Zm/AA33/1-228 · · · · · · · · · · · · · · · · · ·	LSLSLP
Z#/AA16/1-289 · · · · · · · · · MGDAAETNKTLHNWMGEPRPRSSDQRDEEETLQ Z#/AA9/1-357 DGKE · · · · RKGREAQDAGRSKNSGGFGG · · · · EED · · AKLEI	LSLOLP
Z <i>m/AA11/1-251</i> Z <i>m/AA34/1-355</i> MLNLA <mark>P</mark> FET <mark>PPL</mark> GRQER <mark>P</mark> TNTIVTAT	MKLKQ
2т/АА18/1-197 Ме 2т/АА30/1-216 Ме 2т/АА17/1-206 Ме	LELGLAP
2m/A41/1-225 MEVAAAASYSYYGLEAADDDVDNLRATE	EN <mark>S</mark> GAEEEDEETVVEQDDDELEL <mark>GL</mark> CL <mark>G</mark> SKQQQQH <mark>PPP</mark> CRILTAR LRLGLPGTEAAEEEEEARQAQKVAA <mark>PPP</mark> LRLGLPGTEEKEEAEE <mark>P</mark> .QHKAA <mark>PPPP</mark>
Zm/AA32/1-226 METVV <mark>O</mark> DLMATEI Zm/AA3/1-202 MEMIDAEI	LR LG LPG TVD
Zm/AA25/1-66 Zm/AA24/1-115 M A G Y G D	L R L G P P G S S N
2m/AA10/1-269 M S P P L E P H D Y IG L SA VAAAA P P T P T P T SSSSSSSS P A P R L T 2m/AA29/1-272 M S P P L E P H D Y IG L SA AAAAA P P T P T SSSSSSS P A P R L T	LILGPPGVN. LRLGLPGSES
2m/AA28/1-255 M S <mark>PP</mark> LE - LDY I <mark>G</mark> LS <mark>PP</mark> AAAAAAA EN DELK <mark>O</mark> T E 2m/AA2/1-237 M AGAD VD VOG	L R L O L P O S O S
Zm/AA5/1-220	L R L <mark>G L PGGGGGG E P</mark> A L <mark>GG E G</mark> R SS SS A S <mark>G</mark> K R <mark>G</mark> F A E T I D L K L K L E PAAV VEAEEEEE
Zm/AA31/1-255 WS IAPSPSPFLPLSGLPRPOSOSGSRRAWSPARCTPPPAMS	VDTERSSTESSAASRLGYEDTTLALTLRLPGSVDTERSSTESSAASRLGYKDTTFALTLRLPGS VDTERSSTESSAASRLGYKDTTFALTLRLPGS ASS-TNSAASPAVSGLDYDDT.ALTLALPGS
Zm/AA33/1-228	RÖNESASV <mark>GAGG</mark> KAVE <mark>GG</mark> NK
Zm/AA3V1-357 AHVLQL <mark>G</mark> RR <mark>P</mark> SAPVVGWPPV <mark>R</mark> SF <mark>RRNLAHHHHG</mark> SSSKOPTE <mark>P</mark> Zm/AA23V1-346 <mark>6</mark> DVL······PVVGWPPVRSFRRNLANASSSKOSLEQQQO	NORKKEDKEEUTIKKAPFVKINNIG IPIG KKUDLSALG SVDELSLB VDKLFROLLAADUDP DNSEASRKEKPACKKNPLVKINNIG IPIG KKUDLAAVDSVERLSLG VKELFHOFLQAQKD. NDDEASCDKAKOTCKRSPLIKINNIG IPIG KKINLSAVDSVQKLSSAVQDLFCGFLDAQKD. SCAVG KVDLLAH.GVASLSRALQAMFIG FLSGDELRTDHEP.LVSLVHMLHGQWRIVGSE
2 <i>m1AA34/1-355</i> RRN IVSAMHVI <mark>T</mark> N KOTAGASSAVAGNGG TPPOSTTA THTGG 2 <i>m1AA6/1-198</i> DLOLGLSESPASSALLVAETNNSIVPSTPRNGALPON 2 <i>m1AA18/1-197</i> LFVCEDODGG.GOORDMOVDHCOSNNVPRKK	SETN <mark>S</mark> AAAAALAAR <mark>P</mark> ALAASSMFAKVHMIGYAIGKKVNLRAQDGYDSLSRILTNMATNFFCP MPPIKPFLRSALTASARRRTLFVKVYMIGVPIGKKLDMLLDGYSSLAKLCHMFKASITY RVGWPPVKCARRRS.GOGGYVKVLLGVPIGKKDDVSIHGSNGELLRTLESMFPSGNQQ
2m/AA30/1-216 LFL R D D D D G D R GOOG D R GOOG D R 2m/AA17/1-206 TTL FL FD D G S C GOR S GOO 2m/AA127/-235 P G TV A S GH P Q S F O V G W P IR TF R M S L F N Q A K E N A S E A O A K	LLVOWPPVKCARRSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Zm/AA8/1-229	SAKSKPAAADEGAPGPAGGGr VKVSMIGAPYL XKVDLGTCGGYRDLREALEAMFCF SGPG AAKNKPAAALA.EEAPAAGGF VKVSMIGAPYL XKVDLKMYKGYRELREALEAMFL.CF SG ADKEDAAA <mark>P</mark> APSCTASAAASNATASA <mark>G</mark> AG SF VKVSMIGAPYL XKUDLRMYKGYRELREALEAMFL.VSSG AAKDEAAAAPGCTASSAAATNTTSSSSAAVVVG SF VKVSMIGAPYL XKVDLRMYRGYRELREALEAMFVSSG
Zm/AA3/1-202	AAKQEAAAAAAQCTASSAAATNTTSSSSAAVVVQSFVKVSMIGAPYLKKVDLRMYRGYRELREALEALF. VSSS EAARRTNNKGEELQGGGGRLYVKVSMIGAPYLKVDLRTYGGYRELRDALDALFG.CFSSSSAS EARRTRRGE.QQGGGGG
2m/AA24/1-115	AFVKVSMIGTPYLSKVDVAAYDDYGELVEALNELFCCCSIG AFVKVSMIGTPYLSKVDVAAYDDYGELVEALNELFCCCSIG AFVKVSMIGTPYLSKVDVAAYDDYGELVEALNELFCCCSIG
2m/AA29/1-272	SRSKAP <mark>A</mark> AEDAASAARPMYVKVSMIGAPYLIKKVDIKMYSSYEDLSVALOKMFSCFIAGO K <mark>O</mark> SKEDAEAKODOGFLYVKVSMIGAPYLIKIDLKTYKNYKDLSTALEKMFSGFSTGK E©SKEDDAKOĞOGFLYVKVSMIGAPYLIKIDLKTYKNYKDLSTALEKMFSGFSTGK
Zm/AA14/1-228	VKSKKEEE <mark>P</mark> EKQQ SAANA <mark>GG</mark> NGSAFVKVSMIGA PYLSKVDLKMYN SYTELSVALKKMFSTFTTS VRSKKEEEPEKQQQ PAAANAFVKVSMIGA PYLSKVDLKTYG SYKDLSAALKKMFGTFVTAT DK <mark>G</mark> AAAANGDKSSPAAGOGAFVKVSLIGA PYLSKVDLKMYRSYQDLSKALENMFSSFTIG SCOS
2 <i>m/AA27/1-1</i> 86 · · · · · · · · · · · TRVVGWPPVRSYRKNALADSSKANRS · · · · · · · · · · · · · · · · · · ·	
2m/AA19/1-198	
2m/4A20/1-234 NOGOEYTLVYEDDEGDOMLVO.DVPWOM 2m/4A33/1-225 LSCCCCCCEHTLVYEDDEGDOMLVO.DVPWVM	- FAATARRIRVLRSSDLNPS- SLRAATRKRAAA - FVATARRIRVLKSSDLSPS- SLRAAR AAAEC
Zm/AA4/1-228 PVIGG DYTLVYEDEGDEGDRVLAG DVPWEM Zm/AA4/6/1-289 LOGTG EYTLVYEDYEG NEVLVG DVPWGM Zm/AA3/1-357 LOGSG EYTLVYEDYEGNEGDRMLVG DVPWGM Zm/AA3/1-357 LOGSG EYTLVYEDNEGDRMLVG DVPWQM Zm/AA3/1-357 LOGSG EYTLVYEDNEGDRMLVG DVPWN	··FVSSVKRLRVLKTSDLSSS··LTAPPG····QKRTVTECPVFTS ··FVSTAKRLRVLRSSELAKGLVGTRPPQIAVAPRRGPPDC·····
2m/AA237-346 L DOIG	FMAS <mark>VKRLYIAQDP</mark> RKTKN
2m/AA48/1-197 VSHERRRRH • PYVVTYEDGEGDWLLVGDDVPWE V 2m/AA430/1-216 ASHERRRLHR PYVVTYEDGEGDWLLVGDDVPWE V 2m/AA47/-206 AASHTTTSHR DVVVTYEDGEGDWLLUG • DVPWD D	- FVKSVKRLKILARTAAGD@LAHC - FVKSVKRLKILARTAAGD@LAHC
2m /AA 12/1-293 SE	- MFIGTCKRLRIMKGSEARLGLGSAKNND
Zm/AA/15/1-226 · · · · · NNLSEFAUTYUD KOGD LML VG - DVPFE · · · · · Zm/AA32/1-226 · · · · · LSEFAUTYED KDGD LML VG - DVPFE · · · · · · · Zm/AA3/1-222 · · · · CDFAUAYED KDGD LML AG - DVPWE · · · · · · · · · · · · CDFAUAYED KDGD LML AG - DVPWE · · · · · · · · · · · · · · · · · · ·	- MFASTC <mark>KKLRIMKRSEAT-GLG</mark> SSSARQQ
Zm (AA 25/1-66 - DHHQHAIAYED K DOD LMLAO DV PWE	MFVSBCKRMRVMRSCEAR.GLSSNA.
2 <i>m/AA10/1-26</i> 3 <mark>0</mark> SKVDALKDQ <mark>EYVLTYEDKDADWMLVO⁶ · DLPWD</mark> ······ 2 <i>m/AA29/1-272</i> <mark>9</mark> SKVDALKDQ <mark>EYVLTYEDKDADWMLVO⁶ · DLPWD</mark> ······ 2 <i>m/AA21/1-244</i> ·······KD <mark>0 EYVLTYED</mark> K <mark>D0 DWMLVO⁶ · DVPWE</mark> ······	-YFTSIC <mark>RKLKIMRGSDAVG</mark> IAPRTIEQT <mark>G</mark> QNK -MFAD <mark>SCRRLRIMKGSDAIGLAP</mark> RAADKSKNRN
Zm (AA 28/1-255 - · · · · · KD GEYVLTYED K DG DWML VG - DV PWD CH IVFR SN C Zm (AA 2/1-237 - · · · V G GA D VVTTYED K DG DWML VG - DV PWE - · · · · · · Zm (AA 14/1-228 - · · · A G DA D DVVTTYED K DG DWML VG - DV PWE - · · · · · · · · · · · · · · · · · ·	- MFVESCRELRIMKSSEAIGLAPRTKDKCKNRS
2m/AA5/1-220 NG	···VETCORLRLMKGSEAVNLAPRAAR·································
Zm/AA31/1-255 D · · · · · · · · · · · · S <mark>BAG</mark> TWWQT · · PAWSP · · · · · · · Zm/AA19/1-198 EY · · · · · · · · · · · · · · · · · ·	
IV	