

Morant et al., alignment for figure 1

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703A7Lj (*) : -----*-----20-----*-----40-----*-----60-----*-----80-----*-----100
703A8Mt (AB) : -----MVTATFVSTLHAAASKIIT-----EFIRSFSLHKNKLPPEPRWFIVGNLQIGS
703A2At (At) : -----MVTTLIALTLHITVSKIIIRD-----RHIGKSPSLDKNNLPPEPRWFIVGNLQIGS
703A1Ph (BA) : -----MILVNASLFAVLQNLNWLWRWLF-----ASACKAQRPPPEPRWFIVGNLQIGS
703A30s (XP) : -----MIDFTNYLIVLFRVYIFVVDYAFIFVQVYVSKLVHF-----SFIERSK--QKINRLLPPEPRWFIVGNLQIGS
703A6Sb (AA) : -----MDPFLSILLCSWHFWVSWKRLN-----CMRRLLPPEPRWFIVGNLQIGS
703A4Pt (*) : -----MDIATLFSLLFLVIVANFILR-----WGNLKSQHKSKRLPPEPRWFIVGNLQIGS
703B2Pp (*) : -----MDFRIS-ELLIPAISEPVESGHAFATCTVIVLISCVFLF-----IRSGTSVNLPPGEKGLPILGNLQIGS
703B1Pp (*) : -----MNLSP-ELLVPIITEMIQGRRIIPATCSVDVALVSSVFLV-----AHFRTPMNLPPGEKAMPILGNLQIGS
703B3Pp (*) : -----MDTLVSLLELFGQVWNWQESRLLMTTCSVDVALVSSVFLF-----SRFRKFLQPPGEKGLPILGNLQIGS
79A1Sb (AAA) : -----MATMEVEAAAATVLAAPLSSSAILKLLFLVITLSYLARALRRPRKSTTKCSSTTCASPAGVGNPLPPGEVPPWVGNFPBML
79D1Me (AAF) : -----MAMNVSTTIGLLNATSFASSSSINTVKILFVITLFIIS-----IVSTIVLQKSAANKEGSKKLLPPGEPTWPLIGNIPBFI
92A6Ps (AAG) : -----MALQVITLPSWVTLFTFAILLFSRRRRR-----QYN-LPPGEKPPWILGNFNHIG
75B1At (At5) : -----MATLFLITLLATVLF--LILRIFSHRRNR-----HNNRLLPPEPRWFIVGNLQIGS
81D1At (At5) : -----MEETNRVWLYSIFSLFHLISFKFKKPK-----KQNLPSPEGWILFICGHRILK
82C2At (At4) : -----MDTSLFSVFPVILVFWIATFKKSKKPK-----HVKAP-APSGAWPILGICHLIS
84A1At (At4) : -----MESSISQTLSKLSDPTTSLVIVWSIFLIFSTTRR-----RRPYPPPRGWPLIGNLMD
98A3At (At2) : -----MSWFLAVATIAAVSVYKLIQRLR-----YKFPPEPRSPHIVGNLYDK
73A5At (At2) : -----MDLLLKESLAVFVAVFFATVSKLRGKK-----LKLPPPELTPFICGNLQIGS
706A1At (At) : -----METASSNFSLSQLNIEEPYSSMLGVAALAVWCYFIQKSK-----SKNGPPLPPEPRWPLIVGNFPBFI
80A1Bs (AAC) : -----MDYINGFVSSVALLV--FLFKFKHTN-----LPPGEPAWPLVGNFPBFI
78A110s (AA) : MAMATATASSCVDATWWAYALPALGADTLCAHPALLAGAVLAFATAAVAWAAS-----PGGPAWAGHRGLGATPTBPPGEVPPWVGNFPBML
76C1At (At2) : -----MDITSGQALTLFCFISCFLLFTTTRSGRI-----SRGATALPPGEPRPILIGNHIVG
83B1At (At4) : -----MDLLIITAGVAAAFAFFTRSTTKK-----SLRLLPPEKGLPILGNHIG
71E1Sb (AAC) : -----MATTATPQLLGGSVPOQWOTCLLMLLVLLVSVYVITLSSRNRSRSGK-----LGAPRLPPEGAQPLIGNHIG
71A12At (At) : -----MEMIMVSLQITLITLTLKQPLKRTAN-----KVLNLPPEPRWPLIGNHIG
705A1At (At) : -----MDAIVVDSQNCFFIILLCSFLSYVFFVKPK-----VNFLLPPEPRWPLIGNHIG
712A1At (At) : -----MDLKNLTKLITLTSLAFPMYALFKWFLKEQG-----SLAATLQSPALPILGICHLIS
93A1Gm (BAA) : -----MAYQVLLCLVSTIVFYLWR-----KQSK-----KNLPPSKALPILGICHLIS
77B1At (At) : -----MDLTDVIFLFAFYFINLWWRRYFAGSSQ-----CSLNPPEPRWPLIGNLQIGS
89A2At (At1) : -----MEIWLIIASLGSQIFHLLRRRNS-----SSPPLPPEPRWPLIGNLQIGS
701A3At (At) : -----MAFFSMISILGFVSSIFHLLRKRK-----NMSEVTLPSVVPVGGPILGICHLIS
51A1At (At2) : -----MDWDYITLTKTSALIIIVFAKLITSSKSKK-----TSVPLPPEVLAQWPPFICSLIRM
710A1At (At) : -----MVFVSIFASLAPYLISAFILFVLEQLSYLFK-----KRNIPPEPRWPLIGNAVALV
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703A7Lj (*) : QLF---HRDASCEKYG---PLVNLKLGKIDAITTNDPPII---REMLTODDVFASRE---RTLAAVHAAGCG---DVALAELGHWRRRRIQVHELITP
703A8Mt (AB) : QLF---HRDASCEKYG---PLVNLKLGKIDAITTNDPPII---REMLTODDVFASRE---RTLAAVHAAGCG---DVALAELGHWRRRRIQVHELITP
703A2At (At) : PLP---HRDASCEKYG---PLVNLKLGKIDAITTNDPPII---REMLTODDVFASRE---RTLAAVHAAGCG---DVALAELGHWRRRRIQVHELITP
703A1Ph (BA) : QLF---HRDASCEKYG---PLVNLKLGKIDAITTNDPPII---REMLTODDVFASRE---RTLAAVHAAGCG---DVALAELGHWRRRRIQVHELITP
703A30s (XP) : PLP---HRDASCEKYG---PLVNLKLGKIDAITTNDPPII---REMLTODDVFASRE---RTLAAVHAAGCG---DVALAELGHWRRRRIQVHELITP
703A6Sb (AA) : PLP---HRDASCEKYG---PLVNLKLGKIDAITTNDPPII---REMLTODDVFASRE---RTLAAVHAAGCG---DVALAELGHWRRRRIQVHELITP
703A4Pt (*) : QQP---HRDASCEKYG---PLVNLKLGKIDAITTNDPPII---REMLTODDVFASRE---RTLAAVHAAGCG---DVALAELGHWRRRRIQVHELITP
703B2Pp (*) : SHP---HRTTAAHKVYG---PLVNLKLGKIDAITTNDPPII---REMLTODDVFASRE---RTLAAVHAAGCG---DVALAELGHWRRRRIQVHELITP
703B1Pp (*) : SHP---HRTTAAHKVYG---PLVNLKLGKIDAITTNDPPII---REMLTODDVFASRE---RTLAAVHAAGCG---DVALAELGHWRRRRIQVHELITP
703B3Pp (*) : SLE---HRTTAAHKVYG---PLVNLKLGKIDAITTNDPPII---REMLTODDVFASRE---RTLAAVHAAGCG---DVALAELGHWRRRRIQVHELITP
79A1Sb (AAA) : LNKP--AFWVHQMREMGT--DQAGVILGSHVHSICPEPIA---REMLTODDVFASRE---RTLAAVHAAGCG---DVALAELGHWRRRRIQVHELITP
79D1Me (AAF) : RYRP--TFWVHQMREMGT--DQAGVILGSHVHSICPEPIA---REMLTODDVFASRE---RTLAAVHAAGCG---DVALAELGHWRRRRIQVHELITP
92A6Ps (AAG) : ---TLPSOSHGCTQK---GPIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
75B1At (At5) : ---TKPHSTSAVVTI---GPIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
81D1At (At5) : P-THRTLSPSETLDHND-GGCVSRLGSRVLYVWSHKVAE-FCFGKNDVVLNRR-QVIIGKHVGNNA-NMIAAPYCHWRRLRRLCTIFHST
82C2At (At4) : G-KEQLLYTGGKADQ---GASLRLGSSSETFVSSFEVA-RDCFTVNDKALASR-ITAAAKHGDCCA-VFGFAPYSAFWRBRRIATLELISN
84A1At (At4) : ---QLTHRGIANAKK---GFCCLRMGFLHMYAVSFEVA-RVWQVDSVSNRR-ATIAISYTLDR-DMAFHRCBFWRMRKVCVWRVSR
98A3At (At2) : P---VREFCYEWAOQS---GPIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
73A5At (At2) : DDLN---HRNVDYAKKRG---DFTLLRMGQRNIVVSSPDIT---REMLTODDVFASRE---RTLAAVHAAGCG---DVALAELGHWRRRRIQVHELITP
706A1At (At) : SD---VLHQQFQAATLKH---GPIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
80A1Bs (AAC) : SKNSPPFLDYSNIAQK---GPIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
78A110s (AA) : RGLPHRALDASRDAAAPR-ARBLMAFVSGETPAVSSCPATA---REVLAHPSADRLLKRSARELIFARAIG---FAPSQYWRRLRRLIATLHSP
76C1At (At2) : KHEHR---SFAPSKTY---GPIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
83B1At (At4) : K---FNPQHFFRRLSKLY---GPIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
71E1Sb (AAC) : P---L-PHNRREARBY---GPIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
71A12At (At) : L---H-PHRSHSLSRY---GPIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
705A1At (At) : S---TLHRSOKSSK---GPIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
712A1At (At) : ---KVLVPSFQSHAHY---GPIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
93A1Gm (BAA) : ---PIPQDYKSTRH---GPIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
77B1At (At1) : FQR-RHFVFLRDRHKVYG---PIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
89A2At (At1) : EGL-CGLESYLRSHHLG---PIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
701A3At (At) : EKK---PHHTTWSLIG---PIVHMHGSKRWVIGSIVEMA---KFIKTHDITLACR---KFSAGKYTTNYS---DITWSQCGYWRQRRMCLLELSA
51A1At (At2) : KGE---VILREEPKLGSVFWVLLHKNITFLIGFVSS-SHFFNAYESELQRE---IYKFNVTPEGP---VFDVDPVWRMQR---FFSSALG
710A1At (At) : RDE---TSFWDKQSSANISGSANVIGKFTVTRDTLSHQIFSNVRPDAHLIG--HFFGKKHFGDHN---LTYMEGDFKSVRRQLAPN-FEP
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Morant et al., alignment for figure 1

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703A7Lj (*) : KRLESFRRHHEAQAHLVQGVMA-QAQTEKL---INLEVLGAFSMNVVIRMILKQVYFGSES---AGPQEAEMFMMHTHEFWLGLVITYGDIYLFVW
703A8Mt (AB) : KRLESFRRHHEAQAHLVQGVMA-RAKSENP---INLEVLGAFSMNVVIRMILKQVYFGSKS---AGPQEAEMFMMHTHEFWLGLVITYGDIYLFVW
703A2At (At) : KRLESFTTQREEDARYLQDVEK-RSETGKPK---INLEVLGAFSMNVVIRMILKQVYFGPSGL---VSPKEAQEFLHHTHKFWLGLVITYGDIYLFVW
703A1Ph (BA) : KRLESFGKRRADQAQSLQEDVMA-KTQKGET---VNLADLIGAFSMNVVIRMILKQVYFGAES---AGPQEAEMFMMHTHEFWLGLVITYGDIYLFVW
703A3Os (XP) : KRLESFAAHRALPAEHLQCFVMA-KAQSCKP---VNLAEVLGAFSMNVVIRMILKQVYFGQS---AGPQEAEMFMMHTHEFWLGLVITYGDIYLFVW
703A6Sb (AA) : KRLESFAAHRALPAEHLQCFVMA-KSHSGKP---VNLAEVLGAFSMNVVIRMILKQVYFGQS---AGPQEAEMFMMHTHEFWLGLVITYGDIYLFVW
703A4Pt (*) : KRLESFANHRADQAQSLQEDVMA-RTQTKPK---VNLAEVLGAFSMNVVIRMILKQVYFGAES---AGPQEAEMFMMHTHEFWLGLVITYGDIYLFVW
703B2Pp (*) : KRLENTRKERTESRCMMMAE-AAQKGEV---VDLMDVAFAGSMTVMCRMILGRREFAATG---KQPKDFKHTHEFWLGLVITYGDIYLFVW
703B1Pp (*) : KRLEITMKERTESRCMMMAE-AAQKGEI---VDMMDVAFAGSMTVMCRMILGRREFAATG---KQPKDFKHTHEFWLGLVITYGDIYLFVW
703B3Pp (*) : KRLESFAGERTESRCMMMAE-AAANSQV---VDMMDVAFAGSMTVMCRMILGRREFAATG---DKPRDFKHTHEFWLGLVITYGDIYLFVW
79A1Sb (AAA) : SRHAWLHDKRTPDADNLTTRYVYN-LATKAATGDVAVDVHVARHYCGVNVIRLRFNRYFEGEPQADG-GPGPMEVLHMDAFTSLGHIYAFCSDIYLFVW
79D1Me (AAF) : ARHKWLHDKRTPDADNLTTRYVYHNN-QFKANKN---VNLATATRYHGGVNVIRKMFNRYFEGKMPDG-GPGPMEVIEHIDAFSLGHIYAFCSDIYLFVW
92A6Ps (AAG) : KRLESYEYIRKOEHHVFEHEFD---SRNKTLLADHSSLSLNVSRMILGRKYLEK---VE-NSIISPDEFKMDDEFLINILNIGDPIYLFVW
75B1At (At5) : HALDEKFKHVOEVCGLTRETVEVR---VGTKPNVIGQVLMNCVVALSRMILGRKYLEK---A-DADHKADEFKMDDEFLINILNIGDPIYLFVW
81D1At (At5) : HFLNCRFLYVREDEVRRLSRSS---RLAGTKKTVLSEPLMMDLFINVSRMILGRKYLEK---EET-TDEEBAKVRKLDADGANTSSGNADVYLFVW
82C2At (At4) : RRLQMLKHVVSDESMVODYLSLWVKKGGSEPVVLDLSMVEDMSLMMVSRMILGRKYLEK---EADAEARCRKGLANFHFVIGITVSDAFKYLEF
84A1At (At4) : KRLESFASVFR-DEVDKMRVRSVSC---NVGKPNVIGQVLMNCVVALSRMILGRKYLEK---S-ACEKQDEFIRIQEFSKGLYAFNVAQDIYLFVW
98A3At (At2) : KRLESRLRPTDEDEVTAMVESYER-DCNLEPNRAGKQLKRYLQAVAFNTRAFKRRFMAEAG---VVDEQGLEFKKLLSNGLKGLYAFNVAQDIYLFVW
73A5At (At2) : NVVQNRCEGEEFDEAASVVEDKPK---NPDSATKGVLLKRYLQAVAFNTRAFKRRFMAEAG---VFLRLKALNGERSLAQSEFASYSQDIYLFVW
706A1At (At) : PTLASYSYTRERETROTIVHSE-MARE---GSPVNLGEOCFLSIFNVSRMILGRKYLEK---RTSLGNELKTLSDSPSEIYQNSDFKYLEF
80A1Bs (AAC) : RMLAQEKNRERVAGNINFMHT---KVG--DVVELSRVDFGCALNVLGHVIFSRDVEY---SDQSEVGMKDLHGDLMTGCDPDAFVYLFVW
78A110s (AA) : RRVAHEPGRQADATAMASAAA---EQSATGAVLDPHQAALNIMGSHFRRYDVSSS-SG-AAADAEALKSMRGEFLKGLYAFNVAQDIYLFVW
76C1At (At2) : QRLEATKADRNKVKELVDFHSE---SSDRESVDSRAVFTITLNLISNTLFSVDLGSY---NAKASINGVQDTISVMDAAETPDANAFVYLFVW
83B1At (At4) : KRLESFVPRDEECQRMVDKLYK---AADQGTVDLSEKLLSFLNIVSRMILGRKYLEK---EYGTMKRFIDITVIGLDFPFDIYLFVW
71E1Sb (AAC) : RRVKAACYARQEMDRLLVADLDR---AAASKASVLDNKHRLDGLITGVAFNIMAS---KQFAKREFOHVDAMMDASFAEDVFNANA
71A12At (At) : KLVASERKREEDENEMKKEK---ASSSSSSSEVSEDFVTLPSVTSRILGRKHS---EDETARDLKKRIRORVIGLDFPFDIYLFVW
705A1At (At) : PQLVRSQDRSEDERFYKLEFD---KAMKESVHHEKASRFVNSVLYKMTGRS---VENNVERIMEITADIGASQKFFVSKMFRKL
712A1At (At) : QMLKADIRSEKLLKLDVSAK---CCREGLPDSGDFIKYLNIVSRMILGRKYLEK---GTDNAEIEIRLKKSLDAGKSLGAGVLYG-P
93A1Gm (BAA) : RMLDQLPVRQEKFRFVSRVER---KGVAGEAEDFGDEMTLNSIVSRMILGRKYLEK---ENDNAEEMKLLSNLAEKMGKNSDIYLFVW
77B1At (At) : PVKQCSWIGSWMQNHKRAKTK---ENVEKGFVEVMSQCRLLTCSLILCFCFAKIS---EKKIENIVKSNLAEKMGKNSDIYLFVW
89A2At (At1) : SEVRSYSHARHWLEIFERFERN---HGDDE-PIVLEHGHYAFALVLMCFDKLD---EKQIKVEERLQRLDLSRNFVDFKYLEF
701A3At (At) : NAQRKRHYVDALLENVSSKHA---HARDHPQEPVNEAEFHEHLFGVALKQAFKRDVSIYVKELGVTLSKDEIEKVLHDMGALDWNDRDFVYLFVW
51A1At (At2) : QQRGAVDQMTKEFDYDFSKWGE---SGEVLAEERITLITLASSCLREVR---DQLFDDVAELFHD--LDKMQPISVIFKYLEF
710A1At (At) : HALSTYSALQQLVLRHLRQWEG---STSGGSRPISLAEVREINLETSTQVYFVYPLD---KEAKNRFRTDYNLFINLGSMAIPIDYLFVW

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703A7Lj (*) : R---WDPYCEKRMREVEK-RVDFHSHTEPRKARKDK-K---GIGKDEEMDFVLDLSPGEGD-----GKEHDDVETKALD-QM
703A8Mt (AB) : R---WDPHCEKRMREVEK-RVDFHSHTEPRKARKDK-K---GIGKDEELDFVLDLSPGEGD-----GKEHDDVETKALD-QM
703A2At (At) : R---WDPSCCEKRMREVEK-RVDFHSHTEPRKARKLEP---EDKNGDMDFVLDLSPGEGD-----GKARMDVETKALD-QM
703A1Ph (BA) : R---WDPHCEKRMREVEK-RVDFHSHTEPRKRN-----GKNVDEGEMDFVLDLSPGEGD-----DGNKGMDVETKALD-QM
703A3Os (XP) : R---WDPYCEKRMREVEK-RVDFHSHTEPRKAREAKKS---ASLDDDN-KEDMDDFVLDLSPGEGD-----GKEHDDVETKALD-QM
703A6Sb (AA) : R---WDPHCEKRMREVEK-RVDFHSHTEPRKAREAKKTRSSLLDDDDGKEDMDDFVLDLSPGEGD-----GKEHDDVETKALD-QM
703A4Pt (*) : R---WDPHCEKRMREVEK-RVDFHSHTEPRKTRKTRK---ETGEEDKMDDFVLDLSPGEGD-----GKEHDDVETKALD-QM
703B2Pp (*) : G---WLDLQCFERDMYKLRGEFEVLDATQHRDLESGLKP-----GGKNDHISVLDLSPGEGD-----GAPHDDKTIKAVT-LDM
703B1Pp (*) : G---WLDLQCFERDMYKLRGEFEVLDATQHRDLAGSKLP-----GGKNDHISVLDLSPGEGD-----GAPHDDKTIKAVT-LDM
703B3Pp (*) : G---WLDLQCFERDMYKLRGEFEVLDATQHRDLAGSKLP-----GGKNDHISVLDLSPGEGD-----GAPHDDKTIKAVT-LDM
79A1Sb (AAA) : R---GLDLDCEHRTIVEEANY-AVNRHHDVTDWRQWKSGER-----QEMEDDLDVLDKDAQ---GNPLTIEBVAQSQDI
79D1Me (AAF) : L---GLDLDCEHRTIVEEANY-TRDYQNLTDRIQWKSGER-----KEMEDDLDVLDKDAQ---GNPLTIEBVAQSQDI
92A6Ps (AAG) : H---FLDFQGVVGRMVISK-KFQFMEHVLDEHIERKGV---KDYVAKMVDVLDLQ---LAEPPDLEVK---DERHGVKFT-QDL
75B1At (At5) : H---WLDLQCFERDMYKLRGEFEVLDATQHRDLAGSKLP-----GGKNDHISVLDLSPGEGD-----GAPHDDKTIKAVT-LDM
81D1At (At5) : R---LFS--SYENRVRKKEGE-ETKFLQCLDDEKRRQQTG---TMTTCHLIV-----LQK---SDIEYTDQIKGIL-LIM
82C2At (At4) : G---WDFQCEHEEMOTGCE-ELDEVILERNENRQQRKVSQ-----TKHNSDFVDMVLS-----LAEQKFSHLQHDATS--STC-LAL
84A1At (At4) : G---WDFQCEHNRVKNRN-DLGFEDLDEHMKKENQNAVDD---GDVDTMVDLDFYSEEAKLVSETADLQNS-IKTRDNRKATL-MV
98A3At (At2) : R---WMPFADCFAFABHGA-RRRRTRALDEHTLAKQSSGAK-----QHVPALDTEK---DQYD---LSEDTITGL-LWM
73A5At (At2) : R---PFRRCYLITCODKDRRTALFKKYVDRFRKIASSKPTGS-----EGLKCALHIDEAE---QKGEINEDMVLIV-ENI
706A1At (At) : SR---FDQGLVQVGHV-KLILLDFRVMSHVKVMGKSEEE---EDLLOYLDRK---DDDEKAPLSMTRVSL-LDM
80A1Bs (AAC) : A---RDLHLKLRKMDQFK-LIKLWEGEVLARRANRNP-----PKMLDVLITAN---DFNEHINAMF-MET
78A110s (AA) : AH---LYDPNHVARCAAVP-RVQAFVGVTRDRLRRDSSSTAADN---ADRVMDLSEEAHEN-----LAEEDMVAV-WEM
76C1At (At2) : R---FLDLQCNVTFVCTE-RVVRVFRGFDIAKIAEKSSQNNPK-----DVSKNDFVENVLDYK-----GDESELSISIEHL-LDM
83B1At (At4) : G---FLDNLITCLSRDKAFK-ELITYLQELDFTLDPNKRQOETE---S---HIDLMOLY-----KDQPFISKFTHEVNRAMI-LDI
71E1Sb (AAC) : AGRADRLSFLARRERFN-ELLVFFEKVDHMDPARVPVDPNG---GD---LVDVLNLC-----KEHDGTLRFRTRDVRATV-LDT
71A12At (At) : A---WIDRINFNARIRV-SQ-GFSDLMDKVVQVHLEAG---NHK---ED---FVDLISE-----SEKSIGFAQQRDIFM-LDM
705A1At (At) : LEKLGSL--FKTEIMVSE-RFSELVERITIIYEKMDGHQGT-----QMPALIAAY-----RDENTYKTRSRHSLTVEF
712A1At (At) : LKVPDFSG--NKRKIVAMSE-KYLLVERIKKREAKAKKDGTR---KILDLLETY-----RDPTEAMKTRNBMSP-LDV
93A1Gm (BAA) : LKVPDFSG--FNKIKETRD-RFVVVDGILKQREERKKNKTEG---TAKQFKMLDVLIDH-----EDENAEIKDKKNAF-LDI
77B1At (At1) : T---PFR-RQVREAREIRKQVCLVPLRNRKRFVDAKENPNEE---MVSPIGAAVVSFRNLIE-----RGGEVGDDEIVT-CSE
89A2At (At1) : T---KILIRKRWQETLQRRQORILLPLIRARRRSLKREKRESE---DKKDYVQSVVTLIDDELPE-----ENRKNNEEHNMLC-SEF
701A3At (At) : K---WPNKSPEARQKHRRRVMNAILQDRLKQNGSESD---DCLNPLMS-----EAKTKESQIALI-WET
51A1At (At2) : F---IPAHNCRDRAGKAKIFSNLATTRKSGDKSEN---MLDCEHDSKYKD-----GRETTESEVTGL-LTAG
710A1At (At) : AFG---EARRVRLGTELG---ICAGKSKARMAAGEEP-----ACLDFVWQAVAE-----NPQVSSGDEELGGL-LDF

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Morant et al., alignment for figure 1

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703A7Lj (*) : AAADTSAVNEWMAAVIHKHVRVHKQBELTVVGP--NRNVESDLPHLYLRCVVRERFRMHFAGFLIHESLRATT---INGYHIAKTRWF
703A8Mt (AB) : AAADTSAVNEWMAAVIHKHVRVHKQBELTVVGP--NRNVESDLPHLYLRCVVRERFRMHFAGFLIHESLRPTT---INGYHISKTRWF
703A2At (At) : AAADTSAVNEWMAAVIHKHVRVHKQBELTVVGP--NRNVESDLPHLYLRCVVRERFRMHFAGFLIHESVRATT---INGYHIAKTRWF
703A1Ph (BA) : AAADTSAVNEWMAAVIHKHVRVHKQBELTVVGP--DRMVESDLVHLVYLRQVVRERFRMHFAGFLIHESLRITK---INGYHIAKTRWF
703A30s (XP) : AAADTSVNEWMAAVIHKHVRVHKQBELTVVGR--DRMVESDLGQLVYLRQVVRERFRMHFAGFLIHESLKPTT---IMGYHIAKTRWF
703A6Sb (AA) : AAADTSVNEWMAAVIHKHVRVHKQBELTVVGR--DRMVESDLVHLVYLRQVVRERFRMHFAGFLIHESLKPTT---IMGYHIAKTRWF
703A4Pt (*) : AAADTSVNEWMAAVIHKHVRVHKQBELTVVGP--NRMVESDLAHLNYLRQVVRERFRMHFAGFLIHESLRATT---INGYHIAKTRWF
703B2Pp (*) : MAGADTSVNEWMAAVIIRNPTORLQKQBELISVVG--ERNVESDVGNFVYLMQVVKERLRLHFAFATFRSMAGTT---INGYHIAKTRWF
703B1Pp (*) : MAGADTSVNEWMAAVIIRNPTORLQKQBELISVVG--ERNVESDINKLYLMQVVKERLRLHFAFATFRSMAGTK---INGYHIAKTRWF
703B3Pp (*) : MAGADTSVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDLNMYLMQVVKERLRLHFAFATFRSMAGTK---INGYHIAKTRWF
79A1Sb (AAA) : TFAAVNPSNAVEWHLAEMVNNPEVAKAMBELRVVGR--ERLVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
79D1Me (AAF) : IITVNPNSNAIEWHLAEMVNNPEVAKAMBELRVVGR--DRNVESDIPNLYVYKACAREARLHFAVAFNVVHVALAETV---IGDYFIPKGSWAV
92A6Ps (AAG) : IAGGESSAVVNEWMAAVIIRNPTORLQKQBELISVVG--ERLVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
75B1At (At5) : FTAGDTSASVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIAQLVYQVWIKENRRLHFAVAFNVVHVALAETV---IGDYFIPKGSWAV
81D1At (At5) : IAGGESSAVVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
82C2At (At4) : IAGGESSAVVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
84A1At (At4) : IAGGESSAVVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
98A3At (At2) : IAGGESSAVVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
73A5At (At2) : NVAAITLWHLAEMVNNPEVAKAMBELRVVGR--GCVVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
706A1At (At) : IAGGESSAVVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
80A1Bs (AAC) : FFGSDTNSNIEWHLAEMVNNPEVAKAMBELRVVGR--SSTVESDHFSELYLQAVVKEIRLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
78A110s (AA) : IFRGDTALVTWHLAEMVNNPEVAKAMBELRVVGR--DGCPSDGVDMVYLMQVVKERLRLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
76C1At (At2) : FTAGDTSASVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
83B1At (At4) : IAGGESSAVVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
71E1Sb (AAC) : FIGADTSASVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
71A12At (At) : FIGADTSASVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
705A1At (At) : FIGADTSASVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
712A1At (At) : FIGADTSASVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
93A1Gm (BAA) : FVAGDTSASVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
77B1At (At1) : IAGGESSAVVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
89A2At (At1) : IAGGESSAVVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
701A3At (At) : IAGGESSAVVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
51A1At (At2) : IAGGESSAVVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI
710A1At (At) : IAGGESSAVVNEWMAAVIIRNPTORLQKQBELISVVG--DRNVESDIPKLVYKACIREARLHFAVAFNVVHVALAAT---IAGYRVKGSRWI

703A7Lj (*) : INTHGGRNTKLMD--VEEFPERHPS-DG---SRVEISHGDFKILPFSAKRRCPGAPLGVTLVLAARLHFCGWEPIKGNPEIDTRVEYGC-M
703A8Mt (AB) : INTHGGRNTKIMD--VDFEFPERHFST-SG---SRVEISHGDFKILPFSAKRRCPGAPLGVTLVLAARLHFCGWEPIKGNPEIDTRVEYGC-M
703A2At (At) : INTHGGRNTKIMD--VDFEFPERHPVW-EGS---GRVEISHGDFKILPFSAKRRCPGAPLGVTLVLAARLHFCGWEPIKGNPEIDTRVEYGC-M
703A1Ph (BA) : INTHGGRNTKIMD--VIDEFPERHHPA-DEL---SRVEISHGDFKILPFSAKRRCPGAPLGVTLVLAARLHFCGWEPIKGNPEIDTRVEYGC-M
703A30s (XP) : INTHGGRNTRIMD--VDAFRPERHPASADG--GRVEISHLDFKILPFSAKRRCPGAPLGVTLVLAARLHFCGWEPIKGNPEIDTRVEYGC-M
703A6Sb (AA) : INTHGGRNTRIMD--VDAFRPERHPA-EEG--ARVEISHLDFKILPFSAKRRCPGAPLGVTLVLAARLHFCGWEPIKGNPEIDTRVEYGC-M
703A4Pt (*) : INTHGGRNTKLMD--VEEFPERHHLA-DG---SRVEISHGDFKILPFSAKRRCPGAPLGVTLVLAARLHFCGWEPIKGNPEIDTRVEYGC-M
703B2Pp (*) : INIISLGRSSETWV--DPLIFPERWANE-----NLTAIHDSGRILPFNGRRCPGYLTTMVLTLARLHGENMSPFPVTSDSIDMEELYC-C
703B1Pp (*) : INIISLGRSSETWV--DPLIFPERWANE-----NLSAIHDMGRILPFNGRRCPGYLTTMVLTLARLHGENMSPFPVTSDSIDMEELYC-C
703B3Pp (*) : MNFMSGRNPELMA--DPLIFPERWANE-----NLAQVDPFERILPFNGRRCPGYLSSMVLSTLARYHGENMSPFPVTSDSIDMEELYC-C
79A1Sb (AAA) : ISTRGGRNTRVMD--BELFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
79D1Me (AAF) : ISTRGGRNTRVMD--BELFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
92A6Ps (AAG) : VNTTARSDNMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
75B1At (At5) : INIATARDPQNS--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
81D1At (At5) : VNAATARDPQNS--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
82C2At (At4) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
84A1At (At4) : INIATARDPQNS--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
98A3At (At2) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
73A5At (At2) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
706A1At (At) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
80A1Bs (AAC) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
78A110s (AA) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
76C1At (At2) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
83B1At (At4) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
71E1Sb (AAC) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
71A12At (At) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
705A1At (At) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
712A1At (At) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
93A1Gm (BAA) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
77B1At (At1) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
89A2At (At1) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
701A3At (At) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
51A1At (At2) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
710A1At (At) : VNVAKGRDPRVMD--DPLFPERHAT---A--ASDVALTENLDFGSESTGRRCIAASLTA-SVWLFGBLQGEFMSKPAQEAVDSESKSD---
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Morant et al., alignment for figure 1

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620
703A7Lj (*) : TPKLHETLVAATERRAKNMYS-----
703A8Mt (AB) : TPKVHETLVAAKERRASHMYD-----
703A2At (At) : TPKAKETLVAIAKERRAAHLYT-----
703A1Ph (BA) : TPKAKETLVAIAKERRPDHLYHSIK---
703A3Os (XP) : TPKAKETLVAVATERRPPQMYGRHGKQV
703A6Sb (AA) : TPKAKETLVAVATERRPPHLYGGGSAS-
703A4Pt (*) : TPKAKETLVAVARERRAEHMYH-----
703B2Pp (*) : TPLRTRRRAVATERRAPHLYSQ-----
703B1Pp (*) : TPLRTRRRTVATERRAPHLYSQ-----
703B3Pp (*) : TPLMRTRRAVATERRPPYLYA-----
79A1Sb (AAA) : -TFMATELVLHAEERRPAHLYPSISI--
79D1Me (AAF) : -TFPATELSAFAKERRAPHLYPTSP---
92A6Ps (AAG) : TPKKIH-----
75B1At (At5) : LQRAVELVHVKERRAPNVVGLGSG--
81D1At (At5) : LVPKATELKAICKERRPFLHKIIS----
82C2At (At4) : LVPKATELEIISERR-LKEGLY----
84A1At (At4) : LAPKATREFAVPTERRICAL-----
98A3At (At2) : VTYMRTVCAVATERRPSDLYKRVPYDM
73A5At (At2) : SHILLNSETIMKERRNC-----
706A1At (At) : VIKLKSVELVAVPERRSDPKLYTA---
80A1Bs (AAC) : SLCKAKERRVVPKERR-----
78A11Os (AA) : -LEMKTELAAATERRRRRAA-----
76C1At (At2) : NFA-----
83B1At (At4) : AHHKKEHVLAPTKEH-----
71E1Sb (AAC) : FHRKTELVVPTKYKNRRAA-----
71A12At (At) : DVCRKTELVAFPSSV-----
705A1At (At) : LITMAHETCTPTIQLPRTQNSLISHL--
712A1At (At) : SAEMARELWONPVDHFNTE-----
93A1Gm (BAA) : LPRANETICVPERRNPFTI-----
77B1At (At1) : LVVVMKNSKCAQIRSE-----
89A2At (At1) : LVVVMKHEKAVERRRCH-----
701A3At (At) : LSQKLYELMAMINERRS-----
51A1At (At2) : VVGAKGNVVRVYKRRPFS-----
710A1At (At) : PKDGCCTVFLSRRVAKYPNFS-----

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