

SUPPORTING INFORMATION FIGURE S3. Alignment of fungal Mmm1 proteins. Conserved cysteines are shaded in grey. A116-124 is shaded in grey in the *N. crassa* protein. The membrane spanning domain of the *N. crassa* protein is underlined and shaded in grey. Residues in the C.g. sequence resulting from a potential missed intron are highlighted. Abbreviations: N.c., *Neurospora crassa*; G.z., *Gibberella zeae*; C.g., *Chaetomium globosum*; S.m., *Sordaria macrospora*; M.o., *Magnaporthe oryzae*; P.a., *Podospora anserina*; F.o. *Fusarium oxysporum*; V.d., *Verticillium dahliae*; A.n., *Aspergillus nidulans*; *Trichophyton tonsurans*; C.i., *Coccidioides immitis*; P.b., *Paracoccidioides brasiliensis*; S.s., *Sclerotinia sclerotiorum*; B.f., *Botryotinia fuckeliana*; P.t., *Pyrenophora teres*; S.c., *Saccharomyces cerevisiae*; *Kluyveromyces lactis*; C.a., *Candida albicans*; S.p., *Schizosaccharomyces pombe*; U.m., *Ustilago maydis*; C.n., *Cryptococcus neoformans*; R.o., *Rhizopus oryzae*; B.d., *Batrachochytrium dendrobatidis*.

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N.c. -----
G.z. -----
C.g. -----
S.m. -----
M.o. -----
P.a. -----
F.o. -----
V.d. -----
A.n. -----
T.t. -----
C.i. -----
P.b. -----
S.s. -----
B.f. -----
P.t. -----
S.c. -----MTDSENESTETDLSIMTFDDYISKELPEHLQRLIMENLKGSTTNDLKQTSNNSEFN 55
K.l. MEMSELLASEVVS SGPDYAKKSV DGLNMTAANGTNDT LMT-LDEYLNKSLPLHLEQLILD 59
C.a. -----MSQDLIETTATTTKIVEAR-----ELGHQIHDSLLEQLKLQQ-EELLQQQRDLFFQ 50
S.p. -----
U.m. -----
C.n. -----
R.o. -----
B.d. -----

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N.c. -----MADICPSRSEP-----TLSFTQGLI 20
G.z. -----MAGDTCQPTEP-----TLSFTQGLI 21
C.g. -----MARDVCP TNSEP TVSRRVVPTLRLRGWDVNVANCRWVYRLSFTQGLI 46
S.m. -----MADICPARSEP-----TLSFTQGLI 20
M.o. -----MTPDSCPVRPEP-----TLSFTQGLI 21
P.a. -----MAQDVCPTRSEP-----SLSFLQGLI 21
F.o. -----MEADTCPRLIEP-----TLSFTQGLI 21
V.d. -----MADKTCPATSEP-----TLSFAQGLV 21
A.n. -----MAFQQGTPGPPVELCSTFTDHDE-----TVSSLSFTQGF 35
T.t. -----MSSPENASCP-----PPQHLSFTQGLL 23
C.i. -----MSN--DTSAQ-----PAQSLSFTQGLL 21
P.b. -----MAGSTSASLQTPYFPSSTQINPVRVDHTLPLPPSQPSLSFTQGLL 45
S.s. -----MWLDDVAS-----ELSFTQGLL 17
B.f. -----MTIPAPIPKAES-----SLSFTQGLL 22
P.t. -----MAEEVPTAVPLATPAGSS-----SLSFTQGF 27
S.c. VSKNGSFKGLDDAIQALQMQSVLHPS-----SLGSLATSSKFSGWSFAQGF 102
K.l. ANQKELFDSAAKSLLSSTLLAKQQQSL-----QIAPIQPQSSFSQSFAEGLI 107
C.a. EQQ-----LQLQQQVTQP-----VSNNGNTWSFTQGLV 78
S.p. -----MIHLPQG-----SFTQGLI 14
U.m. -----MQQPQQDLQIGLPYAPVQPPIPSPAAYFAYLPSPSRWTFTQGLI 45
C.n. -----MSETFSPNLTFTEGFV 16
R.o. -----

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B.d.

N.c. LGQLSVVLLLAAFIKFFIFGDPPSPEVVASIRATDRRSRTLAHKKS-----ILSLRETN 74
G.z. VGQLSVVLLVLAAFIKFFIFGDPPSPDVTASLRATERRSRTLAHKRS-----LLSLRSPG 75
C.g. LGQISVVLLIAAFIKFFIFGDPPSPEITASIRAAERRSRTLAHKRS-----LLSLRESS 100
S.m. LGQLSVVLLLAAFIKFFIFGDPPSPEVVASIRATDRRSRTLAHKKS-----ILSLRETN 74
M.o. VGQISVVVLLIAAFIKFFIFGDPPSAEETASLRASERRSRTLAHKKS-----LLSLRTSN 75
P.a. LGQLSVVLLIAAFIKFFIFGEAPSAEETASIRATERRSRTLAHKKS-----LLSLRSAA 75
F.o. VGQLSVVLLVLAAFIKFFIFGDPPSADVTASLRATERRSRTLAHKRS-----LLSIRSPA 75
V.d. LGQLSVVLLVLAAFIKFFIFGDPPSPEVTASLRATERRSRTLAHKKS-----LVGLRAAT 75
A.n. LGQLSVVLLIGAFIKFFIFGEAPPPSRG--LRASTHRRSNSIFS--QDAPPPRSREKP 91
T.t. LGQLSVVLLIGAFIKFFIFGEAPSSSSRGISQRAAPRKRSYSANSTLFRDAASRLKESA 83
C.i. VGQLSVVLLIGAFIKFFIFGEASPPSSRSQTRRTSPHKRSYSISG--ARDLGSRSLEKEP 79
P.b. VGQLSVVLLIGAFIKFFIFGEAPPPSRGLSNRTSTHPRSYSINAA-STDSSPRPLREKP 104
S.s. LGQLSIVILIGAFIKFFIFGDPPSPDVSAALRATERRSRTLAHKRS-----LLTLRSST 71
B.f. LGQLSIVILIGAFIKFFIFGDPPSPDVTAALRATERRSRTLAHKRS-----LLTLRSST 76
P.t. LGQLSIAILIFCFIKFFIFGDEPSADDRALHLNLSLRRARTLAHQQS-----YKQLQTRA 81
S.c. VGQLSIVLLIFFFLKFFIFGDEPSKSNPKPAASRHRSKFKEYPFI-----SRE 151
K.l. VGQLSVIVALIFVIKFFVFSEGGTKTATAKSVGS--ASSFMS--T-----KNS 152
C.a. IGQVSVIFIIIVFVKFFVFADSSSHIPKPLDG--ATGVIVK-----RNK 122
S.p. VGQLLTLAIIVVFLRFFFCSPIPKSVANSFKQTGNETPDETPSTP-----60
U.m. VGQVSMVIVALLLIRYVIFEDSATALEKERLMLKVSQRRSKLHAKALLQDARKANSAAA 105
C.n. LGQASFLIILLFIRYVVFSPSEQIDHEG-----WRKRR 50
R.o. -----MLLVQKARYIPSRPSLN-----TAP 20
B.d. -----MHQRIAVSKPK-----PVS 14

N.c. ALQLVQNP----ALNKKH--VLRPG---PPILTIGSILSKTYKVDSHQPESLDWFNVII 125
G.z. NR----QDR---ELNRKKSTVLRN----PPALTIGSILSKTYYNVDSHQPESLDWFNVII 124
C.g. TRRAGQQP----TLNRKKSSILRPS---PPPLTIGSILDKTYKVDSHQPESLDWFNVII 153
S.m. ALQLVQNP----ALNKKH--VLRPG---PPTLTIGSILSKTYKVDSHQPESLDWFNVII 125
M.o. QRPGSQQQQS--VLNRKKSSILRSG---PPSLTIGSILNKTYRVESHQPESLDWFNVII 130
P.a. TQRQGSQPPALPALNKKKSSILRSN---PPTLTIGSILDKTYKVDSHQPESLDWFNVII 132
F.o. NRGDRSQDR---SLSRKKSTVLRN----PPTLTIGSILSKAYYNVDSHQPESLDWFNVII 128
V.d. GR---PGQP---SLNKKKSSVLRN----PYNLTIGSILSKTYYNVDSHQPESLDWFNVII 125
A.n. STSNVLRPVP--SSATNTRSILRKTYYSAPNPNS---SKHRIHHSSHQPESLDWFNVII 146
T.t. S-SNVLRPVP--SSSTNKSILRKTYYNAPTNFQ--KNGRNLHHSTHQPESLDWFNVII 139
C.i. S-SNVLRPVP--SSSTNTRSILRKTYYSANPTNFTSKHGRHRPHSTHQPESLDWFNVII 136
P.b. STSNILRPVP--SSSTNTRSILRKTYYSATPHPTPKHGRPRLYHSSHQPESLDWFNVII 162
S.s. PRHASQS-----LNRKRSSVLRN----PAPLTTNAILSKTYYNVDSHQPESLDWFNVII 121
B.f. PRRASQP-----LNRKRSSVLRN----PAPLTTNAILSKTYYNVDSHQPESLDWFNVII 126
P.t. NSTSLSLR-----HKPSTSIRKGEETRGGPSIATILAKTYYNVKGHQPESLDWFNVII 135
S.c. FLTSLVRKGA-----KQHYELNEEAENEHLQELALILEKTYYNVDVHPAESLDWFNVI 205
K.l. ILSTIIKRG-----KDGLEVDK-DNEKSRQINSILEKTYYNVETHSPESLDWFNVI 205
C.a. NKKHSNGQFA-----NDGENEDDTSLDNSQSKISSILEKTYYNVNNHASESLDWFNVI 176
S.p. -----LSNKKRYKPLTILEPHILNLLYDVNEHEPESLDWFNVI 101
U.m. SAAAAAAPSP----ASHPLRKSHRLASDTRAMFANILDKTAYDLSSHLPEADWLVNMF 161
C.n. AERADLLSN-----HTPPPLSNLLSKTSYDMSIHPAESSDWVNVLL 91
R.o. SVAAAAALPN-----DHITLTKTYDVIIHPPPESTDWLVNLL 55
B.d. AQQRRRTIDS-----LILGKIYNTSQHPFESCNWLNILI 48

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N.c. AQTIAQFRSDA-----QHDDAILSSLSKALNG-----TARPDFLD 160
G.z. GQTIAQFRSDA-----QHDDAILDLSLTKALNG-----GSRPDFID 159
C.g. AQTIAQFRSDA-----QHDDAILTSLTKALNG-----TSRPDFVD 188
S.m. AQTIAQFRSDA-----QHDDAILSSLSKALNG-----TARPDFLD 160
M.o. AQTIAQFRSDA-----QHDDAILTSLTKALNG-----TSRPDFLD 165
P.a. AQTIAQFRSDA-----QHDDAILTSLTKALNG-----TSRPDFVD 167
F.o. AQTIAQFRSDA-----QHDDAILDLSLTKALNG-----DSRPDFID 163
V.d. AQTIAQFRSDA-----QHDDAILSSLTKALNG-----TSRPDFVD 160
A.n. AQTIAQYRQTAYLLKDSPTSSILHSLTAALNNP-----EKKPSFID 187
T.t. AQLIAQYRQTAYLLKDSPTSSILDSTLDTLNNV-----EKKPSWID 180

C.i. AQTIAQYRQTAYILKDSPTSSILES LATTLNNP-----EKKPSFID 177
P.b. AQTIAQYRQTAYILKDSPTSSILASLSETLNNP-----EKKPSFID 203
S.s. AQTIAQFRADA-----QHDDAILTSLTKALNG-----GNRPDFLD 156
B.f. AQTIAQFRADA-----QHDDAILTSLTKVLNG-----GNRPDFLD 161
P.t. AQTIAQLRADA-----RQDDAILTSLTEVLNT-----GSKPDWIG 170
S.c. AQIIQQFRSEA-----WHRDNILHSLNDFIGRKS-----PDLPEYLD 242
K.l. AQTIHQFREEA-----LQKNNILNSLNDFIERRS-----NELPQYLD 242
C.a. AQTISQLRSEA-----LLKDNIIYHSLNNFLTN-----AKLPDFID 211
S.p. AQALIQFRYDA-----CSNDVALRKLETVLNKG-----AQDKSMVD 137
U.m. AQAIAGYREDVLTGG--VSSHHTASDAIPSPNPLEPQKERTARDLMEEILNRATSSFLD 219
C.n. AQILQGYRNDLLSEG--GEEGARQRIEGWLNPK-----GENSLWLD 130
R.o. AQVILQYRQDAS-----INNRMSCALDSVFNSG-----VRPSFVG 90
B.d. AQFLTLRLTDAEFG-----LKSVSMLDSILNSA-----WKPSFLG 83
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N.c. EIKVTELSLGEDFPFIFSNCR IIPVDEDGLSFGTGKAFDANMATREGARLQARMDVDLS-D 219
G.z. EIRVTELSLGEDFPILSNCR IIPVDEDGVS LGHGKKFDPKAARDGTRLQARMDVDLS-D 218
C.g. EIRVTELSLGEDFPFIFSNCR IIPVDEDGLNLQSGKGLDANMATREGARLQARMDVDLS-D 247
S.m. EIKVTELSLGEDFPFIFSNCR IIPVDEDGLSFGTGKAFDANMATREGARLQARMDVDLS-D 219
M.o. EIRVTELSLGEDFPFIFSNCR IIPVDEDGLDFGPGKAFDANMATRDGGTLQARMDVDLS-D 224
P.a. EIRVSELSLGEDFPFIFSNCR IIPVDEDGLQFGAGKAFDPKQAAREGARLQARMDVDLS-D 226
F.o. EIRVTELSLGEDFPILSNCR IIPVDEDGVS LAPGKKFDATAARDGLRLQARMDVDLS-D 222
V.d. EIRVTKLSLGEDFPFIFSNCR IIPVDEDGLSLGNSKTI DASAATREGAKLQARMDVDLS-D 219
A.n. KITVTDISLGEFFP FIFSNCR IIAVDDP-----MSDGGRLQALLDVMSDD 232
T.t. RINVTDISIGEEFFP FIFSNCR VIAVDDP-----NSDGGRLQALMDVDLSDD 225
C.i. DITVTDISLGEFFP FIFSNCR VIAIDDP-----SSDGGRLQALMDVDLSDD 222
P.b. IIKVTDISLGEFFP FIFSNCR VIAVEDP-----NSDGGRLQALMDVDLSDD 248
S.s. EIKVTELSLGEDFPFIFSNCR IIPVDEDGITLGR----EGGAAGREHGRLQARMDVDLS-D 211
B.f. EIKVTELSLGEDFPFIFSNCR IIPVDEDGMTLGR----EGGAAGREHGRLQARMDVDLS-D 216
P.t. EIKVTEIALGDEFFP FIFSNCR VMPA-EDGFWYGGP-----NTGNDKERLQARMDVDLS-D 222
S.c. TIKITELDTGDDFP FIFSNCR IQYSP-----NSGNKKLEAKIDIDLN-D 284
K.l. QIKITEVDIGDDFP FIFSNCR IQYSP-----NSNKKRLEAKIDIDLN-D 284
C.a. TINLTEIDIGDDFP FIFSNCR IKYG-----EDLKRLEAKIDVDLS-D 251
S.p. HIYVRDLSLGDGFPVFSHCRVLP HQHN-----SSQLRAEMLVSLT-D 178
U.m. PIRVTEADFGDAYPIFTNARVRPADDT-----GRTRIEIDVDYS-D 259
C.n. PIDVTSLSLGTSYPLLSNARIRPADGQ-----GRLRAEIDVDYL-D 170
R.o. PIHVTELNLGQEFPIFSRARIRPSDEA-----GSTRAEIDFEYS-D 130
B.d. DISITNFSLGE EYPTLKNARVFAEPE-----SGMKIHVDFSFID-D 123
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N.c. MITLAVETKLLLNYPKRLSAVLPVALAVSVVRFSGTLSISFIPSN----- 264
G.z. MLTLAVETKLLLNYPKKLSAVLPVALAVSVVRFSGTLSISFIPSN----- 263
C.g. MITLAVETKLLLNYPKRLSAVLPVALAVSVVRFSGTLSISFVPSN----- 292
S.m. MITLAVETKLLLNYPKRLSAVLPVALAVSVVRFSGTLSISFIPSN----- 264
M.o. MITLALETKLLLNYPKKLTAVLPVALAVSVVRFSGTLAISFIPSN----- 269
P.a. MITLAVETKLLLNYPKRLSAVLPVALAVSVVRFSGTLSISFNPSN----- 271
F.o. MLTLAVRTKLILNYPKKLSAVLPVELAVSVIRFSGTLSISFIPSN----- 267
V.d. LLTLALETKLLLNYPKKLSAVLPVALTVSVRRFSGTLSVSVFIPSN----- 264
A.n. NLSIAVETSLVLNYPKPCSAI LPVALSISVVRFSGTLCISLVPAS-----T 278
T.t. NLSLAIETNLLLNYPKPASAVLPVALSVSVVRFSGTLCISFVPSP-----G 271
C.i. NLSLAIETNLLLNYPKPYSAI LPVALSVSVVRFSGTLCISFVPGT-----T 268
P.b. NLSLAIETSLLLNYPKPFAVLPVALAVSVVRFSGTLCISFVPGP-----R 294
S.s. FITLAVETKLLLNYPKPLVAVLPVALAVSVMRFSGTLSISFVPGS----- 256
B.f. FITLAVETKLLLNYPKPLVAVLPVALAVSVVRFSGTLSISFVPGS----- 261
P.t. VITIGVETLNLNWPKPMSAVLPVALAVSIVRFSGTLAMSFIPSSPPSTTAPMPSPTCN 282
S.c. HLTGLVETKLLLNYPKPGIAALPINLVSVIRFQAACLTVSLTN----- 327
K.l. RLALGIETKLLLNYPKPFAALPIKLTVSVIRFQAACLTVSLTT----- 327
C.a. TLTLGIATKLLLNYQPRPLTAVLPVALSVIVRFSGCLTVSLINTKDI DLKNVDKTSNMNG 311
S.p. NINCTVDTKLLLNYPKPAFATLPLSITVRI CKFVGKVSFLTIVYS----- 225
U.m. QITLAIDTKLLINFPKPRFAVLPVSLGLTIVRFSGTLAIELFSSD----- 304
C.n. SLSMTLSTAVLVNFPKPRFAVLPVTLGVELVSI GGTMSVQLHEPI----- 215
R.o. QVTLGIETQLILNWPKQAFVLPVSLVLSVVRFSGTLTIELINP----- 174
B.d. QLTGLIDTQMLINYPKPGMAALPISIVLSIVKFSGT FVIEFVSKP----- 168

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N.c. -----PSNNE-----PAK 272
G.z. -----PSQST-----PTR 271
C.g. -----PSENT-----PTK 300
S.m. -----PSNNE-----PAK 272
M.o. -----PSQST-----PTK 277
P.a. -----PSENT-----PTK 279
F.o. -----PSQST-----PTR 275
V.d. -----PSQST-----PTM 272
A.n. PPLHTPSPMPSPPTAGAQPAAGAQPTDGGDIP----PKSSS-----KSN 318
T.t. TTS----ESSNPPPHSEGNQEP---RPGQED----PRRPSSKDGIRS-----GIPKTS 314
C.i. QTSTHLATSPSNIDPTLQTNDYSGANRRGNRR---QERTDTEQATQANNAGTTGIPKTS 324
P.b. TSDQTMSP IPTPHDTTSEAI DDQSSDQPSPAQNPDGPKDAHANTSNTTDASSKHGIPKTS 354
S.s. -----PLNGS-----PTT 264
B.f. -----PLNGS-----PTT 269
P.t. THRSSSPSRPTSSSGAPP-----HRPTT 305
S.c. --AEEFAS TNGSSSENGMEGNS-----GYF 351
K.l. --DEQFVPTSEETN-DDEMGNDK-----GY 350
C.a. YSKENANGDGASSNNDDEDDG-----GTA 337
S.p. ---LYDSLHPSPGGLKHQVLRITVIMIFYSP-----SNGAGQPAY 263
U.m. -----PNATV 309
C.n. -----EDRQH 220
R.o. -----PETTT 179
B.d. -----ILPVC 173

N.c. MIFTFLDDYRLDFSIRS-----LLGSR SRLQDVPKIAQLVE 308
G.z. MIFNFLDDYRLDFSIRS-----LLGSR SRLQDVPKIAQLIE 307
C.g. MTFTFLDDYRLDFSIRS-----LMGSR SRLQDVPKIAQLVE 336
S.m. MIFTFLDDYRLDFSIRS-----LLGSR SRLQDVPKIAQLVE 308
M.o. MVFNFLDDYRLDFSIRS-----LVGSR SRLQDVPKIAQLVE 313
P.a. MTFTFLDDYRLDFSIRS-----LLGSR SRLQDVPKIAQLVE 315
F.o. MIFNFLDDYRLDFEIRS-----LLGSR SKLHNVPKIAQLVE 311
V.d. MTFNFLDDYRLDFSIGS-----LLGSR SKLEDVPKIAQLIE 308
A.n. IAFSFLPDYRLDLSVRS-----LIGSR SRLQDVPKVAQLVE 354
T.t. LAFSFLPDYRLDISVRS-----LIGSR SRLQDVPKVAQLVE 350
C.i. LAFSFLPDYRLDLSVRS-----LIGSR SRLQDVPKVAQLVE 360
P.b. LAFSFLPDYRLDLSVRS-----LIGSR SRLQDVPKVAQLVE 390
S.s. LAFCFLLDDYRLDLSIRS-----LVGSR SRLQDVPKIAQLIE 300
B.f. LAFCFLLDDYRLDLSIRS-----LVGSR SRLQDVPKIAQLIE 305
P.t. LAFTFLDDYRLDLSVRS-----LVGSR SRLQDVPKIAQLIE 341
S.c. LMFSFSPEYRMEFEIKS-----LIGSR SKLENIPKIGSVIE 387
K.l. LMFSFNPEYRMELEVKS-----LIGSR SKLENIPKIASLIE 386
C.a. LMFSFSPDYRLEFIVKS-----LIGSR AKLQDVPKISSLIE 373
S.p. MNLSFDPNFVISLQVSS-----LVGAR SKLQDIPKITQLIE 299
U.m. LPTANPNPSSSSSSSATSPPRSRHLHFSLHPDFALEASATSLIGSR AKLQDIPKIEQLLI 369
C.n. IHVNLLPDFHLNLKVTS-----LLGSR AKLQDIPKLEQLIV 256
R.o. KP-----KIPLERYIAI 191
B.d. QQPLYKSQASETSTS-----DLGHHTYVSV 198

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N.c. SRLHRWFDERC VEP RFQEIALPNMWP RKKNTRG---GDETISDVER-----S 352
G.z. SRLHRWFDERAVEPRFQEIALPSLWPRKKNTRG---PDDGLAEGSV-----P 351
C.g. SRLHRWFDERC VEP RFQEIALPSMWP RKKNTRG---GDEAIADAER-----S 380
S.m. SRLHRWFDERC VEP RFQEIALPNMWP RKKNTRG---GDETISDVER-----S 352
M.o. SRLHRWFDERC VEP RFQEIPLPSMWP RKKNARG---GDDAIADVER-----S 357
P.a. SRLHRWFDERC VEP RFQEIELPSMWP RKKNTRG---GDEIIANIEQ-----S 359
F.o. ARLHRWFDERAVEPRFQEIALPSLWPRKKNTRG---PEDASTERSE-----S 355
V.d. ARLHRWFDERC VEP RFQEIALPSLWPRKKNTRG---PDDGMAEGNIG-----S 353
A.n. ARVHAWFEERVVEPRVQVGLPDLWPRMGRTGVRT-GDESETGSNTASRPAMSVDMSS--S 411
T.t. ARVQSWFEDRVVEPRVQLVALPGIWP RMGRTGVRA-QEDHDAVSDSDDP-EAKAAKSGFT 408
C.i. ARVQAWFEERVVEPRVQVVALPGIWP RMGRTGVRG-QEEQQEVGSSGNAGVSTANVSMGL 419

P.b. ARVQSWFEERVVEPRVQVVLGPNIWPRMGRGTGLRSSQEEPEAGSGSVEIPVMTSPGADGV 450
S.s. ARLHTWFDERCVEPRFQQIELPSLWPRKKNTRG---GEDLDTGSEAG-----G 345
B.f. ARLHTWFDERCVEPRFQQIELPSLWPRKKNTRG---GEDLDTGSDAG-----G 350
P.t. SRVHAWFDERAVEPRFQQIVLPSLWPRKHNTTRGGA-PEDTEAAVEGEEGLDEDDFAVDG 400
S.c. YQIKKWFVERCVEPRFQFVRLPSMWPRSKNTR---EKPTL----- 426
K.l. YQISKWFVERCVEPRFQFVKLPSMWPRSKNTRK---EKTDTDDSVS----- 429
C.a. NQLRTWFIERCVEPRFQVRLPSLWPRKKNTRKREPVTKKTTTTPSTT----- 419
S.p. SRIRQWFTNRQVSPQFQQIAIPNLWPTSAKEGHARSHAPQEESNED----- 346
U.m. SRLRGWIMDRFVWPRYWSLTLPLNLVPSAASRSFSAAAAANRHTDAASVGSSSGGHGINV 429
C.n. SRLRNLVQDRFVHPNHISLALPRILSPSVSSTPILEGLGEGAVDAMKDAVSDGMKRMVED 316
R.o. SSYSDFILD-----LQIKVPNMWK----- 210
B.d. SVLDDFLLD-----FDVRSLLG----- 215

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N.c. MSKAKG-----VDIAKDVREEARKEIEAEAHGGADRV-----PDS 387
G.z. IGRSKG-----RDASRPQ-EEARG---DAEIRDR-----GT 379
C.g. MGKSKG-----MEMAKEMRTEARREVEAETDVRADRG-----HES 415
S.m. MNKTKG-----VDIAKDVREEARKEIEAEAHGGADRV-----PDS 387
M.o. MSKAKG-----ADVARDLR-----REVLVEAEARQAAQ-----RDS 388
P.a. INKAHG-----GAIAKEAR---QELDTETDG----- 382
F.o. IGRSRG-----NDAGRDHR-EEIRGRGGDAEIRDRGA-----GGT 389
V.d. VGRSKG-----RDVQDIR-AEARK-EVEAEASSRTD-----RAQ 386
A.n. PGHLQGD-----GGNHEEELFRFGLGPRPPLPFDVAVSRTSSYQVE-----TGA 454
T.t. PVNANRD-----GPQTPRDLNMDGLRYRRNGGGQSTPDNYENLP-----QGD 451
C.i. ARDAGAE-----GSHATRDADMEGLRYRRNASPGDETSQVRYSPQ-----NQD 462
P.b. SGGGGSG-----GGSGGGGGMGRGIDRGLSGREAGYEALRYRHAA-----CGG 493
S.s. IGRARS-----RDVERDLREEARKEVEAETGVRVGRSKLGVSLDVPDVGLD-GGS 394
B.f. IGRARS-----RDVERDLREEARKEVEAETGIRVGRSKLGVSLDVPDE-----GS 395
P.t. NGTAPGSTSYIPTPIAENATLEERIEAEGAKMREAEIRAGVRKPSASQERSRGRDDRAG 460
S.c. -----
K.l. -----VKSND----- 434
C.a. -----VNGTSAATVTTTTPGEYVNSNI----- 439
S.p. -----
U.m. GTGVERTDASVIQPGHHE SARQEMLHAASERPS-----LASSRPPHVRSSSSGLRANGM 483
C.n. FMGENPVEGALNGQEEQWLLDDDFPPTPLVQPPGTFPTLSVSSRQSHRQSLPPSRPQSTT 376
R.o. -----EQEEQEE----- 217
B.d. -----HRTKVKDLPKLTSLSISN-----SLRSVFISEMVFACKMIKIP 253

N.c. LRYRHRPRADEEFPGAGSMGSMG-SMP----- 415
G.z. IRQRRGTRGSDSD--FSMPGSLPSFQIPTP----- 408
C.g. LRYRRRPQTDDSFSTSGSMGSMPLDIPPT----- 445
S.m. LRYRHRPRADEEFPGAGSMGSMG-SMP----- 415
M.o. LRYRR-PRADDAFP---MPGSLAVDD----- 410
P.a. LRYRRRPVGDYTSVSGSMGSLPGIDMPT----- 412
F.o. VRHRRGTRSNDSDD--FSMPGSLPDFQVAAS----- 418
V.d. ESLRR-RRLRSEDE--LIMPGSLPDFVQ----- 411
A.n. PRSPSLTRERSLG-DDFHMPGSMPEAPGAQ----- 483
T.t. GHPQPTSG-----EQFRIPGSLPGTSAIA----- 475
C.i. SREQACRD-----DPFRIPGSLPDVVPVT----- 486
P.b. HQNQSGRDGGRGNEQFAMPGSMPTVTET----- 523
S.s. EEGLRFRRRSRGRGDEYAMPGSMPLSMA----- 423
B.f. EDGLRFRRKSAGR-DEYAMPGSMPLSMT----- 423
P.t. MRWRGEQRERTTGPRPKLQSRSTTTGIVKAI PGALPR----- 497
S.c. -----
K.l. -----
C.a. -----
S.p. -----
U.m. GSVEAWRAHAAGVYNQPSHQHATSLNQAALLRAHVGGGGATDCAPGSDVNIEVPGSYRGS 543
C.n. QGQPQLFYRRPLIHPTQSYPHYNTYTLDPQIPHVSYSRHPPRGSHVHNPETPVPQRPSH 436
R.o. -----
B.d. NGEELFGDIANAVDENSHDVFNLQENGSETLKSA----- 287

N.c.	-----	
G.z.	-----	
C.g.	-----	
S.m.	-----	
M.o.	-----	
P.a.	-----	
F.o.	-----	
V.d.	-----	
A.n.	-----	
T.t.	-----	
C.i.	-----	
P.b.	-----	
S.s.	-----	
B.f.	-----	
P.t.	-----	
S.c.	-----	
K.l.	-----	
C.a.	-----	
S.p.	-----	
U.m.	VAGAGIELASSNASSVLPTGAHHSSGLRNRPGFVQ---	579
C.n.	GQGRMSTTSSLTPSQSQSQRFRFRGQFASGVTPGQVGTSR	475
R.o.	-----	
B.d.	-----	