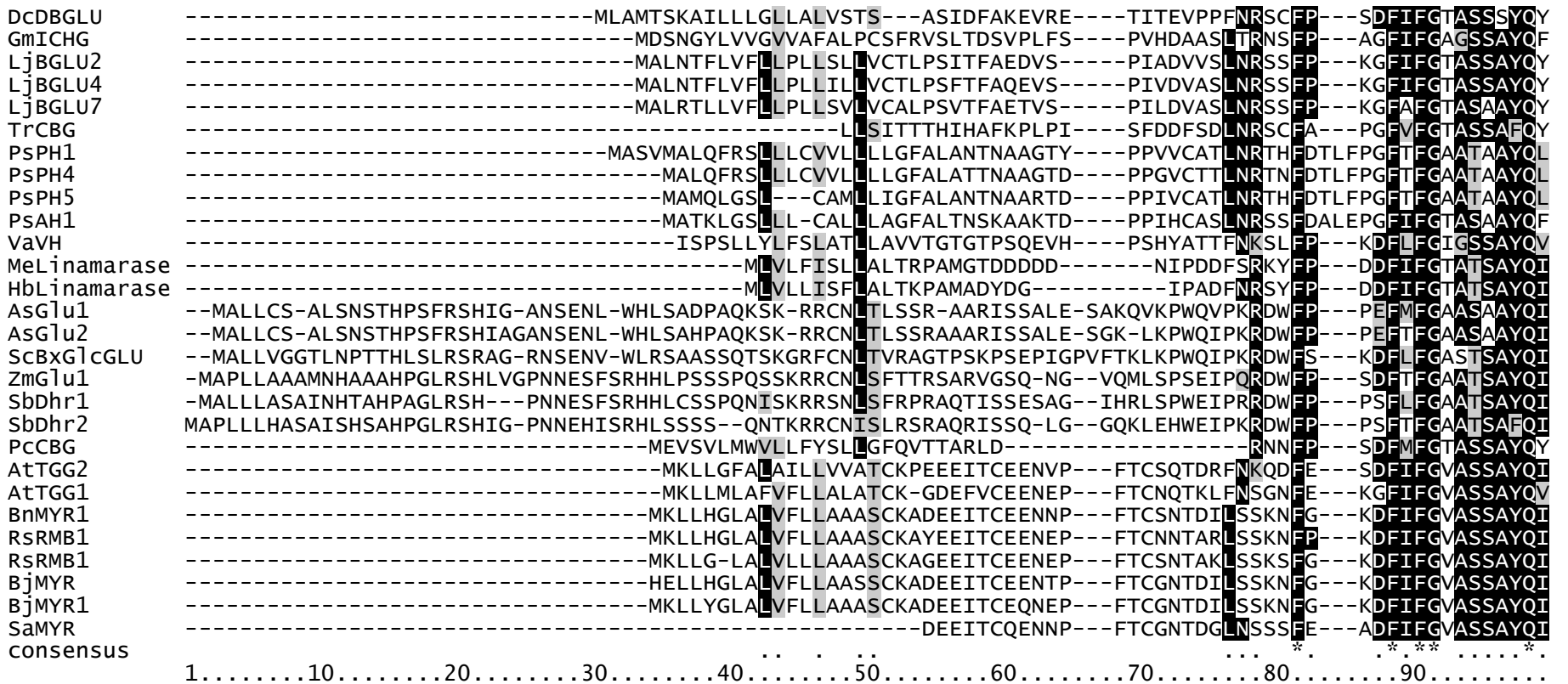


Vinther Morant et al., Figure 7 Alignment

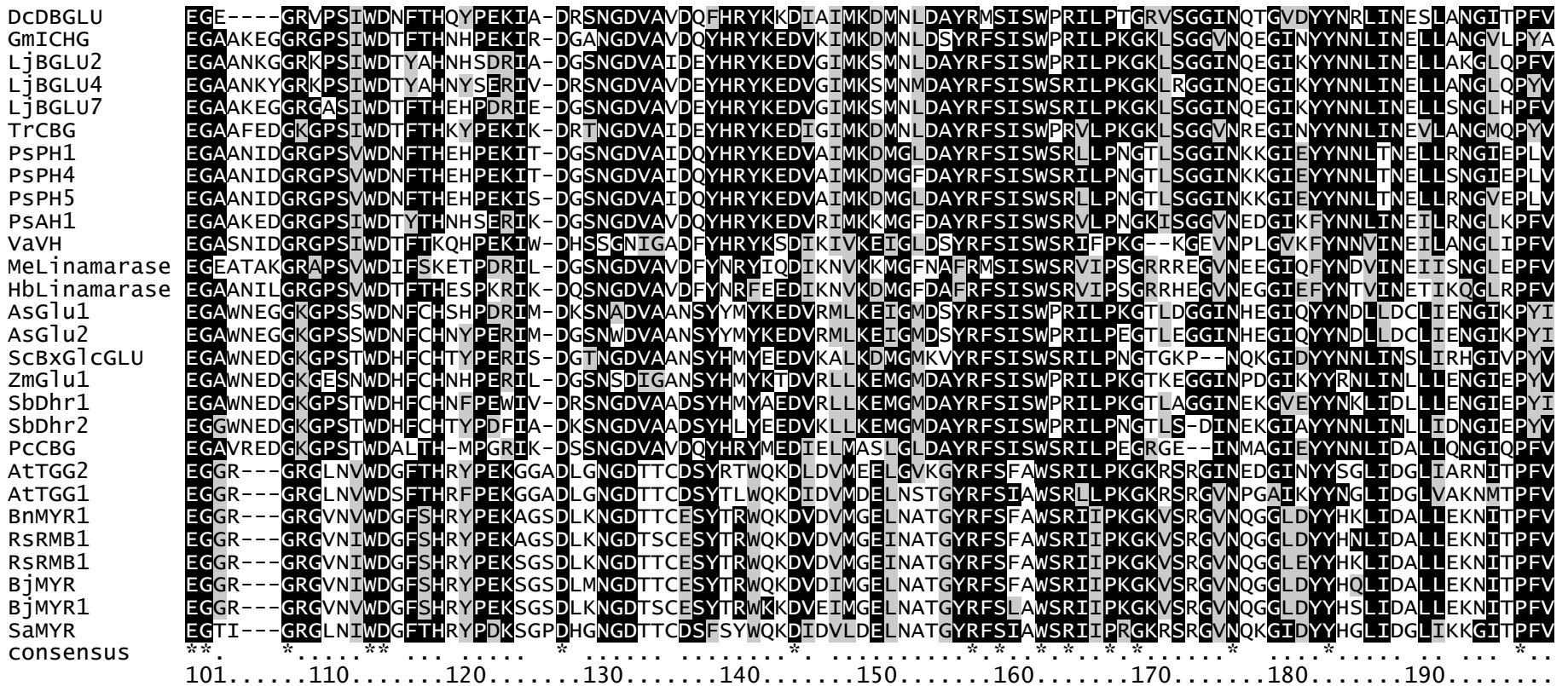


ClustalX 1.83

Pairwise Settings – Gap opening penalty: 13.50, Gap extension penalty: 0.75, Protein Weight Matrix: Gonnet 250

Multiple Alignment Settings – Gap opening penalty: 15.00, Gap extension penalty: 1.00, Protein Weight Matrix: Gonnet Series

Vinther Morant et al., Figure 7 Alignment



ClustalX 1.83

Pairwise Settings – Gap opening penalty: 13.50, Gap extension penalty: 0.75, Protein Weight Matrix: Gonnet 250

Multiple Alignment Settings – Gap opening penalty: 15.00, Gap extension penalty: 1.00, Protein Weight Matrix: Gonnet Series

Vinther Morant et al., Figure 7 Alignment

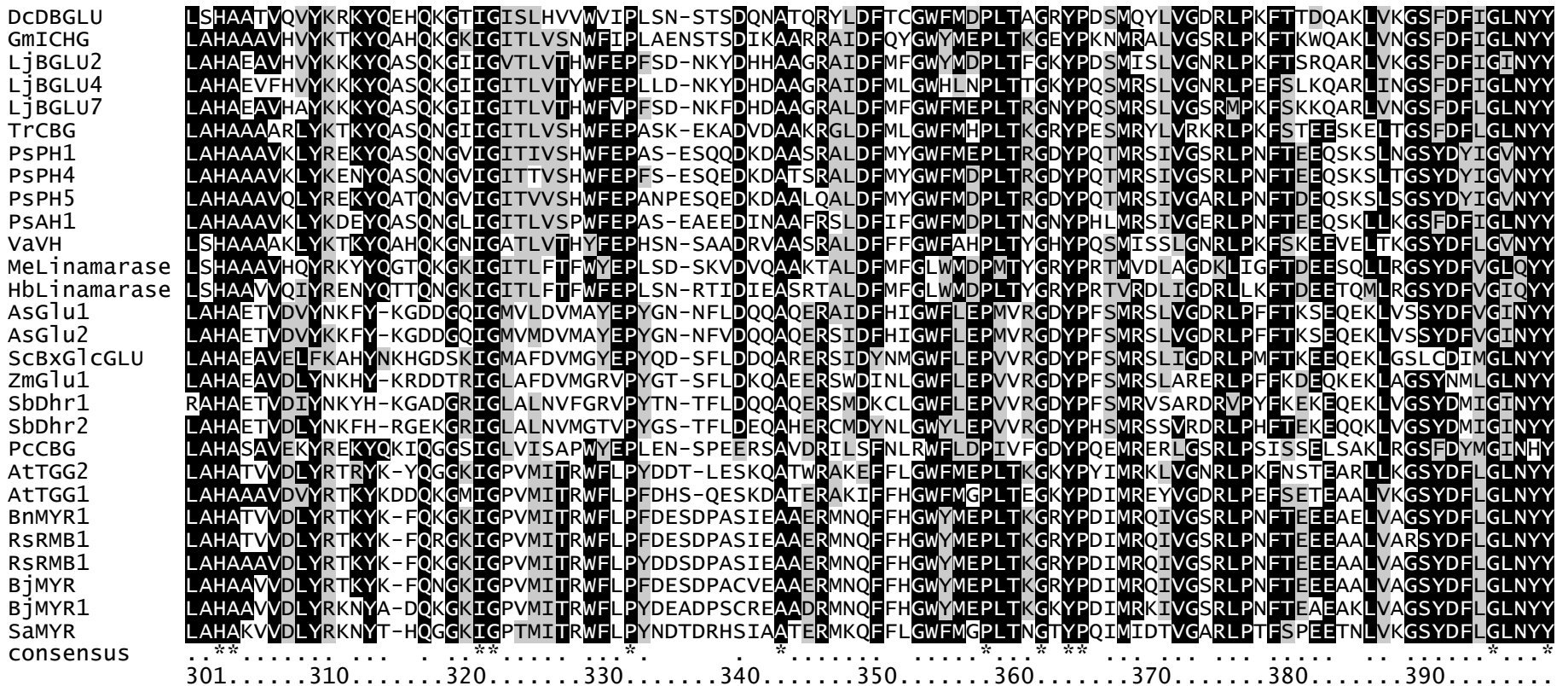


ClustalX 1.83

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Vinther Morant et al., Figure 7 Alignment

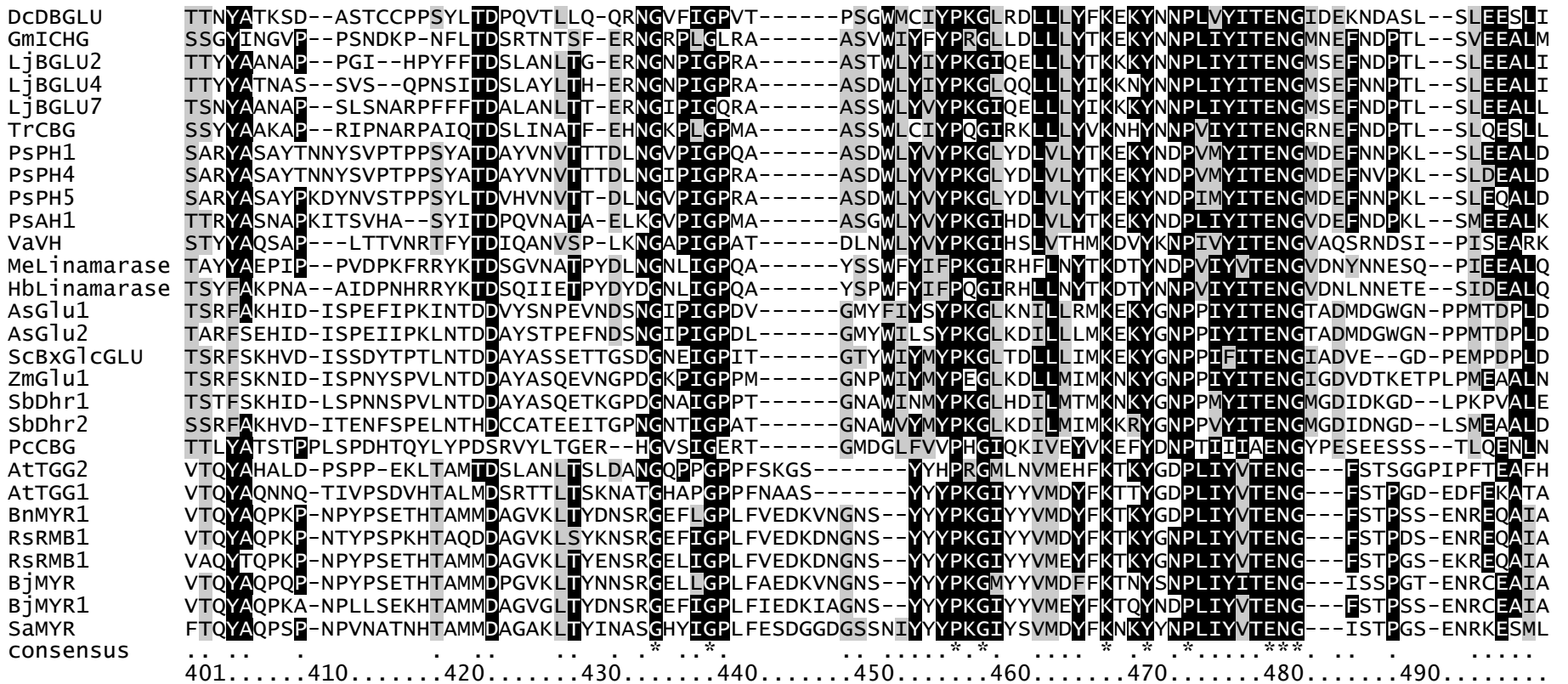


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Vinther Morant et al., Figure 7 Alignment

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DcDBGLU      DTYRIDSYRHLFYVRYAIRS-GANVKGFFAWSLLDNFWEAEGYTSRFGLYFVNYTT-L-NRYPKLSATWFKYFLARDQESAKLEILAPKARWSLSTMIK
GmICHG       DTIYRIDYRHLFFYLRSATKA-GANVKGFFAWSLDCNEWFAGFTVRFGLNFDYKDGL-KRYPKLSAQWYKNFLKRN-----
LjBGLU2     DTFRIDYFRHLFYLRSAIRN-GSNVKGYFAWSLLDNYEWSGGYTVRFGMNFVDYKNGL-KRYKLSAKWFTNFKRY-----
LjBGLU4     DTFRIDYFRHLFYLQSAIRD-GSNVKGYFAWSLLDNYEWSGGYTVRFGMNFVDYENGL-KRYKLSAKWFTNFKRY-----
LjBGLU7     DTFRIDYRHLFYLQSAIRD-GANVKGYFAWSLLDNFEWASGYTRFGINFADYKNGS-KRYKLSAKWFKNFKRY-----
TrCBG       DTPRIDYRHLFYVLTATGD-GNVKGYFAWSLFDNMEWDSGYTVRFGLVFVDFKNNL-KRHPKLSAHWFKSFLKK-----
PsPH1       DANRIDYRHLCYLQAATKE-GANVQGYFAWSLLDNFEWSEGYTVRFGINYYDYDNGL-ERHSKLSSTHWFKSFLKRSSISKKKIRRCGNNAKATKFVY
PsPH4       DANRIDYRHLCYLQAATKE-GANVQGYFAWSLLDNFEWSEGYTVRFGINYYEYDSSL-ERHSKLSKHWFKSFLKKSSISKKKIRRSNGTNARATKFVY
PsPH5       DVNRIDYRHLCYLQAATKE-GANVQGYFAWSLLDNFEWSEGYTVRFGINYYDYDNGL-ERHSKLSSTHWFKSFLKRSSISKKKIRRCGNNGRATKFVY
PsAH1       DTNRIDFYRHLCYLQAATIK-GSKVKGYFAWSFLDNFEWDAGYTVRFGINYYDYDNDL-KRHSKLSSTYWFWSFLKKYERSTKEIQMFVESKLEHQKFS
VaVH        DGIRISYHDNHLKFLQGIKD-GANVKGYFAWSFSDSYEWDAGYTRFGIYYDFKNDL-RRYPKYSALWLQKFLK-----
MeLinamarase DDFRISYKKHMWNALGSLKNYGVKLGKGYFAWSYLDNFEWNIQYTSRFGLYYVDYKNNL-TRYPKSAHWFTKFLNISVNANNIYELTSKDSRKGKGFVY
HbLinamarase DEFVRNYYRKHMMNALGSLKEYNVNIKGYFAWSYLDNFEWNIQYTSRFGLYYVDYKNNL-TRIPKSSAFWFAAFLNPES-SKKITQTTSRNSRKGKGFYI
AsG1u1      DPLRIEYLQOHMTAIKEATDLGRRTLGRHFTWSLIDNFEWSLGYLSRFGIVYIDRNDGC-KRIMKKSAKWLKEFNG-ATKLNKILGASSCCSGVTHGG
AsG1u2      DPLRIEYLQOHMTAIKEATDLG-ADVRGHFTWSLIDNFEWSMGLYSRFGIVYIDRNDGF-KRIMKKSAKWLKEFNG-ATKEVNKILGASSCCSGELMWF
ScBxG1cGLU DWKRLDYLQRHISAVKDAIDQG-ADVRGHFTWGLIDNFEWGSYSSRFGLVYIDKEDGN-KRKLKKSAKWFAKFNS-VPKTLKTTNNNATVTASVSV--
ZmG1u1      DYKRLDYIQRHIAATLKESTDLG-SNVQGYFAWSLLDNFEWFAGFTERYGIVYVDRENGC-TRYMKESAKWLKEFN--TAKKPSKKILTPA-----
SbDhr1      DHTRLDYIQRHLSVLKQSTDLG-ADVRGYFAWSLLDNFEWSSGYTERFGIVYVDRENGC-ERTMKRSARWLQEFNGAAKKVENNKILTPAGQLN-----
SbDhr2      DHIRLDYLQRHISVLKDSIDSG-ANVRGHFTWLLDNFEWSSGYTERFGIVYVDRENGC-KRTLKRSARWLKEFNG-AAKRPGNLIKPNFSEINKIKVVT
PcCBG       DVRRIRFHGDCLSYLSAATKNG-SDVRGYFVWSLLDNFEWAFGYTRFGLYHVDFISDQ-KRYPKLSAQWFRQFLQ---HDDQGSIRSSSSI-----
AtTGG2      DYNRIDYLCSHLCFLRKATKEKRVNVKGYFVWSLGDNYEFCNGYTVRFGLSYVDFNNVTADRDLKASGLWYQSFLRDTTK---NQDILRSSLPFKNGDRK
AtTGG1      DYKRIDYLCSHLCFLRKVIKEKNVNVKGYFAWSLGDNYEFCNGFTVRFGLSYVDFANITGDRDLKASGKWFQKFINVTDEDSTNQDLLRSSVSSKNRDRK
BnMYR1      DYKRIDYLCSHLCFLRKVIKEKGNVNRGYFAWALGDNYEFCCKGFTVRFGLSYVNWEDLD-DRNLKESGKQYQRFINGTVKNVAKQDFLRSSLSSQSQKRR
RsRMB1      DYRIDYLCSHLCFLRKVIKEKGNVNRGYFAWALGDNYEFCCKGFTVRFGLSYVNWADLN-DRNLKESGKQYQRFISGTVKNPAKQDFLRSSLSSQSQKRR
RsRMB1      DYKRIDYLCSHLCFLRKVIKEKGNVNRGYFAWALGDNYEFCCKGFTVRFGLSYVNWDDL-DRNLKESGQWYQRFINGTVKNPAKQDFLRSSLSSQSQK-R
BjMYR       DYKRIDYLCSHLCFLRKVIKEKGNVNRGYFAWALGDNYEFCCKGFTVRFGLSYVNWDDL-DRNLKESGKQYQRFINGTVKNHANQDFLRSSLSSQSQKRR
BjMYR1      DYKRIDYLCSHLCFLRKVIKDRGNVNRGYFAWALGDNYEFCCKGFTVRFGLSYVNWDDL-DRNLKESGKQYQRFINGTSKNPTKQDFLRSSLFLKARR
SaMYR       DYTRIDYLCSHLCFLNKVIKEKDVNVKGYLAWALGDNYEFNNGFTVRFGLSYINWNNVT-DRDLKKSQWYQKFIISP-----
consensus  *      *      *      *      *      *      *      *      *      *      *      *      *      *      *
501.....510.....520.....530.....540.....550.....560.....570.....580.....590.....

```

ClustalX 1.83

Pairwise Settings – Gap opening penalty: 13.50, Gap extension penalty: 0.75, Protein Weight Matrix: Gonnet 250

Multiple Alignment Settings – Gap opening penalty: 15.00, Gap extension penalty: 1.00, Protein Weight Matrix: Gonnet Series

Vinther Morant et al., Figure 7 Alignment

```

DcDBGLU      EEKTKPKRGIEGF-
GmICHG       -----
LjBGLU2     -----
LjBGLU4     -----
LjBGLU7     -----
TrCBG        -----
PsPH1        QM-----
PsPH4        QM-----
PsPH5        QI-----
PsAH1        QMMNKVQSSLAVVV
VaVH         -----
MeLinamarase M-----
HbLinamarase M-----
AsGlu1       GTA-----
AsGlu2       LVQNPYGK-----
ScBxGlcGLU   -----
ZmGlu1       -----
SbDhr1       -----
SbDhr2       PA-----
PCCBG        -----
AtTGG2       SLT-----
AtTGG1       SLADA-----
BnMYR1       FADA-----
RsRMB1       LADA-----
RsRMB1       LADA-----
BjMYR        LAC-----
BjMYR1       GLLADA-----
SaMYR        -----
consensus    601.....610..

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ClustalX 1.83

Pairwise Settings – Gap opening penalty: 13.50, Gap extension penalty: 0.75, Protein Weight Matrix: Gonnet 250

Multiple Alignment Settings – Gap opening penalty: 15.00, Gap extension penalty: 1.00, Protein Weight Matrix: Gonnet Series