGDGNNDKN-RDANDQVGNDAQAAGNA-	705
MCM6_Glyma15g16570	KLLKTSIISVESSEIDLSEFQEQNHDDGAGGGNENDNN-RDANYQEGNDTAQ-QAAGNG-	704
AtMCM2	RVLLDSFISTQKFGVQRTLRESFKRYIT-----YKKD-----F----	853
BoMCM2_1	RVLLDSFISTQKFGVQRTLRESFKRYIT-----YKKD-----Y----	841
BrMCM2_1	RVLLDSFISTQKFGVQRTLRESFKRYIT-----YKKD-----Y----	844
BoMCM2_2	RVLLDSFISTQKFGVQRTLRESFKRYIT-----YKKD-----Y----	839
BrMCM2_2	RVLLDSFISTQKFGVQRTLRESFKRYIT-----YKKD-----Y----	848
ZmMCM2	RVLLDSFISTQKFGVQKALQKNFRKYMT-----FKKD-----Y----	877
PsMCM2	RVLLDSFISTQKFGVQKALQKSFRKYIT-----FKKD-----Y----	854
MCM2_Glyma07g36680	RVLLESFISTQKFGVQKALQKSFRKYMT-----FKKD-----Y----	849
MCM2_Glyma17g03920	RVLLESFISTQKFGVQKALQKSFRKYMT-----FKKD-----Y----	855
ZmMCM5	RLFNVSTVDAARSGINEHLNLSPEIANEIKQAEAIKRRMGIGSH-----I	684
AtMCM5	KLFDSTMTDAARSGINQQINITGEMANEIKQAEAIKRRMGIGAR-----L	682
BoMCM5	KLFDSTMTDAARSGINQQINITSEMANEIKQAEAIKRRMGIGAR-----L	682
BrMCM5	KLFDSTMTDAARSGINQQINITSEMANEIKQAEAIKRRMGIGAR-----L	682
PsMCM5	RLFVSTMTDAARSGINQLTPEMAHEIQAEAIKRRIGIGNH-----I	687
MCM5_Glyma13g22420	RLFTVSTMTDAARSGINQQINLTPDMANEIKQAEAIKRRIGIGNH-----I	687
MCM5_Glyma17g11220	RLFTVSTMTDAARSGINQQINLTPDMANEIKQAEAIKRRIGIGNH-----I	687
ZmMCM3	QVLNFAIYHKELTEMEEREQKEMEMK---QQAHE---DAGA-----TGGTVD	678
AtMCM3	KLMNFAIYHQELTEMDEREQERERE---QAEQERTPSGRRGNQRRNN--EDGAENDTA	681
BrMCM3_1	KLMNFAIYHQELTEMDEREQERERE---QTEQERTPRG---NQRSD--DNEQENVSA	681
BoMCM3	KLMNFAIYHQELTEMDEREQERERE---QSEQERTPSG---HR-----GNQENVSV	676
BrMCM3_2	KLMNFAIYHQELTEMDEREQERERE---QSEQERTPSG---HR-----GNQENVSV	676
MCM3_Glyma05g25980	KVLNFAIYHKELTEMEEREQEREREL---DR---KRKADHDENDGPDHGPDKRRGPKD	687
MCM3_Glyma08g08920	KVLNFAIYHKELTEMEEREQEREREL---DR---KRKADHDENDGPDHGPDKRRGPKD	687
PsMCM3	KILNFAIYHKELTEMDEREEREKER---EREQERKRKA-DAENNGPDRGSKSK-----	618
AtMCM7	RLMQMSKISLYADDRQ-KAGLDAISDITY-SIIRDEAARSNKTHVS-----Y----	674
BoMCM7_2	RLMQMSKISLYADDRQ-KAGLDAISDITY-SIIRDEAARSNKTHVS-----Y----	676
BrMCM7_1	RLMQMSKISLYADDRQ-KAGLDAISDITY-SIIRDEAARSNKTHVS-----Y----	676
BoMCM7_1	RLMQMSKISLYVDDRQ-KAGLDAISDITY-SIIRDEAARSNKTHVS-----Y----	676
BrMCM7_2	RLMQMSKISLYADDRQ-KAGLDAISDITY-SIIRDEAARSNKTHVS-----Y----	669
ZmMCM7	RLMQMSKISLYSDDRQ-RSGLDAISDIY-SILRDEAARTSSMDVR-----Y----	676
PsMCM7	RLMQMSKISLYSDDRQ-RSGLDAISDIY-SILRDEAARSNKMDVN-----Y----	676
MCM7_Glyma03g37770	RLMQMSKISLYSEDRQ-KSGLDAISDIY-SILRDEAARGNRMDVS-----Y----	676
MCM7_Glyma19g40370	RLMQMSKISLYSEDRQ-KSGLDAISDIY-SILRDEAARGNRMDVS-----Y----	676
ZmMCM4	RLLEVAMQQSATDHATGTIDMDLINTGI---SASERQRRENLVAA-----T-----	790
AtMCM4	RLLRVAMQQSATDHATGTIDMDLINTGV---SASERMRRDTFASS-----I-----	784
BoMCM4	RLLRVAMQQSATDHATGTIDMDLINTGV---SASERMRRDILASS-----I-----	762
BrMCM4	RLLRVAMQQSATDHATGTIDMDLINTGV---SASERMRRDILVSS-----I-----	762
MCM4_Glyma11g12110	RLLEVAMQQSATDHSTGTIDMDLITGV---SASERMRRRESLQQA-----T-----	774
MCM4_Glyma12g04320	RLLEVAMQQSATDHSTGTIDMDLITGV---SASERMRRRESLQQA-----T-----	778
PsMCM4	RLLEVAMQQSAMDIKTGTIDMDLITGV---SASERIRRESLIQD-----T-----	773

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BoMCM6_2	-----EPA---SAT-ADKGAVAPKLVINEEYDKITQALVI	560
BoMCM6_1	-----EPA---PATAADNGAAAPKLVISEEYDRITQALVL	730
AtMCM6	-----EPA---SAT-ADNGAAAQKLVISEEYDRITQALVI	729
BrMCM6	-----EAA---PAT-ADNGAAAPKLVISEEYDRITQALVL	729
ZmMCM6	-----AENDQ---AADNGKKKLVITEHFQVQTALVM	731
PsMCM6	-----GDNEKAADESNPQRKSTVTDEYFQRI TRALVT	724
MCM6_Glyma09g05240	-NDQVGN DATQQTANDQVGNDAQAAGPAGNNGNSADGSKPQVRKLVMSDEYYQVTSALIM	764
MCM6_Glyma15g16570	-----NDQVGNDAQAATGNNNGNPADGSKPQVRKLVMSDEYYQVTSALIM	750
AtMCM2	--NSLLLVL---KEL-----VKNALKF-----EEIISGS--NSGLPTI	885
BoMCM2_1	--NSLLLVL---KEL-----VKNALKF-----EEIITGS--NSGLSSI	873
BrMCM2_1	--NSLLLVL---KEL-----VKNALKF-----EEIITGS--NSGLSSI	876

BoMCM2_2	--NSLLLVL	---KEL---	VKNAMKF	---EEIITGS--	NSGLPSI	871	
BrMCM2_2	--NSLLLVL	---KEL---	VKNAMKF	---EEIITGS--	NSGLPFI	880	
ZmMCM2	--NELLLLL	---RTL---	VKDAVHF	---EEIMAGS--	ASRLTHV	909	
PsMCM2	--NDMLIYIL	---QEL---	VKSAIKF	---EEIVAGS--	TSSLTHV	886	
MCM2_Glyma07g36680	--NELLLYIL	---REL---	VKNALHF	---EEIVTGS--	ASGLTHI	881	
MCM2_Glyma17g03920	--NELLLYIL	---REL---	VKNALHF	---EEIVTGS--	ASGLTHI	887	
ZmMCM5	SERRLIDDL	---RMG---	MNES	---IVRR---		705	
AtMCM5	SERRLIEDLA	---RMG---	MNDS	---MVRR---		703	
BoMCM5	SERRLIEDLA	---RMG---	MNDS	---MVRR---		703	
BrMCM5	SERRLIEDLA	---RMG---	MNDS	---MVRR---		703	
PsMCM5	SERRLIDDL	---RMG---	MNDS	---IVRR---		708	
MCM5_Glyma13g22420	SERRLIDDL	---RMG---	MNES	---IVRR---		708	
MCM5_Glyma17g11220	SERRLIDDL	---RMG---	MNES	---IVRR---		708	
ZmMCM3	GHGSSGNDPM	---DVD---	VGSN	--DQ-NV--	SAERIEAFEALLGQHVL	716	
AtMCM3	NVDSETADPM	---EVD---	EPSVEQFSG	--TV--	SAARIETFERVFGQHMR	722	
BrMCM3_1	NAESETADPM	---DVD---	EPPAEQFSG	--TV--	SAARIETFERVFGQHMR	722	
BoMCM3	NVESETADPM	---DVD---	EPPSEQFSG	--TV--	SAARIESFERVFGQHMR	717	
BrMCM3_2	NVESETADPM	---DVD---	EPPSEQFSG	--TV--	SAARIESFERVFGQHMR	717	
MCM3_Glyma05g25980	KRRSTSTDAM	---DVD---	DNSAAQAAV	--GL--	TPERIEEFNSLFNQHM	728	
MCM3_Glyma08g08920	KRGPTSTDAM	---EVD---	DNSATHAAV	--GP--	TPERIEEFNSLFNQHM	728	
PsMCM3	--RDSTSEAM	---ELD---	DTSAAPPV	--GL--	TPERIEAFNSLFGQHMR	657	
AtMCM7	--ANALNWS	---RKG---	YS	---E-AQ--	LKECLEEYAALN--	VW	704
BoMCM7_2	--ANALNWS	---RKG---	YS	---E-AQ--	LKECLEEYAALN--	VW	706
BrMCM7_1	--ANALNWS	---RKG---	YS	---E-AQ--	LKECLEEYAALN--	VW	706
BoMCM7_1	--ANALNWS	---RKG---	YS	---E-AQ--	LKECLEEYAALN--	VW	706
BrMCM7_2	--ANALNWS	---RKG---	YS	---E-AQ--	LKECLEEYAALN--	VW	699
ZmMCM7	--AHALNLIS	---RKG---	YS	---E-AQ--	LKECLEEYASLN--	VW	706
PsMCM7	--RDALNWS	---RKG---	YS	---E-AQ--	LKECLEEYAALN--	VW	706
MCM7_Glyma03g37770	--AHALNWS	---RKG---	YS	---E-AQ--	LKECLEEYAALN--	VW	706
MCM7_Glyma19g40370	--AHALNWS	---RKG---	YS	---E-AQ--	LKECLEEYAALN--	VW	706
ZmMCM4	--RNLIAEKM	---QLG---	GP	---S-MR--	MIELLEELRKQS--	SM	820
AtMCM4	--RDIALEKM	---QIG---	GS	---S-MR--	LSELLEELKKHGGNINT		817
BoMCM4	--RDI TLEKM	---QIG---	GS	---A-MR--	LSELLEELKKHGGNINT		795
BrMCM4	--RDI TLEKM	---QIG---	GS	---A-MR--	LSELLEELKKHGGNINT		795
MCM4_Glyma11g12110	--RNIIMEKM	---QIG---	GP	---S-MR--	LLELLEELKKQD--	TGS	805
MCM4_Glyma12g04320	--RNIIMEKM	---QIG---	GQ	---S-MR--	LLELLEELKKQD--	TGS	809
PsMCM4	--RNIILEKM	---QIG---	GR	---S-MR--	LLEILEELKNQS--	PGN	804

BoMCM6_2	RLRQHEETVS	-----	KDSSELPGMR	-----	QKELIRWYIDQQNEKK	596
BoMCM6_1	RLRQHEETVN	-----	KDSSELPGMR	-----	QKELIRWYIDQQNEKK	766
AtMCM6	RLRQHEETVN	-----	KDSSELPGIR	-----	QKELIRWFIDQQNEKK	765
BrMCM6	RLRQHEETVK	-----	KDCSELPGMR	-----	QKELIRWYIDQQNEKK	765
ZmMCM6	RLRQHEESVK	-----	KDGDLAGMK	-----	QGDLIWYVEQQNAKG	767
PsMCM6	RLRQHEETVV	-----	EQGSDLAGMR	-----	QRDLIKWYVDQQNEKN	760
MCM6_Glyma09g05240	RLRQHEEAVV	-----	QGNLSGMR	-----	QKDLIQWYVDQQNERN	799
MCM6_Glyma15g16570	RLRQHEEAVV	-----	QGDLSGMR	-----	QKDLIQWYVDQQNERN	785
AtMCM2	EVKIEELQTKAKEYDIADLRPFSSSTDFSAKHFELDHGRGMICKPKRLITW	-----		-----		936
BoMCM2_1	EVKIEELQTKANEYDLADLRPFSSSTDFAKAHFELDHGLGVIKFPRRLVTW	-----		-----		924
BrMCM2_1	KVKIEELQTKANEYDLADLRPFSSKDFAKAHFELDHGLGVIKFPRRLVTW	-----		-----		927
BoMCM2_2	EVKIEELQTKANEYDIADLRPFSSSTDFAKAHFELDQVLGVIKCPRRLVTW	-----		-----		922
BrMCM2_2	EVKIEELQTKANEYDIADLRPFSSSTDFAKARFELDQVLGVIKCPRRLVTW	-----		-----		931
ZmMCM2	EVKLEDLRNKAEYEIYDLKPFSSACFRDNGFLDEGRGIIRHPLAE	-----		-----		957
PsMCM2	EVKVDDL FVKAQEHD IYDLKPFSSQFSKSNY ILDEERAVIRHNLV	-----		-----		933
MCM2_Glyma07g36680	DVKVDDL YNKAEQEHD IYDLKPFSSSHFSRANFVLDEERRVIRHHLTR*	-----		-----		929
MCM2_Glyma17g03920	DVKVDDL YHKAQEHD IYDLKPFSSSHFSRANFVLDEERRVIRHHLTR*	-----		-----		935
ZmMCM5	-----A-----		LLIMHQRDEVEYKRER	-----		722
AtMCM5	-----A-----		LLIMHQRGEVEYQRER	-----		720
BoMCM5	-----A-----		LLIMHQRGEVEYQRER	-----		720
BrMCM5	-----A-----		LLIMHQRGEVEYQRER	-----		720
PsMCM5	-----A-----		LLIMHQRDEVEYKRER	-----		725

MCM5_Glyma13g22420	-----A-----	LIIMHQRDEIEYKRER	725
MCM5_Glyma17g11220	-----A-----	LIIMHQRDEIEYKRER	725
ZmMCM3	ANHIDQMSID	EIEQMVNREST--APYTRSQVEFILERMQDAN	756
AtMCM3	THRLDDISIA	DIETVVNNNGVGASRYSADEIMALLEKLQDDN	764
BrMCM3_1	TNRLDDISIA	DIETVVNNNGVGASRYSADEIMALLEKLQDDN	764
BoMCM3	TNRLDDISIA	DIETVVNNNGVGASRYSADEIMALLEKLQDDN	759
BrMCM3_2	TNRLDDISIA	DIETVVNNNGVGASRYSADEIMALLEKLQDDN	759
MCM3_Glyma05g25980	ANRLDQITVV	NLVNVIN-RGEDPPSYSAADVLLLLLERLQDDN	769
MCM3_Glyma08g08920	ANRLEQITIA	NLGNVIN-RGQPPPYSAADILLLELERLQDDN	769
PsMCM3	ANPLDQISIA	DIEDVIN-RGADS-TYSSADILLLEKLQEDN	697
AtMCM7	QIDPHTFDIR	FI	716
BoMCM7_2	QIDPNTFDIR	FI	718
BrMCM7_1	QIDPNTFDIR	FI	718
BoMCM7_1	QIDPNTFDIR	FI	718
BrMCM7_2	QIDPNTFDIR	FI	711
ZmMCM7	QIHPSTFDIH	FIDA	720
PsMCM7	QIHPQTFDIK	FIDA	720
MCM7_Glyma03g37770	QIHPHTFDIR	FIDA*	720
MCM7_Glyma19g40370	QIHPHTFDIR	FIDA*	720
ZmMCM4	EIHMHRLGA	LGTLMTGAVVIHGDNVRRV	850
AtMCM4	EIHLHDVKA	VATLASEGFLVAEGDRIKRV	847
BoMCM4	EIHLHDVKA	VGTLASEGFLVTEGDRIKRI	825
BrMCM4	EIHLHDVKA	VGTLASEGFLVTEGDRIKRI	825
MCM4_Glyma11g12110	EVHLNDRNA	IATLATEGFVTMHGDIVKRS*	835
MCM4_Glyma12g04320	DVHLNDRNA	IATLAAEGFVTMHGDSVKRS*	839
PsMCM4	EIHLNDRNA	VSTLASEGFLSVAGESVKRT	834
BoMCM6_2	KYSSQEQVKLDIKKLRAIIESFVCKEGHLIVLANEQEEATEAEE	-TRRKSSQORDERILAV	655
BoMCM6_1	KYTSQEQVKLDIKKLRAIIECYPMCKPKQVKNQEEEMRG	-----SWPL	810
AtMCM6	KYSSQEQVKLDIKKLRAIIESLVCKEGHLIVLANEQEEAAEAE	-TKKKSSQORDERILAV	824
BrMCM6	KYTSQEQVKLDIKKLRAIIESLVCKEGHLIVLSNEQEAEGE	-----EPRRRDERILAV	818
ZmMCM6	AYSSTAIEVKEEVKCIKAIIEERLIQREGHLIVIDEGTAAAAEDGSGA	---RRTSESRILAV	824
PsMCM6	NYSSIEEAKTEVSVQIKAIIEILIRREGHLIVVDDGRQAAAAEAGAEQTESAARNDRILAV		820
MCM6_Glyma09g05240	NYSSMEEVQAEISKIKAIIESLIRREGHLIVVDDGQAAAAA	---EPPGAPRNYRILAV	855
MCM6_Glyma15g16570	NYSSMDEVQAEISKIKAIIESLIRREGHLIVVDNGEAAAAA	---EPPGAPRNYRILAV	841
AtMCM2	-----	-----	936
BoMCM2_1	-----	-----	924
BrMCM2_1	-----	-----	927
BoMCM2_2	-----	-----	922
BrMCM2_2	-----	-----	931
ZmMCM2	-----	-----	957
PsMCM2	-----	-----	933
MCM2_Glyma07g36680	-----	-----	929
MCM2_Glyma17g03920	-----	-----	935
ZmMCM5	HVI	VRKA	729
AtMCM5	RSI	VRKA	727
BoMCM5	RSI	VRKA	727
BrMCM5	RSI	VRKA	727
PsMCM5	RVL	FRKA	732
MCM5_Glyma13g22420	RVV	FRKA*	732
MCM5_Glyma17g11220	RVV	FRKA*	732
ZmMCM3	RVM	IRDGVVRII	768
AtMCM3	KVM	ISDGKVHII	776
BrMCM3_1	KVM	ISDGKVHII	776
BoMCM3	KVM	ISDGKVHII	771
BrMCM3_2	KVM	ISDGKVHII	771
MCM3_Glyma05g25980	RVM	ITDGVVHMIS*	782
MCM3_Glyma08g08920	RVM	ITDGVVHMIS*	782
PsMCM3	RLM	IVAGMVHMIS	710
AtMCM7	-----	-----	716

BoMCM7_2	-----	718
BrMCM7_1	-----	718
BoMCM7_1	-----	718
BrMCM7_2	-----	711
ZmMCM7	-----	720
PsMCM7	-----	720
MCM7_Glyma03g37770	-----	720
MCM7_Glyma19g40370	-----	720
ZmMCM4	-----	850
AtMCM4	-----	847
BoMCM4	-----	825
BrMCM4	-----	825
MCM4_Glyma11g12110	-----	835
MCM4_Glyma12g04320	-----	839
PsMCM4	-----	834

BoMCM6_2	ASNYVTE-	662
BoMCM6_1	LPTM----	814
AtMCM6	APNYVIE-	831
BrMCM6	APNYVIE-	825
ZmMCM6	NPNYVID-	831
PsMCM6	APHYVVD-	827
MCM6_Glyma09g05240	APNYVID*	862
MCM6_Glyma15g16570	APNYVID*	848
AtMCM2	-----	936
BoMCM2_1	-----	924
BrMCM2_1	-----	927
BoMCM2_2	-----	922
BrMCM2_2	-----	931
ZmMCM2	-----	957
PsMCM2	-----	933
MCM2_Glyma07g36680	-----	929
MCM2_Glyma17g03920	-----	935
ZmMCM5	-----	729
AtMCM5	-----	727
BoMCM5	-----	727
BrMCM5	-----	727
PsMCM5	-----	732
MCM5_Glyma13g22420	-----	732
MCM5_Glyma17g11220	-----	732
ZmMCM3	-----	768
AtMCM3	-----	776
BrMCM3_1	-----	776
BoMCM3	-----	771
BrMCM3_2	-----	771
MCM3_Glyma05g25980	-----	782
MCM3_Glyma08g08920	-----	782
PsMCM3	-----	710
AtMCM7	-----	716
BoMCM7_2	-----	718
BrMCM7_1	-----	718
BoMCM7_1	-----	718
BrMCM7_2	-----	711
ZmMCM7	-----	720
PsMCM7	-----	720
MCM7_Glyma03g37770	-----	720
MCM7_Glyma19g40370	-----	720
ZmMCM4	-----	850
AtMCM4	-----	847
BoMCM4	-----	825

BrMCM4	-----	825
MCM4_Glyma11g12110	-----	835
MCM4_Glyma12g04320	-----	839
PsMCM4	-----	834