Table S1. Percent Identity/Similarity of insect MCOs

		1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	AgMCO1		71.9	44.9	51.2	55.5	51.7	47.9	36.7	36.7	36.5	36.2	35.6	35.8	36.5
2	AaAAEL007802	83.3		47.8	55.8	55.2	54.1	51.7	37	37.3	36.7	36.7	35.9	36	37.1
3	AmLOC724890	58.1	62.9		53	44.6	51.8	52.9	34.9	34.7	34.2	35.2	34.7	34.6	35.1
4	BmMCO1	65.1	69.2	67.7		51.3	89	56.6	39.4	39.6	38.3	39.4	38.6	39.3	38.8
5	DmCG3759	71.8	74.7	59.1	67		53.4	48.6	36	35.8	35.6	34.7	35.5	35.1	35.9
6	MsLac1	65	69.8	67.2	96.4	67.7		55.6	38.9	38.8	38.2	37.8	38	38.3	38
7	TcLac1	63	66.4	68.3	73.9	65	72.2		39.3	38.8	38.1	38.4	38.7	38.2	39.2
8	AgMCO2A	55	57	53.6	62.7	55.3	62.7	62		97.6	84.2	87.6	93.3	87	86.4
9	AaLac1	54.3	56.4	53.4	62.9	55.6	62.9	61.5	98.8		84.1	87.8	93.1	87	86.4
10	AmLOC410365	53.2	55.3	52.2	61.7	54.8	60.6	60.1	93.8	93.1		83.8	83.6	82.6	84.1
11	BmLac2	53.8	56.5	53.3	63.2	55.2	62	61.5	94.6	94.5	92.6		88	95.8	86.5
12	DmCG30437-PA	54.1	56.2	53.3	62	55.3	61.8	61.8	97.5	97	93.5	93.3		86.6	87.4
13	MsLac2	53.5	56.2	52.7	62.9	54.2	61.2	61.2	93.8	93.3	91.8	97.8	92.6		85.3
14	TcLac2A	54.5	57.5	52.7	61.7	55.3	61.1	61.4	94.6	94.3	92.4	93.8	94.3	93.5	
15	AgMCO3	51.9	53.6	52.8	58.5	54.2	57.5	58.5	61.3	60.8	61.6	62.4	60.6	62	61.8
16	AgMCO4	51	53.5	52.7	58.5	52.9	57.2	57.2	61	61.2	61	61	59.8	60	59.8
17	AgMCO5	51	53.5	50.7	57.1	51.7	57.3	55.7	60.4	59.9	59.8	58.9	59.9	58.1	60.3
18	AaLac2	52.5	55.3	53.6	57.8	53.5	57.3	56.4	61.8	61.6	61.4	61.6	61.9	60.9	61.8
19	AaAAEL001632	53.2	55	52.1	59.2	53.8	58.5	57.4	62.5	63	61.3	62.8	62.6	62	62.3
20	AaAAEL001640	50.6	53	51.9	56.6	53.6	55.6	55.3	59.8	59.8	58.9	59.8	59.4	58.9	59.4
21	AmLOC552811	48.2	52.2	51.7	57.5	50.3	57.5	56.3	64.4	64.2	62.8	64.5	63.7	64	64.3
22	PhLac1	52.6	54.4	51	57.3	54.7	57.2	54.8	66.5	66.7	66.8	66.3	66.3	66.3	66.8
23	DmCG5959	51.8	52.9	52.4	55.5	52	55.8	56	55.1	55.1	52.5	54.8	54.5	54.2	54.9
24	DmCG32557	49.6	53.3	52.3	55.7	50.8	54.7	56	52.6	52.9	53.4	53.3	52.9	51.8	53.2

The matrix was generated using the MatGAT v2.0 program (Campanella et al., 2003)
Percent identity is given above the diagonal and percent similarity below.
The MCO1 group is highlighted in yellow, the MCO2 group is highlighted in blue, and the mosquito-specific group is highlighted in rose.

Table S1 (continued)

		15	16	17	18	19	20	21	22	23	24
1	AgMCO1	35.4	34.9	34.6	36.8	35.7	33.4	33.8	33.5	33.9	34.9
2	AaAAEL007802	35.7	35.8	35.5	35	37.7	35	34	34.6	35.9	35.5
3	AmLOC724890	35.2	33.1	34.7	35.5	32.9	34.8	32	34.5	32.7	34.5
4	BmMCO1	39.1	38.9	37.3	37.8	37.4	36.8	38.3	38.2	34.4	37.6
5	DmCG3759	37.3	33.9	33.4	34.6	34.2	35.2	33.4	34.3	34.6	36.1
6	MsLac1	38.8	39.4	37.8	38.6	37.8	37	37.1	38.1	34.9	37.6
7	TcLac1	37.4	37.3	37.5	36.9	38.1	37.6	36.2	35.3	36.4	37.1
8	AgMCO2A	42.5	40.5	41.6	41.1	41.5	42.6	43.4	48.1	33.5	33.6
9	AaLac1	42.7	41	41.3	40.9	41.9	42.8	43.3	47.7	33.2	33.4
10	AmLOC410365	40.9	40.8	41.4	39.3	40.9	42.1	43.3	50.6	31.7	33.9
11	BmLac2	42.8	40.8	40.4	39.5	41.4	42	43.8	48.1	33.7	32.9
12	DmCG30437-PA	42.2	40.4	41.6	40.9	42.3	43.1	43	48.6	33	32.9
13	MsLac2	42.7	40.7	40.4	39.5	41.8	41.9	43.6	48.2	33.2	32.7
14	TcLac2A	42.4	40.7	41.2	41	40.6	41.3	42.8	48.9	32.3	32.7
15	AgMCO3		49.7	45.6	64.5	48.9	45.1	39.4	37.9	31.8	31.9
16	AgMCO4	65.6		60.5	46.6	70.9	56.1	36.2	36.1	32.6	33.2
17	AgMCO5	61.9	74.7		44	59.4	61.5	36	35.2	33	33
18	AaLac2	78.5	65	62.1		45.6	42.5	39	36.6	32.6	33.5
19	AaAAEL001632	67.2	84.3	75.4	65.9		57.3	35.5	35.7	33.3	33.8
20	AaAAEL001640	62.8	71.7	74.2	61.9	71.8		37.9	35.1	31.3	33.3
21	AmLOC552811	58.3	54.7	55.5	57.1	54.8	57.4		38.2	31.5	32.2
22	PhLac1	55.9	55.6	55.2	54.9	57.2	54.8	56		31.2	32.1
23	DmCG5959	50.8	50.4	50.1	53.3	52.1	50.8	52	51.4		40.3
24	DmCG32557	49.9	51.9	49.3	51.1	52.5	50.1	52.2	49.6	60.4	

Figure S1. Intron/exon structure of MCO genes. Exons are represented by boxes that are drawn to scale, and their sizes (in bp) are indicated above the boxes. Introns are denoted by short lines, and their sizes (in bp) are indicated below the lines. Untranslated regions are shown in gray. The alternative exons of MCO2 are color coded to show analogous exons. The exons for MCO3, MCO4 and MCO5 are color coded to illustrate the relationship between the exons of these three genes. Note that the color code for MCO2 is different than the one for MCO3-5. MCO3 shares three intron positions with MCO4 and 5, and MCO4 and 5 share eight intron positions; MCO3, 4 and 5 share more intron locations with MCO2 than with MCO1 (see also Figure 1).

Figure S2. Alignment of insect MCO sequences. Sequences were aligned using the program ClustalW and adjusted by eye. The amino and carboxyl ends, which were highly variable, were left out of the phylogenetic analysis. Sequences blocked in grey were also omitted from the analysis because these regions aligned poorly due to high sequence variability. Numbers left and right of the alignment indicate amino acid position with respect to the start methionine. Asterisks (*) below the alignment indicate identical residues at that position while colons (:) and periods (.) indicate strong and weak conservative substitutions. Accession numbers for the sequences are given in the Materials and Methods section of the main text. A gap in the AmLOC724890 sequence of approximately 70 amino acids after position 210 is likely an error in the gene prediction as this occurs in a region containing several conserved residues. The missing sequence is likely encoded by the partial gene prediction LOC727569 (GenBank accession no. XP_001123278) which was not mapped to any linkage group; residues 7-100 and 171-208 of LOC727569 are a perfect match to residues 117-248 of LOC724890. However, inclusion or omission of the missing amino acids had no effect on the phylogenetic analysis, therefore, the LOC724890 sequence was used unaltered as deposited in GenBank.

Figure S3. Alignment of MCO2 isoforms. The carboxyl-terminal variable region of MCO2 proteins encoded by alternatively spliced exons was aligned using the program ClustalW and adjusted by eye. Numbers and symbols are the same as in Figure S2. Accession numbers for the sequences are given in the Materials and Methods section of the main text.

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AgMCO1          289  CKRACTLGRKPETCYYRFRLEWYRTLSKACYNCPY-NA----------------TDCERP  331
AgMCO2A         151  CARACREGEPPRICYYHFTVEYYTVLGAACQVCTPNAT----------------NTVWSH  194
AgMCO3           50  CLRECDNTQP-RICHFSWTMEHYHVMGPACRDCAKGNH----------------TDCYHP   92
AgMCO4           71  CDRICTEREAPRVCYFRWIAEHYAAMGSACGDCRWGNR----------------SHCFHP  114
AgMCO5           70  CDRHCVPGDPPLTCHFRWKLENYATMGSACWDCRLGNR----------------AHCFHP  113
AaLac1          145  CARACREGEPPRICYYHFTAEYYTVLGAACQVCTPNAT----------------NTVWSH  188
AaLac2           61  CMRSCEDTQP-RVCYFKWVLEHYHSMGPACKRCADGVH----------------SDCYLP  103
AaAAEL007802    241  CRRECMRGRKPMNCYYRFKMEWYETLSKACYECPY-NV----------------TDCERP  283
AaAAEL001632      9  CDRVCNATETPRICYFSWVAENYAAMGSACKDCRWGNH----------------TDCSHP   52
AaAAEL001640     66  CDRTCSVDEPSRICYYKWVLESYAAMGSACWDCIRGNR----------------THCFHP  109
AmLOC724890      47  CRRNCVDEAPPMQCHYIFRLEAYHTMSKACYDCPF-NV----------------TDCFRK   89
AmLOC410365     133  CARACRENEPPRICYYHFTLEYYTVLGAACQICTPNAT----------------NVVWSD  176
AmLOC552811      36  CVRNCTDNEQPKICYYFFHIEFYTTVGPACDIQGSN------------------------   71
BmMCO1          137  CERECKEGEDPMVCYYHFNLEWYQTMSKACFNCPF-NE----------------TDCFRP  179
BmLac2          157  CARACRENEPPRICYYHFTLEFYTVLGAACQVCTPNAT----------------NVVWSH  200
DmCG3759        245  CNRDCQVGAEPMTCRYKFVVEWYQTFSKACYDCPR-NL----------------TDCSRP  287
DmCG30437-PA    180  CARACREGEPPRICYYHFTLEYYTVLGAACQVCTPNAT----------------NTVWSH  223
DmCG5959        102  CRRVCQQGQS-QNCYYQLVVHNYQRLGPECQRCQF-DE----------------RACASE  143
DmCG32557        67  CRRDCADKQP-MTCYYYMVVHYDDTMAETCKRYLQSKFRFKLSGKEYIDGIALATQLAAN  125
MsLac1          148  CERECKEGEEPMVCYYHFNLEWYQTMSKACYNCPF-NE----------------TDCSRP  190
MsLac2          153  CARACRENEPPRICYYHFTLELYTVMGAACQVCAPNAT----------------NVVWSH  196
PhLac1           51  CARACIDGEPPKTCYYHFTVEYYSTLTEACKLCQQEAR----------------SRVTPD   94
TcLac1           44  CARKCVKDSVPMTCRYTFLLEWYHTLSKACYDCPY-NT----------------QDCYRE   86
TcLac2A         108  CARACREGEPPRICYYHFTLELYTVLGAACQVCTPNAT----------------NTVWSH  151
SpLOC586543      54  WFRDCT-GSAPMSCEYTFVVEWYYTMAKACYDCPC-NL----------------SDCERV   95
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AgMCO1          332  -HCITGDGVRR-NVAVINRMMPGPAIEVCENDIIVVDVENHLM-GESTTIHWHGLHQRRT  388
AgMCO2A         195  CQCVLADGVER-GILTVNRMIPGPSIQVCENDRVVIDVENHME-GMELTIHWHGIWQRGT  252
AgMCO3           93  -ACITADGVER-GVMSLNRKIPGPTISVCRHDLIVVDITNAMA-GTSAAIHWHGLHQRAT  149
AgMCO4          115  -QCITADGMER-GVLALNRRIPGPTIHVCRHDLIVVDVVNHME-GLESTIHWHGAHQYDT  171
AgMCO5          114  -QCITANGLER-GVFAINRRVPGPPIHVCKHDSIVVDVENQLE-GLGSTIHWHGFHQKAT  170
AaLac1          189  CQCVLADGVER-GILTINRMIPGPSIQVCENDRVVIDVENHME-GMELTIHWHGIWQRGT  246
AaLac2          104  -ACLTADGFER-GVMSINRQVPGPAIQVCKDDLIVVDMTNAMG-GTATAMHWHGLHQRDT  160
AaAAEL007802    284  -HCIAADGVSR-SVIVINRMMPGPSIEVCENDIITVDVENHLM-GDSTTIHWHGLHQKRT  340
AaAAEL001632     53  -QCITADGMER-PVVSLNRQMPGPAVIVCRNDIIVIDLLNHME-GSSTTIHWHGMHQTQT  109
AaAAEL001640    110  -QCVTANGMER-SIVSINRKMPGPLIFVCQGDTIVVDVSNEME-GMSATIHWHGFRQMQS  166
AmLOC724890      90  -HCIPADGIER-SILVVNRQMPGPAIEVCQGDRITVDVINLLH-SESTTMHWHGQHHVKT  146
AmLOC410365     177  CQCVLADGVER-GILTANRMIPGPSIQVCQGDKVVIDVENHIE-GMEVTIHWHGVWQRGS  234
AmLOC552811      72  -QCILADGIEK-TLIPINRQLPGPPIEVCLNDRVVVDVQNAAM-GMEATIHWHGLFQNGF  128
BmMCO1          180  -DCIPADGMNR-PLNVINRKMPGPAIEVCQHDRVIVDVENDLM-TEGTTVHWHGQHQKGT  236
BmLac2          201  CQCVLADGVER-GILTANRMLPGPSIQVCENDKVVIDVENHME-GMEVTIHWHGIWQRGS  258
DmCG3759        288  -HCVMGDGLER-SITVVNRMMPGPAIEVCEGDEIVVDVKNHLL-GESTSIHWHGLHQKKT  344
DmCG30437-PA    224  CQCVLADGVER-GILTANRMIPGPSIQVCENDKVVIDVENHME-GMEVTIHWHGIWQRGS  281
DmCG5959        144  -HCIYGDGVAN-PVMAVNRMVPGPSIELCENDTVVVDVLNYLS--EPTTMHWHGVHMHRT  199
DmCG32557       126  DDCKYADGLES-EVMVVNGQLPGMNIEVCYGDTVVADVINSMH--ETTTIHWHGMHQRLT  182
MsLac1          191  -DCIPADGMNR-ALSVVNRKMPGPAIEVCQDDRIIVDVENDLM-TEGTTVHWHGQHQRGT  247
MsLac2          197  CQCVLADGVER-GILTANRMLPGPSIQACENDKVVIDVENHME-GMEVTIHWHGIWQRGS  254
PhLac1           95  CQCIQADGYEKSGLITVNRMYPGPGIMACLGDNIVVDVENRVL-GNAVTVHFHGVYQRNY  153
TcLac1           87  -DCIPGDGNKR-SIIVVNRKMPGPSVEVCLGDEVIIDVVNHLS-SDSTTIHWHGHHQKNS  143
TcLac2A         152  CQCVLADGVER-GILTANRMIPGPSIQVCEGDKVVIDVENHIE-GNEVTLHWHGVWQRGS  209
SpLOC586543      96  -HCVPADGVPR-QIMVANRALPGPAIEVCEGDEVIVNAVNSMDNGESITLHWHGIYQTSN  153
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AgMCO1          389  PYMDGVPHVSQCPISPGTTFRYTFRADNPGTHFWHSHTGMQRGDGAFGALIIR--KDNDI  446
AgMCO2A         253  QYYDGVPFVTQCPIQQGNTFRYQWTG-NAGTHFWHAHTGLQKLDGLYGSIVVRQPPSRDP  311
AgMCO3          150  PYMDGVPFITQCPIGFGNTFRYAFLATEPGTQFYHSHSGHHKVNGHYGALIVREPKRVDP  209
AgMCO4          172  PWMDGVPMITQCPIPNGAAFRYAFNASEPGTQLYHSHSGHQKANGHYGLFVIRSP--TDI  229
AgMCO5          171  PWMDGVPMVTQCPIPQDTTFRYQFTAVEAGTQFYHSHAGFQKANGHYGMVVVRDP--SDL  228
AaLac1          247  QYFDGVPFVTQCPIQQGNTFRYQWTG-NAGTHFWHAHTGLQKLDGLYGSIVVRQPPSRDP  305
AaLac2          161  PHMDGVPFVTQCPIEFMSTFRYAFWATEPGTQFYHSHAGHHKVNGHYGAMIIRQPEVNDP  220
AaAAEL007802    341  PYMDGVPHISQCPISPGTTFRYTFKADNAGTHFWHSHTGMQRGDGAFGPLIIR--RDNDP  398
AaAAEL001632    110  PWMDGVPMVTQCPIPAGNTFRYVFNASEHGTQFYHSHAGHQKANGHFGLLVVRHP--TDL  167
AaAAEL001640    167  PWMDGVPMVTQCPIAPSTTFRYRFVAEEAGTHWYHSHSGYHMANGHLGAAVVRNP--LDV  224
AmLOC724890     147  PYMDGVPYVSQCPILPGSTFRYDFIATEAGTHFWHSHSGFQRGDGVFGPLIVRTPPKANW  206
AmLOC410365     235  QYYDGVPFVTQCPIQEGSTFRYQWTAGNEGTHFWHAHTGLQKMDGLYGSIVIRQPPSKDP  294
AmLOC552811     129  QYYDGVPYVTQCPIASSSTFRYDFVVKNSGTHFYHSHISTHMLDGQIGSFIVKDPPRKNP  188
BmMCO1          237  PYMDGTPYVTQCPIPPETTFRYQFNATHTGTHFWHSHSGMRADGAAGAFIVRKPKSQDP  296
BmLac2          259  QYYDGVPFVTQCPIQQGNTFRYQWG-NAGTHFWHAHTGLQKLDGLYGSIVVRQPPSKDP  317
DmCG3759        345  PYMDGVPHITQCPITPHATFRYSFPADLSGTHFWHSHTGMQRGDGVFGALIIRKPKTAEP  404
DmCG30437-PA    282  QYYDGVPFVTQCPIQQGNTFRYQWTG-NAGTHFWHAHTGLQKLDGLYGSVVVRQPPSRDP  340
DmCG5959        200  PEMDGAPFITQYPLQPGEVQRHEFKVDRSGSLWYHSHVGWQRGFGVAGAFVVRQTSQENQ  259
DmCG32557       183  PFMDGVPHVTQYPIEAGQAFRYRFEVDHGGTNWWHSHTEHQRAFGLAGPLVVRMPPKLNP  242
MsLac1          248  PYMDGTPYVTQCPILPETTFRYQFTARHSGTHFWHSHSGMQRADGAAGAFIIRKPKSQEP  307
MsLac2          255  QYYDGVPFVTQCPIQQGNTFRYQWQG-NAGTHFWHAHTGLQKLDGLYGSIVVRQPPSKDP  313
PhLac1          154  QYSDGVPFVTQCPIQEGSTFRYQWKAENSGTHLWHAHTGLHKGEGLMGPLIIREPKSTEP  213
TcLac1          144  PYMDGVPFVTQCPIHPGMTFRYHFNVHNSGTHFWHSHSGFQRSDGTFGPFIVRVPEEDNP  203
TcLac2A         210  QYYDGVPFVTQCPIQQGNTFRYQWIAGNAGTHFWHAHTGLQKMDGLYGSVVIRQPPAKDP  269
SpLOC586543     154  QYMDGVFMVTQCPILPRTTFRYNFSADHAGTHFWHAHTGMHRADGLFGAMIIRQSKQVDA  213
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AgMCO1          447  QELLYDHDLSEHVITVQDWGHEQGVSLFASHHHSTG-DNKPPNLLINGRGKYFQRFAKTT  505
AgMCO2A         312  NSHLYDFDLTTHIMLVSDWLHEDAAERYPGRLAVNT-GQDPESLLINGKGQFRDPNTGFM  370
AgMCO3          210  NGDLYHYDTPAHVILGSDWMHIDGEMFMPG--LPSAGGIMPINLLINGKGTYHD-PKKNE  266
AgMCO4          230  NRHLYDYDLSEHHIIISDWTLDLVEKFVPG--LQS-STVRMDSILINGRGRHFDEEEHEL  286
AgMCO5          229  NQAHYDYDLSEHRIIIADWTLDMVEKWVPG--IQT-DSMRVDSILINGRGRYFNETTGTR  285
AaLac1          306  NSHLYDFDLTTHIMLVSDWLHEDAAERYPGRLAVNT-GQDPESLLINGKGQFRDPNTGFM  364
AaLac2          221  NAKLYDFDLPEHLIVASDWMHVDGEMYMPG--LPNGDGILPVNLLINGRGTWLK-HNGN-  276
AaAAEL007802    399  QQILYDHDLSEHVITVQDWGHVAGNQMFTAHHHSTG-DNKPPNILINGRGKYFKRYPKIS  457
AaAAEL001632    168  NMNLYDYDLSEHHIIIADWTLDMAEKFVPG--LQS-HTIQMDSILINGRGRHFDEEEQEL  224
AaAAEL001640    225  NMALYDFDLSEHVMLISDWTLDSAERWVPG--QQS-SQMAVDSILINGRGRYTKEETGTK  281
AmLOC724890     207  HKDL--------------------------------------------------------  210
AmLOC410365     295  NSNLYDYDLTTHVVLISDWFHENAAERFPGRLAVNT-GQAPESVLINGKGQFRDPNTGFM  353
AmLOC552811     189  HRDLYDKDE--IVIFLSDWIHELSFERYPGYYRYNVLGQTAENILINGLGNYTNAN-GNT  245
BmMCO1          297  HGHLYDYDRTDHVMIVTDWIHELSVGMFTDHHHSSG-DNKPPTLLINGVGR-FRVFNNDT  354
BmLac2          318  NSHLYDYDLTTHVMLISDWLHEDAAERYPGRLAVNT-GQDPESVLINGKGQFRDPNTGFM  376
DmCG3759        405  HGGLYDFDLSEHVMIVQDWIHDTGASIFSYHHHSRG-DNKPHNLLVNGKGRYYNRIWAEA  463
DmCG30437-PA    341  NSHLYDFDLTTHIMLISDWLHEDAAERYPGRLAVNT-GQDPESMLINGKGQFRDPNTGFM  399
DmCG5959        260  HSQLYDYDLVEHTLMIQDIFYEYNLQDVRN-------------ILVNGKGRNHLSQLPDN  306
DmCG32557       243  HAHLYDFDMSEHVIMIQDWVHNFVESVAEN-------------ILINGRGN-LKKGVKA  288
MsLac1          308  YESLYDYDRSDHVMIVTDWIHQLAVGMFTDHHHSSG-DNKPPTLLINGVGR-FKIFNNDT  365
MsLac2          314  NSHLYDYDLTTHVMLISDWLHDDAAERYPGRLAVNT-GQDPESVLINGKGQFRDPNTGFM  372
PhLac1          214  NHDLWDHDDIDNVIFLSDWFHRSSADHFPGNFHREP-GQEPDNFLINGMGQWTDPDTGET  272
TcLac1          204  HAKLYDYDLSSHVITILDWTKEDGTDKFMSHIHNDG-DNKPDTILVNGFGR-FKHFVGAD  261
TcLac2A         270  NSHLYDYDLTTHVMLLSDWMHEDATERFPGRLAVNT-GQDPESLLINGKGQFRDPNTGFM  328
SpLOC586543     214  QGLLYDYDLPEHKVVLIDWTHQGHVSIYLDQHFRGT-EDDPKSILINGKGA-FAVYGNDA  271
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AgMCO1          506  PLTTTTTSTEEPALEPETIMAVEPESTTLMEELPTTTVPITDAITPDDTELLQASSNTNL  565
AgMCO2A         371  TN---------------------------------------------------------  372
AgMCO3          267  TTQ--------------------------------------------------------  269
AgMCO4          287  QTQ--------------------------------------------------------  289
AgMCO5          286  AD---------------------------------------------------------  287
AaLac1          365  TN---------------------------------------------------------  366
AaLac2          277  RTN--------------------------------------------------------  279
AaAAEL007802    458  TISVNRD----------------------------------TANDAELIQSSPSKGL    480
AaAAEL001632    225  QQ---------------------------------------------------------  226
AaAAEL001640    282  VDY--------------------------------------------------------  284
AmLOC724890     210  -                                                            210
AmLOC410365     354  TN---------------------------------------------------------  355
AmLOC552811     246  TN---------------------------------------------------------  247
BmMCO1          355  EKP--------------------------------------------------------  357
BmLac2          377  TN---------------------------------------------------------  378
DmCG3759        464  KQAHRRAEER---------------------------TTQPVEPLPKSQVDFVQ       490
DmCG30437-PA    400  TN---------------------------------------------------------  401
DmCG5959        307  DNR--------------------------------------------------------  309
DmCG32557       289  AKP--------------------------------------------------------  291
MsLac1          366  EKP--------------------------------------------------------  368
MsLac2          373  TN---------------------------------------------------------  374
PhLac1          273  TN---------------------------------------------------------  274
TcLac1          262  NST--------------------------------------------------------  264
TcLac2A         329  TN---------------------------------------------------------  330
SpLOC586543     272  STS--------------------------------------------------------  274


AgMCO1          566  KTVLRAEEVR---HRTKRQSRTVNFNAIVVPESKHIPLKVFHVDKGRRYRFRLINAEFLN  622
AgMCO2A         373  ----------------------------------TPLEIFTITPGRRYRFRMINAFASV  397
AgMCO3          270  ----------------------------------TPLEVYTVRRGARFRFRFINAASHV  294
AgMCO4          290  ----------------------------------APLTVYRVKKGYRYRFRLVSSGSQF  314
AgMCO5          288  ----------------------------------APLTVYQVEYGKRYRFRLISSGSQY  312
AaLac1          367  ----------------------------------TPLEIFTITPGRRYRFRMINAFASV  391
AaLac2          280  ----------------------------------APREVYRVRKGGRYRFRFINAASHV  304
AaAAEL007802    481  KQVTATNLSMRPLARMKRQSRTVNFNAVVVPESEHIPLKVFHVEPKKRYRFRLINAEFLN  540
AaAAEL001632    227  ----------------------------------SPLTVYRVEQWKRYRFRMISSGSQF  251
AaAAEL001640    285  ----------------------------------TPLTVFRVRRNYRYRFRLISGGSQY  309
AmLOC724890     211  -------------------------------------------YRFRLVNAEFLN      222
AmLOC410365     356  ----------------------------------TPLEVFTITPGRRYRFRLINSFGSV  380
AmLOC552811     248  ----------------------------------GSLKVFTVKKGERHIRMINSFSTV  272
BmMCO1          358  -----------------------------LYMKAARFNVEQGHRYRFRVINAEFLN    384
BmLac2          379  ----------------------------------TPLEVFTITPGRRYRFRMINAFASV  403
DmCG3759        491  TLPRQARLAKTNTTKLFPVNSRQKRGNLNEIPLELVPHQIYTVRRGFRYRFRIINAEYLN  550
DmCG30437-PA    402  ----------------------------------TPLEIFTITPGRRYRFRMINAFASV  426
DmCG5959        310  ----------------------------------HRYERLRVTPGYRYRMRVILNGIAN  334
DmCG32557       292  ----------------------------------TLYAHFPVVRGGRYRFRVIFNGVSN  316
MsLac1          369  -----------------------------VYMKAARFNVEQGYRYRFRVINAEFLN    395
MsLac2          375  ----------------------------------TPLETFTITAGRRYRFRMINAFASV  399
PhLac1          275  ----------------------------------TSYAHFNVTNGKSYKFRLINGAGMT  299
TcLac1          265  -----------------------------VFVPTARFTVEQGYRYRFRVINAGFLN    291
TcLac2A         331  ----------------------------------TPLEVFTITPGRRYRFRMINSFASV  355
SpLOC586543     275  ---------------------------------TVTPREIYNVTQGKRYRFRVISSAIAN 301
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AgMCO1         623 CPVELSIENHNLTVIASDGFGIQPLEDLGSFVSYAGERFDFIVKANQPIGNYLIRFRGLM 682
AgMCO2A        398 CPAQVTIEGHALTVIATDGEPVHP-AQVNTIISFSGERYDFVITADQPVGAYWIQLRGLG 456
AgMCO3         295 CPLQLQIEDHMMEVIASDSFHLQP-RKVDTLVSTSGERYDFVLEANGVKDTYWVRLRSLG 353
AgMCO4         315 CPFQLQIEKHRMQLIVTDGGAVQP-TMVDTLISTSGERYDFVLSANQKPGTYWVRVRAIG 373
AgMCO5         313 CPFQMQIQNHSMLIISTDGGTVQPHTVDTLVSISGERYDFVLTANQPPGNYWVRVRGIG 372
AaLac1         392 CPAQVTIEGHGLTVIATDGEPVLP-VQVNTIISFSGERYDFVISADQQVGAYWIQLRGLG 450
AaLac2         305 CPLELQIANHTLEIIASDSYNLQP-ISANTLVTTSGERYDFVVNADQPTDDYWIRLRAIG 363
AaAAEL007802   541 CPVELSVEGHNLTVISSDSFDINPVEDLASIVSYAGERFDFILRANQPVGNYLMRFRGLM 600
AaAAEL001632   252 CPFQLQIEAHRMQIISTDGGAVQP-VTVDTVISTSGERYDFVLHADQKPGDYWVRVRAVG 310
AaAAEL001640   310 CPFQLQIENHRMLVISTDGGAVKP-HMVDTLISISGERYDFVINADQPVGNYWVRVRGAG 368
AmLOC724890    223 CPIEISIDNHTMRVISSDGRDIEAVE-AESLVSYAGERFDFVVETSQNIDNFWIRFRGLM 281
AmLOC410365    381 CPSQITFEGHSLTIIATDGEAVQP-VTVDTIISFSGERYDFVINADQPVGAYWIQVRSLG 439
AmLOC552811    273 CLTELRIEKHKLIIIAQDGENVKP-KPVDKIVTSTGERVDFILVANQSVDSYWIQARGLG 331
BmMCO1         385 CPIELSVDGHNITVISSDGYDLEPIA-ATSLVTYAGERYDFILDANNEIDNYWIRFRGLM 443
BmLac2         404 CPAQITFEGHNLTVIATDGEPVQP-VQVNTIISFSGERYDFVIEANNIPGAYWIQVRGLG 462
DmCG3759       551 CPIVVSIDGHNLTAINSDGFDIEAMD-VGSIVTYSGERFDFVLNANLEVGNYWIRLKGLM 609
DmCG30437-PA   427 CPAQVTIEGHGMTVIATDGEPVHP-VDVNTIISFSGERYDFVISADQPVGAYWIQLRGLG 485
DmCG5959       335 CPVEFSIEQHRLLMISTDGNDIEP-VLADGFFLTSAERFDFVLEANQYKKNYWIRIKGYE 393
DmCG32557      317 CPISFSIDKHDLVVIASDGNDIEP-VEVQRIMFHGAERFDFVLHANQEVSNYWIRVKGYS 375
MsLac1         396 CPIEMSVDGHNITVIASDGYDLEPIT-ATSLVTYAGERYDFILDANNEIDNYWIRFRGLM 454
MsLac2         400 CPAQVTFEGHNLTVIATDGEPVQP-VQVNTIISFSGERYDFVIEANNIPGAYWIQVRGLG 458
PhLac1         300 CPLMLTIEGHKMHIIASDGQPLEL-VTVNTITSFAAERYDFVLNANKPIGNYWIQLRADG 358
TcLac1         292 CPIEVSIDNHTLSVISTDGSDFNATE-VDSLVTYAGERFDFIVTADQPQDVYWMHFRGLM 350
TcLac2A        356 CPAQLTIQGHDLTLIATDGEPVHP-VRVNTIISFSGERYDFVINADQTPGAYWIQLRGLG 414
SpLOC586543    302 VPMKVSVDGHNITLISSDGDDFEPLE-VDAFFLYGGERYDFILNASQEVGNYWLKVEGSK 360
                    .  .   *  :    *   *.   .              .    .** **:: :.      : ::  ..

AgMCO1         683 DCDERFTSAYQFAVLRYRGAPT-------------DTEYESWPPYD----YEAPGVQLNS 725
AgMCO2A        457 ECG--IKRAQQLAILRYARGP-------------YQPASPPPTYD---VGLPQGVVMNP 497
AgMCO3         354 PCA--DLQLEQFAVLRYTTGP--FIN--------DAFPTGAPPTYEEP--FRNVATANH 398
AgMCO4         374 FCN--IERREEFAVLSYEDEAHHVPE------EVLAYPKRTPPSWDDR---FPSGTVLNN 422
AgMCO5         373 FCD--QMRVEDFAILSYRTPETAIPAAGLTVEQTLAYPTEPMPTYDEP---YPDGIVFNH 427
AaLac1         451 ECG--IKRAQQLAILRYARGP-------------YQPASPPPTYD---VGLPQGVVLNP 491
AaLac2         364 PCD--YRQISQVAVLSYQPMSVPEED--------IAFTDKEIPHYQDQL--FLNDVYVNH 411
AaAAEL007802   601 DCDERFTSAYQVAVLRYKGAP-------------EVEYEQWPNYD----FPLEGMQLNS 642
AaAAEL001632   311 FCN--IQRKEEFAVLSYRSSSE-ISD------EELAFPVQVPPTWDEP---FPDGMTLNH 358
AaAAEL001640   369 FCS--TLSVETFAILSYADPSIST--------ESLMYPTLEPPEYGNA---YPMGQTLNE 415
AmLOC724890    282 DCDERFTKAYQVAILRYEGAT-------------NKDPNGLVGYEYKSNYSTDGQRINA 327
AmLOC410365    440 ECG--IPRAQQLGILRYARGP-------------YQPTTTAPTYD---FGLPQGVVLNP 480
AmLOC552811    332 ECA--TTFMQQLAILKYENGP-------------FRPSTPLPNYN----DTIDGVIYNG 371
BmMCO1         444 DCDEVFTKAKQVGVLHYEGAM-------------EVEPAGDPTWE---ELHNEGLQLNA 486
BmLac2         463 ECG--IKRAQQLGILRYARGP-------------YQPSSLAPTYD---VGIPQGVVMNP 503
DmCG3759       610 DCSEVFTSAFQVAILRYEGAP-------------DEEPTAELSYG----HKAEGIELNV 651
DmCG30437-PA   486 ECG--IRRAQQLAILRYARGP-------------YQPASSPPTYD---VGIPQGVVMNP 526
DmCG5959       394 QCE--NRNIYQGAVLSYRGSARS-----------ELPQGDILDKPSSRAADEDLILVND 439
DmCG32557      376 FCA--KNQLHQEAVLHYRDADTR-----------ALDT-----HTLSYAYDAPGKTLNE 416
MsLac1         455 DCDEIYTRAKQVAVLHYEGAM-------------DLEPPGDPSWF---ELHNEGLQLNA 497
MsLac2         459 ECG--IKRAQQLGILRYARGP-------------YQPSLPAPTYD---IGIPQGVVMNP 499
PhLac1         359 PCI--NRKMQQFAVLHYTSAP-------------VEPQRSRITFDGP-TSLDTGVILNP 401
TcLac1         351 DCDERFTRAYQVAVLEYKGTQ-------------TNYPSYEPTYD---NSRREGKQLNP 393
TcLac2A        415 ECG--IRRVQQLGILRYAKGP-------------YQPSQAPPTYD---YGIPQGVVLNP 455
SpLOC586543    361 QGSGLVG----LAVIRYQGAA-------------DEVPPADPSVD------RQGLVYQD 396
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AgMCO1         726  LN--RGPGA--ENV-ITIAETSAL------DQEDLLLLRNETDYKFYVYYDFYGKDNPH-  773
AgMCO2A        498  LD-AQCNVQ--RDDAICVSQLKNAKE------IDRALLQDKPDVKIFLPFRFYLYRPEE-  547
AgMCO3         399  PN-ATCGRP--EFGDYCITDFQAYDT-------DEDVINGVPDHQLTFGFYNYPVSFES-  447
AgMCO4         423  PN-ATCYVP--GDDDLCVADLESHEVH-----RDDDLIDAAPNKTFRILFNTFTADPAV-  473
AgMCO5         428  QT-APCYTP--NDTYICAADLEAYEVF-----RDTGLIDAVPDRTFFLGFHVIEANNSL-  478
AaLac1         492  LD-AQCNVQ--RDDAICVSQLKNAKD------IDRALLQEKPDVKIFLPFRFYLYRPEE-  541
AaLac2         412  PN-TTCGVS--KP-DVCITDFQAYET-------DDDVINGVPDMQFILGFENYPMKFED-  459
AaAAEL007802   643  LN--KGTGH--SDT-MSIAETSSR------DQEDLLLLREKTDFKFYVYYDFYAKDNPH-  690
AaAAEL001632   359  PN-STCYQP--GDQFVCASDLEAHEVQ-----RDDALIDAVPDKKFYVAFNTFTADTSL-  409
AaAAEL001640   416  QT-ATCYNS--EDQFTCAADLETHEAH-----RDDKLINATPDVRLFLGFKMMHPDNRW-  466
AmLOC724890    328  LN--EGTET--NNS-ISIPLLKAM------DKNDKSN-TADPDYQFYVSYDFYKKDNPH-  374
AmLOC410365    481  LD-AICNRQ--REDAICVSQLKNARQ------IDQGILQQRPDVKIFLPFRFLFYRPEE-  530
AmLOC552811    372  LNGTLCNTN-ITEPVLCINQLESLES------EN-DLLKVEPDERHILPFWFFNYTDTSK  423
BmMCO1         487  LN--KGEEE--DET-ISVAEMKSL------DGYDESL-KEIADYQFYVAYDFYAKNNSH-  533
BmLac2         504  LD-ARCNIS--RNDAICVSQLKNAQN------IDPAILQERPDVKIFLPFRFFVYRPEM-  553
DmCG3759       652  MN--RGPGY--PDT-KTVAEMRALPIYDHVSGIDHDTLKPEADYKFFIYYDFYTKNNPD-  705
DmCG30437-PA   527  LD-AQCNRQ--RNDAICVSQLKNALE------IDRGILAEKPDVKIFLPFRFFVYRAED-  576
DmCG5959       440  FR------------FKPANSTAISSL----RQSLDKDNNVGTVALRSVDPVPWTRYTK-  481
DmCG32557      417  LG------------DDASGARAG-------------NSISLANLNAQRPEPEVAPS--  447
MsLac1         498  LN--KGEEE--NET-ISVAEMRSL------AGYDDSL-KEIADYQFYIAYDFYAKNNSH-  544
MsLac2         500  LD-ARCNIL--RNDAICVSQLKNAKH------IDPAILQERPDIKIFLPFRFFVYGPET-  549
PhLac1         402  LN-VRCFEQKLRTYIRCMSDLVNAKP------IPQEILKDKADVQIFMNFGFNGYDPND-  453
TcLac1         394  LN--KGTEA--DSSFVTLPQLHSL------DEWDDTL-KEKADFQYYVSYDFYKMNHPV-  441
TcLac2A        456  LD-ARCNEI--RPDAICVSQLKNALS------IDKGILREKPDVKIFLPFRFHIYTPED-  505
SpLOC586543    397  VD--QEPNV--FPS---VNDLRSLG-------------------------TSKLNNPT-  422


AgMCO1         774  ---FHVPSLYGFQQVVNNTNRLYTPQLNHISMRMPPVPFLPGKDVLDE--SQFCNETSVR  828
AgMCO2A        548  --LFQPNTYNRFLVAPTGDHVISL--IDEISYLSAPAPLLSQYDDINP--EQFCNGDNRP  601
AgMCO3         448  --MFESNRYEHYMNIYGSVMMQGA--INNISLAYPPFSLLTQPEKIR--DDTFCDEDNRP  501
AgMCO4         474  --LFSDQGYVRYMTVVLTLNNIGV--TNNISMVFPDFPLLTQPELIG-GDGMFCNNTHRP  528
AgMCO5         479  --LFSDRGTSHYATVREGFNTIGA--TNMISFVPPSFPLLIQPELIVDENAQFCNVSHRP  534
AaLac1         542  --LFQPNTYNRFLVAPTGDHVISL--IDEISYLSAPAPLLSQYDDINP--EQFCNGDNRP  595
AaLac2         460  --AFGMGSHEHFMNIHDDIVLQGA--INNISFTYPPFSLLTQTDLIT--EGMFCDEDSWP  513
AaAAEL007802   691  ---FHVPDLYGFKDVINNTNRLFTPQLNHISMRMPKIPMMPGKDELDE--SLFCNASSLM  745
AaAAEL001632   410  --LFSNDGYVRYMTVALTLNNIGI--TNNISMVYPSFPPLTQPELLPTMENAFCNVSSRP  465
AaAAEL001640   467  --LFSEYKP--FITVREDFNTIAA--ANNISFRYPSFPLLIQPDLIIDENKQFCNSTHLP  520
AmLOC724890    375  ---FHRGKLYGFNQVKN-TKQVLTPQLNHISMKLPPMPLLSQRDFIDS--DQFCNSSTVQ  428
AmLOC410365    531  --VFQPQTYNRFLVAPTGDHVISL--VDEISFTFPPAPPLSQIDDIPP--EQFCNGDNRP  584
AmLOC552811    424  NRLFNSSSYLPFFNANDRSQLLSI--FNDIAYENPASNLLTQSSSYR----AICK-KNQL  476
BmMCO1         534  ---FHRSPYYGYYQVPEKVNRLYTPQLNHISMKMPSSPLLVAR--PTP--DHFCNASSIE  586
BmLac2         554  --LFQPNTYNRYLVAPGGDHVISL--IDEISYMSPPAPLISQYDDINP--DQFCNGDNRP  607
DmCG3759       706  ---FHDKDLYAMDMEMTQQNRLYTPQLNHITLNFPSLALLPSRSQLKD--SDFCNETSLM  760
DmCG30437-PA   577  --LFQPNTYNRFLVAPTGDHVISL--IDEISYLSAPAPLTSQYNDINP--DQFCNGDNRP  630
DmCG5959       482  ----FLTHYSSFGSRTAPNGE-VLFQISDISYNSPGISLLQGRHLYQDD-RYFCNKSSLA  535
DmCG32557      448  -----VTFYTSMNAFEVRQGEGFRFQMDDISFSMPKMSLLQTRNLGVG--QFFCNRSQQA  500
MsLac1         545  ---FHRSPYYGYYQVPEQVNRLYTPQLNHISMKMPTSPLLITR--PSP--ENFCNASSID  597
MsLac2         550  --LFQPNTYNRYLVAPSGDHVISL--IDEISYMSPPAPLLSQYDDINP--EQFCNGDNRP  603
PhLac1         454  --LFQPGRYLPYHVAGGG-ESVAM--MGNISNFYPASPLLSQRSDIPD--DQICSIADRE  506
TcLac1         442  ---YHKDPHYGFHNVTNTTLQNLTPQLNYISMKLQSFPLLSQRHQIDA--KMFCNESSVS  496
TcLac2A        506  --LFAPNTYNRHLVAPNGDHVISL--IDEISYMAPPAPLISQYDDIDP--QQFCNGDNRP  559
SpLOC586543    423  ---FNDADLYPLGPSGPGWGEQTLPQINNRTFHFPGFPLLSQFDDERA--AEGYYDDILC  477
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AgMCO1          829  DR------NCRQEF-CECSHVLQIPLHATVEMVMIDEGF-TFDANHPFHLHGHAFRVVGM  880
AgMCO2A         602  AD-------CGAN--CMCTHKVDIPLNAIVEVVLVDEVQ-QPNLSHPFHLHGYAYNVVGI  651
AgMCO3          502  DS-------CSDRQLCTCTHRVKINLGDIVELYILDLTPSVNDLNHPFHLHGYQMFVMEM  554
AgMCO4          529  AR-------CKPHHACFCLHRLKVALNDVVEMSLIDDAEVVRDLYHPFHLHGHRFIVTGM  581
AgMCO5          535  AY-------CTDDHLCFCTHRMKVKHNDVIEIVLYDTAEVRQKFYHPFHLHGHRFIVTDS  587
AaLac1          596  AD-------CGAN--CMCTHKVDIPLNAIVEVVLVDEVQ-QPNLSHPFHLHGYAYNVIGI  645
AaLac2          514  ER-------CQTRDHCTCIHRLKIPLHALVELYILDLTPEVNDLNHPFHLHGYQMYVMEM  566
AaAAEL007802    746  EQGI----NCREEF-CECSHVVQVPLNSTVEMVLIDEGF-TFDANHPFHLHGHAFRVVGM  799
AaAAEL001632    466  AQ-------CPMERACFCVHRLKVDLNDIVEMSLIDDAEVIRELYHPFHLHGHRFIVTGM  518
AaAAEL001640    521  PG-------CDRLHLCFCTHRIKVKLNDIVELTLYDTAYERQNFYHPFHIHGHRFIITDM  573
AmLOC724890     429  G--------CVQDY-CACTHVLRVNLDSVVEIILVDEGF-AYDANHPFHLHGYQFRVIAM  478
AmLOC410365     585  AD-------CGAN--CMCTHQVDIPHNAVVEVVLVDEVQ-QPNLSHPFHLHGYAFNVIGI  634
AmLOC552811     477  ST-------CTEP--CTCAQIIKTKLNNVVELVMYDAIP-QTDLDHPFHLHGFAFQVFSV  526
BmMCO1          587  ES-------CKEGY-CECSHVLSVKLNSVVEVVIVDEGI-TFDANHPFHLHGHSFRVVGL  637
BmLac2          608  AN-------CGQN--CMCTHKVDIPLNAVVEIVLVDEVQ-IANLSHPFHLHGYSYNVIGI  657
DmCG3759        761  DQGI----DCRQEF-CKCHHVLQVPLGAVVEMIIVDEGF-QYYANHPFHLHGNAFRVMGL  814
DmCG30437-PA    631  AD-------CGPN--CMCTHKIDIPLNAIVEVVLVDEVQ-QPNLSHPFHLHGYGFSVIGI  680
DmCG5959        536  AEGR----NCEREL-CECVNVMRLPAYRPLEMVVANYLD----STHPFHIHGFTFRLVGQ  586
DmCG32557       501  DLGF----NCRQRH-CQCSNVIQVPANQQVEFVISSLSQ----TPHPIHLHGYTFRVVGM  551
MsLac1          598  EG-------CKEGY-CECPHVLSVKLNAIVEVIIVDEGV-TFDANHPFHLHGHSFRVVGL  648
MsLac2          604  AN-------CGQN--CMCTHKVDIPLNAVVEIVLVDEVQ-ITNLSHPFHLHGYAYNVIGI  653
PhLac1          507  AK-------CGKAYPCQCVHIERIPLNSVTELILTDEAK-IANLSHPFHLHGQPFYLFGE  558
TcLac1          497  N--------CENEY-CECTHVVNIPLGTVVEMVLIDKGY-AYDANHPFHLHGHSFRVVAM  546
TcLac2A         560  AD-------CQQN--CMCTHKVDIPLNAIVEIVLVDEVQ-QPNLSHPFHLHGYAFNVIGI  609
SpLOC586543     478  EVEQDGFENCDTEF-CACTQYIKVDLGQTLEIILIDVGAGPFPVNHPFHLHGHAFRILAQ  536
                     *      *  *  :           *. :  .         **:*:**     :

AgMCO1          881  DRV--SRNTTIEDIRRMDEEG------RLPRRLK-------------------RAPIKD  912
AgMCO2A         652  GRS-PDSNVKKINLKHALDLD----RRGLLHR-------QYN------------LPPLKD  687
AgMCO3          555  SQDR-RVPITLEIAQNIAR------QRLLSRN-------------------TVALPPRKD  588
AgMCO4          582  GQLP-QFGTQSEKVDFVER-----ARRYSRTMP-----------------SDHNPPYKD  617
AgMCO5          588  GSFP--SDILTDQIAYLRN-------LRTVRRP-----------------NAHCPPYKD  620
AaLac1          646  GRS-PDSNVKKINLKHALDLD----RRGLLHR-------QYN------------LPPLKD  681
AaLac2          567  GQDR-STPITMERAQKIAR------RQSLHRTR-----------------VTTMPPKKD  601
AaAAEL007802    800  ERL--AGNITAEEVKRLDEEG------KIKRRLK-------------------GAPIKD  831
AaAAEL001632    519  GQLPTRIKHSSEKLRWIKDEELKPVVRRTRGMP-----------------DGHNPPYKD  560
AaAAEL001640    574  GRLP--ESAINSRLKYLQG-------RNFTQRP-----------------NGHNPPFKD  606
AmLOC724890     479  ERI--GENVTVDKVKALDKKG------AIRRNLD-------------------HAPLKD  510
AmLOC410365     635  GRS-PDKNVKKINLKHALDLD----KRGLLNR-------QFN------------LPPAKD  670
AmLOC552811     527  GQFWPIRNISRQDINEVIQEH----TERLRRG-------EYK-----------NPPGKD  563
BmMCO1          638  RRL--ASDTTIEEVKAFDEAG------LLKRNLK-------------------NAPIKD  669
BmLac2          658  GRS-PDQNVKKINLKHALDLD----RRGLLER-------HLKQGD---------LPPAKD  696
DmCG3759        815  ERL--GENVTVEMIKQLDQFN------LLKRNLD-------------------NPPVKD  846
DmCG30437-PA    681  GRS-PDSSVKKINLKHALDLD----RRGLLHR-------QYN-----------LPPTKD  716
DmCG5959        587  GVLGNLNDLRNIQELDRRG--------RLPRLSEDS-----------------AAVAKD  620
DmCG32557       552  GVLGEQ-KIGQIEQIDKKT--------PLPRRAK-------------------GAPLKD  582
MsLac1          649  RRL--NRTTTIEEIKAFDEAG------LLKRNLK-------------------NAPIKD  680
MsLac2          654  GRS-PDQNVKKINLKHALDLD----RRGLLER-------HLKQGD---------LPPAKD  692
PhLac1          559  GDA-DLHGVKTINVETVKELE----KQGKLNRYPTSVAVEHNDVEGPVPPKVAARFPAKD  613
TcLac1          547  ERV--GSHVNVSEILKMDQNG------QIKRNLV-------------------DAPLKD  578
TcLac2A         610  GRS-PDQNVKKINLKHALDLD----RQGLLHR-------QFN-----------LPPAKD  645
SpLOC586543     537  GRS--ETGSTKEDIIRLDENG------GIVRNYD-------------------NPPEKD  568
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AgMCO1          913  TVTIPDGGYTIIRFIANNPGYWLFHCHIEFHAEIGMSLVLKVGDSSEMLPAPANFPTC  970
AgMCO2A         688  TIAVPNNGYVVLRFRADNPGFWLFHCHFLFHIVIGMNLILQVGTHADLPPVPPNFPTC  745
AgMCO3          589  TVSIPSRGYARVRFRADNPGFWLMHCHYEWHTAVGMALVLQVGETSEMVKAPADFPKC  646
AgMCO4          618  TVSVPSRGYTRIRFRADNPGFWLVHCHFEWHLGIGMSFVLQVGELDEMKQAPKDFPRC  675
AgMCO5          621  TQSIPNRGYVRIRFRADNPGFWLVHCHFEWHLADGMGLVLQIGEPDEMLKPPANFPRC  678
AaLac1          682  TIAVPNNGYVVLRFRADNPGFWLFHCHFLFHIVIGMNLILQVGTLQDLPPVPPNFPTC  739
AaLac2          602  TVSVPSKGYTRVRFVADNPGFWLMHCHYEWHTAVGMVLVLQVGEPGSFVKPPAGFPTC  659
AaAAEL007802    832  TVTIPDGGYTIIRFIANNPGYWLFHCHIEFHAEIGMSLVLKVGDKSEMVAAPHNFPTC  889
AaAAEL001632    561  TVSIPSRGYTKIRFRADNPGFWLVHCHFEWHLGIGMSFILQVGEIDQMIKTPPGFPTC  618
AaAAEL001640    607  TISIPNEGFVKTRFRASNPGFWFVHCHFEWHLGTGMGLVLQVGEVYQMLKAPPGFPRC  664
AmLOC724890     511  TVTVPDGGYTVVRFHANNPGYWLFHCHIEFHAEVGMSLIFKVGEHKDMLPVPRNFPLC  568
AmLOC410365     671  TIAVPNNGYVIFRFRADNPGYWLFHCHFLFHILIGMNLILHVGTHADLPPIPPNFPRC  728
AmLOC552811     564  TAKIPMGGYVIVRFKADNPGWWLLHCHFSWHHITGMELVILVGDENDLPPIPKNFPKC  621
BmMCO1          670  TVTVPDGGYTVIRFKADNPGYWLFHCHIEFHVEVGMALVFKVGDHKDMPPVPREFPKC  727
BmLac2          697  TIAVPNNGYVILRFRATNPGFWLLHCHFLFHIVIGMSLVLQVGTQGDLPPVPPNFPTC  754
DmCG3759        847  TVTIPDGGYTIIRFEASNPGYWLFHCHIEFHAEIGMALVFKVGNDDQMVPVPENFPTC  904
DmCG30437-PA    717  TIAVPNNGYVVLRFRADNPGFWLFHCHFLFHIVIGMNLILQVGTNADLPPVPPGFPTC  774
DmCG5959        621  TVQIPGQGYIIVRFISNNPGFWLYHCHVEAHAVQGMVAVLKIGEDHQMKNIPARV-RC  677
DmCG32557       583  SVQVPAFGYTILRFYSNSPGYWMFHCHISPHSENGMAAVVRVGEDVEMKMCPVS--NC  638
MsLac1          681  TVTVPDGGYTVIRFKADNPGYWLFHCHIEFHVEVGMALVFKVGEHKDMAPLPRDFPTC  738
MsLac2          693  TIAVPNSGYVILRFRATNPGFWLLHCHFLFHIVIGMSLVLQVGTQADLPPVPPGFPTC  750
PhLac1          614  TYAVPNSGYSIIRFWATNPGYWLFHCHFEFHALMGMMTIFHVGEPEDLPPVPPGFPKC  671
TcLac1          579  TVTVPDGGFTIIRFKATNPGYWLFHCHIEFHVEVGMALVFKIGEDYEMPPVPKDFPQC  636
TcLac2A         646  TIAVPNNGYVVLRLRANNPGFWLFHCHFLFHIVIGMNLVLQVGTHADLPPVPPNFPTC  703
SpLOC586543     569  TVMTPSGGYTVVEFVAANPGWWMLHCHMEDHLEDGMGMLVRVGNQSDLPPVPEGFPRC  626
                     :    *    *:      .: : .**:*: ***    *    **  :. :*   .:   *       *
```

Figure S2. Alignment of insect MCO sequences

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AgMCO1          722 QLNSLNRGPG--AENVITIAETSALDQEDLLLLRNETDYKFYVYYDFYGKDNPHFHVPSL 779
AgMCO2A         494 VMNPLDAQCNVQRDDAICVSQLKNAKEIDRALLQDKPDVKIFLPFRFYLRPEELFQPNT  553
AgMCO2B         494 VMNPLDAVCNVPRPDAVCVSNLRNAKKADKAVLSERPDVKIFLPFRFYFYRVEELFTPNT 553
AaLac1          488 VLNPLDAQCNVQRDDAICVSQLKNAKDIDRALLQEKPDVKIFLPFRFYLRPEELFQPNT  547
AaAAEL007415    488 VLNPLDAVCNVPRPDAICVSNLRSAKKLDKAVLTERPDVKIFLPFRFYFYRVEELFTPNT 547
AmLOC410365     477 VLNPLDAICNRQREDAICVSQLKNARQIDQGILQQRPDVKIFLPFRFLFYRPEEVFQPQT 536
BmLac2A         500 VMNPLDARCNISRNDAICVSQLKNAQNIDPAILQERPDVKIFLPFRFFVYRPEMLFQPNT 559
BmLac2B         499 VMNPLDAICDVKRNDAVCVSNLKSARPVDKALLQDRPDVKIFLPFRFHFYKPKDLFKENT 558
DmCG30437-PA    523 VMNPLDAQCNRQRNDAICVSQLKNALEIDRGILAEKPDVKIFLPFRFFVYRAEDLFQPNT 582
DmLac2B         523 ILNPLDAICDRKRADAVCVSNLKNAKKVDKGVLVERPDVKIFLPFRFFVYEPKALFIPNT 582
TcLac2A         452 VLNPLDARCNEIRPDAICVSQLKNALSIDKGILREKPDVKIFLPFRFHIYTPEDLFAPNT 511
TcLac2B         452 VLNPLDAICNKPRKDAVCVSQLRNAKKVDEAILEERPDVKIFLPFRFLFYKPEDIFRPNT 511
                    :*.*:    .      :.: :::       *   :* :..* *::: : *     .. .


AgMCO1          780 YGFQQVVNNTNRLYTPQLNHISMRMPPVPFLPGKDVLDESQFCNETSVRDRNCRQEFCEC 839
AgMCO2A         554 YNRFLVAPTGDHVIS-LIDEISYLSAPAPLLSQYDDINPEQFCNGD-NRPADCGAN-CMC 610
AgMCO2B         554 YNKFLVAPGGDHLIS-LIDEISYVSPPSPMLSQINDIPPEQFCNGD-NRPPDCGPN-CMC 610
AaLac1          548 YNRFLVAPTGDHVIS-LIDEISYLSAPAPLLSQYDDINPEQFCNGD-NRPADCGAN-CMC 604
AaAAEL007415    548 YNKFLVAPGGDHLIS-LIDEISYVSPPSPMLSQIEDIPPEQFCNGD-NRPPDCGPN-CMC 604
AmLOC410365     537 YNRFLVAPTGDHVIS-LVDEISFTFPPAPPLSQIDDIPPEQFCNGD-NRPADCGAN-CMC 593
BmLac2A         560 YNRYLVAPGGDHVIS-LIDEISYMSPPAPLISQYDDINPDQFCNGD-NRPANCGQN-CMC 616
BmLac2B         559 YRNFLVAPGGDHVLS-LVDEISYSAPPAPPLSQMHELSPDLFCNGD-NRPPNCAVD-CRC 615
DmCG30437-PA    583 YNRFLVAPTGDHVIS-LIDEISYLSAPAPLTSQYNDINPDQFCNGD-NRPADCGPN-CMC 639
DmLac2B         583 YNRFLVVPSGDHLTS-LVDEISYISPPAPPLSQIDDIPPEYFCNGD-NRPPNCGPN-CEC 639
TcLac2A         512 YNRHLVAPNGDHVIS-LIDEISYMAPPAPLISQYDDIDPQQFCNGD-NRPADCQQN-CMC 568
TcLac2B         512 YNRFLAATGGDHVIS-LIDEISFTFPPSPPLSQIHDLSPDQFCNGD-NRPPDCGQN-CMC 568
                    *     ..   ::: :  ::.**   .* *  .  . :  .***    *   :*  : * *


AgMCO1          840 SHVLQIPLHATVEMVMIDEGFTFDANHPFHLHGHAFRVVGMDRVS----RNTTIEDIRRM 895
AgMCO2A         611 THKVDIPLNAIVEVVLVDEVQQPNLSHPFHLHGYAYNVVGIGRSPDSNVKKINLKHALDL 670
AgMCO2B         611 THKVDIPLNAIVEVVLVDEVQQENLSHPFHLHGHAFHVIGMGRSPDSTVKKINLRHTLDL 670
AaLac1          605 THKVDIPLNAIVEVVLVDEVQQPNLSHPFHLHGYAYNVIGIGRSPDSNVKKINLKHALDL 664
AaAAEL007415    605 THTVDIPLNAIVEVVLVDEVQQDNLSHPFHLHGHSFNVIGMGRSPDTTVKKINLRHALDL 664
AmLOC410365     594 THQVDIPHNAVVEVVLVDEVQQPNLSHPFHLHGYAFNVIGIGRSPDKNVKKINLKHALDL 653
BmLac2A         617 THKVDIPLNAVVEIVLVDEVQIANLSHPFHLHGYSYNVIGIGRSPDQNVKKINLKHALDL 676
BmLac2B         616 THMIDVPLNSIVEIVLVDEVQSPNLSHPFHLHGTSYNVIGMGRSPDKNIKKINLKHALDL 675
DmCG30437-PA    640 THKIDIPLNAIVEVVLVDEVQQPNLSHPFHLHGYGFSVIGIGRSPDSSVKKINLKHALDL 699
DmLac2B         640 THMVDIPLGAIVEVVLVDEVQQVNLSHPFHLHGTAFYVVGLGRSPDKSIKKINLKHALEL 699
TcLac2A         569 THKVDIPLNAIVEIVLVDEVQQPNLSHPFHLHGYAFNVIGIGRSPDQNVKKINLKHALDL 628
TcLac2B         569 THQVDIPLNAIVEVVLVDEVQSPNLSHPFHLHGYAFNVVGIGRSPDQNVKKINLKHALDL 628
                    :*  :::*   :  **:*::**     :  .*******  .:  *:*:.*  .      ::  .:..    :


AgMCO1          896 DEEGRLPRRLK---RAPIKDTVTIPDGGYTIIRFIANNPGYWLFHCHIEFHAEIGMSLVL 952
AgMCO2A         671 DRRGLLHRQYN---LPPLKDTIAVPNNGYVVLRFRADNPGFWLFHCHFLFHIVIGMNLIL 727
AgMCO2B         671 DRRGLLNRQFN---LPPLKDTIAVPNNGYVVLRFRADNPGYWLFHCHFQHIVIGMNLVV 727
AaLac1          665 DRRGLLHRQYN---LPPLKDTIAVPNNGYVVLRFRADNPGFWLFHCHFLFHIVIGMNLIL 721
AaAAEL007415    665 DRRGLLNRQFN---LPPLKDTVAVPNNGYVVMRFRANNPGYWLFHCHFQHIVIGMNLVV 721
AmLOC410365     654 DKRGLLNRQFN---LPPAKDTIAVPNNGYVIFRFRADNPGYWLFHCHFLFHILIGMNLIL 710
BmLac2A         677 DRRGLLERHLKQGDLPPAKDTIAVPNNGYVILRFRATNPGFWLLHCHFLFHIVIGMSLVL 736
BmLac2B         676 DRKGLLHRQYN---LPPHKDTLAVPNNGYVVLRLKADNPGYWLFHCHFIYHIVIGMSLIL 732
DmCG30437-PA    700 DRRGLLHRQYN---LPPTKDTIAVPNNGYVVLRFRADNPGFWLFHCHFLFHIVIGMNLIL 756
DmLac2B         700 DQMGMLERHFS---KPPLKDTIAVPNNGYVVIRFRADNPGYWLFHCHFLFHIVIGMNLIF 756
TcLac2A         629 DRQGLLHRQFN---LPPAKDTIAVPNNGYVVLRLANNPGFWLFHCHFLFHIVIGMNLVL 685
TcLac2B         629 DRRGLLHRQFN---LPPSKDTIAVPNNGYVIFRFRADNPGYWLFHCHFLFHIVIGMNLII 685
                    *.  * * *:  .      .*  ***:::*:.**.::*: *  ***:**:***: :*   ***.*:.
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AgMCO1          951  KVGDSSEMLPAPANFPTCYDFKPKLGQLGSGGARHG  988
AgMCO2A         728  QVGTHADLPPVPPNFPTCGDHLPPIN----------  753
AgMCO2B         728  HIGTHADLPPVPPNFPRCGNHIPPIKYN--------  755
AaLac1          722  QVGTLQDLPPVPPNFPTCGDHLPPIQ----------  747
AaAAEL007415    722  HVGSKADLPPVPPNFPRCGNHIPPIRFN--------  749
AmLOC410365     711  HVGTHADLPPIPPNFPRCGDHLPAITPPSLSLDSFH  746
BmLac2A         737  QVGTQGDLPPVPPNFPTCGDHLPAIPLH--------  764
BmLac2B         733  HIGTQGDLPPVPPNFPRCGHHLPTISPPFYPIH---  765
DmCG30437-PA    757  QVGTNADLPPVPPGFPTCGDHTPSIPIN--------  784
DmLac2B         757  HIGTTADLPPVPPRFPTCGDHVPPVTWY--------  784
TcLac2A         686  QVGTHADLPPVPPNFPTCGDHVPEINSNPNLV----  717
TcLac2B         686  HVGTQLIYRPFS-HFPRCGNHLPPISLH--------  712
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Figure S3. Alignment of MCO2 isoforms.