

gi |112817628| ref |NP_001019679.2| MGKHKHKA---WRSSVEDYTDTPLEKPLKLVKVGGSSEVTELGSGHDSYDDRSHERERHREKHKKSEK---HLDEERRRKEEKKRREKE 99
gi |109457691| ref |XP_217740.4| MGKHKHKA---WRSSVEDYTDTPLEKPLKLVKVGGSSEVTELGSGHDSYDDRSHERERHREKHKKSEK---HLDEERRRKEEKKRREKE 99
gi |57770383| ref |NP_076413.2| ---MKG---YQSLVFNF---FFLKLS 17
gi |114692424| ref |XP_001139048.1| ---MKG---YQSLVFNF---FFLKLS 17
gi |74003131| ref |XP_851785.1| ---MKGR---KQWLLWDYTDKPLEKPLKLVKVGGSSEVTELGSGHDSYDDRSHERERHREKHKKSEK---HLDEERRRKEEKKRREKE 92
gi |194676433| ref |XP_872879.3| MGKHKHKA---WRSSVEDYTDTPLEKPLKLVKVGGSSEVTELGSGHDSYDDRSHERERHREKHKKSEK---HLDEERRRKEEKKRREKE 99
gi |118086323| ref |XP_418893.2| MGKHKHKA---WRSSVEDYTDTPLEKPLKLVKVGGSSEVTELGSGHDSYDDRSHERERHREKHKKSEK---HLDEERRRKEEKKRREKE 150
gi |41053660| ref |NP_956569.1| MGKHKHKA---WRSSVEDYTDTPLEKPLKLVKVGGSSEVTELGSGHDSYDDRSHERERHREKHKKSEK---HLDEERRRKEEKKRREKE 99



gi |112817628| ref |NP_001019679.2| HC---DSEGEADAFDPGKKVEVEPPDRPVRACRTQP---AENESTPIQRLLHEFLRQLQRKDPHGFFAFPVDAIAPGYSMIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNAMY 215
gi |109457691| ref |XP_217740.4| HC---DSEGEADAFDPGKKVEVEPPDRPVRACRTQP---AENESTPIQRLLHEFLRQLQRKDPHGFFAFPVDAIAPGYSMIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNAMY 215
gi |57770383| ref |NP_076413.2| ---DSEGEADAFDPGKKVEVEPPDRPVRACRTQP---AENESTPIQRLLHEFLRQLQRKDPHGFFAFPVDAIAPGYSMIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNAMY 99
gi |114692424| ref |XP_001139048.1| ---DSEGEADAFDPGKKVEVEPPDRPVRACRTQP---AENESTPIQRLLHEFLRQLQRKDPHGFFAFPVDAIAPGYSMIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNAMY 99
gi |74003131| ref |XP_851785.1| HG---DTEGETDDFDPGKKVEVEPPDRPVRACRTQP---AENESTPIQRLLHEFLRQLQRKDPHGFFAFPVDAIAPGYSMIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNAMY 208
gi |194676433| ref |XP_872879.3| HC---DTEGEADDFDPGKKVEVEPPDRPVRACRTQP---AENESTPIQRLLHEFLRQLQRKDPHGFFAFPVDAIAPGYSMIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNAMY 207
gi |118086323| ref |XP_418893.2| QC---DTEGETDDFDPGKKVEVEPPDRPVRACRTQPGEHSENESTPIQRLLHEFLRQLQRKDPHGFFAFPVDAIAPGYSMIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNAMY 269
gi |41053660| ref |NP_956569.1| QSETASTAPVPEFLPKPVVVEEKKRKRDFESESADRFHFAVVEVEQPADRPVACRTQP---ENEAIPHQLLEFLRQLQRKDPHGFFAFPVDAIAPGYSMIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNAMY 245



gi |112817628| ref |NP_001019679.2| NRPDVIYKLAKKILHAGFKMMSK---AALLGSEDPAEPEVPEVVPVQVETAKKSKK---PSRE-VISCMFPEGNACSLDSTAEHVLALVEHADEARDRINRFLPGGKMGVLLKLDGDSLLYSVVNAP 343
gi |109457691| ref |XP_217740.4| NRPDVIYKLAKKILHAGFKMMSK---AALLGSEDPAEPEVPEVVPVQVETAKKSKK---PSRE-VISCMFPEGNACSLDSTAEHVLALVEHADEARDRINRFLPGGKMGVLLKLDGDSLLYSVVNAP 342
gi |57770383| ref |NP_076413.2| NRPDVIYKLAKKILHAGFKMMSK---AALLGSEDPAEPEVPEVVPVQVETAKKSKK---PSRE-VISCMFPEGNACSLDSTAEHVLALVEHADEARDRINRFLPGGKMGVLLKLDGDSLLYSVVNAP 247
gi |114692424| ref |XP_001139048.1| NRPDVIYKLAKKILHAGFKMMSK---AALLGSEDPAEPEVPEVVPVQVETAKKSKK---PSRE-VISCMFPEGNACSLDSTAEHVLALVEHADEARDRINRFLPGGKMGVLLKLDGDSLLYSVVNAP 247
gi |74003131| ref |XP_851785.1| NRPDVIYKLAKKILHAGFKMMSK---AALLGSEDPAEPEVPEVVPVQVETAKKSKR---PSRE-VISCMFPEGNACSLDSTAEHVLALVEHADEARDRINRFLPGGKMGVLLKLDGDSLLYSVVNAP 356
gi |194676433| ref |XP_872879.3| NRPDVIYKLAKKILHAGFKMMSK---AALLGSEDPAEPEVPEVVPVQVETAKKSKR---PSRE-VISCMFPEGNACSLDSTAEHVLALVEHADEARDRINRFLPGGKMGVLLKLDGDSLLYSVVNAP 335
gi |118086323| ref |XP_418893.2| NRPDVIYKLAKKILHAGFKMMSK---AALLGSEDPAEPEVPEVVPVQVETAKKSKK---QNEK-VISCMFPEGNACSLDSTAEHVLALVEHADEARDRINRFLPGGKMGVLLKLDGDSLLYSVVNAP 397
gi |41053660| ref |NP_956569.1| NRPDVIYKLAKKILHAGFKMMSK---AALLGDDIAPPEVPEVVPVQVETAKKSKK---QVKEPIISDMYLEGNACSLDSTAEHVLALVEHADEARDRINRFLPGGKMGVLLKLDGDSLLYSVVNAP 374



gi |112817628| ref |NP_001019679.2| PDADDEEHPVDLSSLSSKLLPGFTTLGFKDERRNKVIFLSSASTALSMQNNVDFGDLKSDDEMELLYSAYGDETVGVCALSLQEFVKDAGSYSKKVVDDLLDQITGGDHSRMLFOLKORRSPMPRPADEM 474
gi |109457691| ref |XP_217740.4| PDADDEEHPVDLSSLSSKLLPGFTTLGFKDERRNKVIFLSSASTALSMQNNVDFGDLKSDDEMELLYSAYGDETVGVCALSLQEFVKDAGSYSKKVVDDLLDQITGGDHSRMLFOLKORRSPMPRPADEM 473
gi |57770383| ref |NP_076413.2| PDADDEEHPVDLSSLSSKLLPGFTTLGFKDERRNKVIFLSSASTALSMQNNVDFGDLKSDDEMELLYSAYGDETVGVCALSLQEFVKDAGSYSKKVVDDLLDQITGGDHSRMLFOLKORRSPMPRPADEM 378
gi |114692424| ref |XP_001139048.1| PDADDEEHPVDLSSLSSKLLPGFTTLGFKDERRNKVIFLSSASTALSMQNNVDFGDLKSDDEMELLYSAYGDETVGVCALSLQEFVKDAGSYSKKVVDDLLDQITGGDHSRMLFOLKORRSPMPRPADEM 378
gi |74003131| ref |XP_851785.1| PDADDEEHPVDLSSLSSKLLPGFTTLGFKDERRNKVIFLSSASTALSMQNNVDFGDLKSDDEMELLYSAYGDETVGVCALSLQEFVKDAGSYSKKVVDDLLDQITGGDHSRMLFOLKORRSPMPRPADEM 487
gi |194676433| ref |XP_872879.3| LDADDEEHPVDLSSLSSKLLPGFTTLGFKDERRNKVIFLSSASTALSMQNNVDFGDLKSDDEMELLYSAYGDETVGVCALSLQEFVKDAGSYSKKVVDDLLDQITGGDHSRMLFOLKORRSPMPRPADEM 466
gi |118086323| ref |XP_418893.2| PEAEDEEHPVDLSSLSSKLLPGFTTLGFKDERRNKVIFLSSASTALSMQNNVDFGDLKSDDEMELLYSAYGDETVGVCALSLQEFVKDAGSYSKKVVDDLLDQITGGDHSRMLFOLKORRSPMPRPADEM 547
gi |41053660| ref |NP_956569.1| PEGEDEEHPVDLSSLANKLIPGLTSLGFKDERRNKVIFLSSASTALSMQNNVDFGDLKSDDEMELLYSAYGDETVGVCALSLQEFVKDAGSYSKKVVDDLLDQITGGDHSRMLFOLKORRSPMPRPADEM 509



gi |112817628| ref |NP_001019679.2| ---VDPLGESGPPVLDVSMKQYVDVSLDVSMLSLGK---VKKELDHDHSHLNLDLAKLLDOLHEAQAERGGSRPSSNLSLSTAS---EREHPGSPSRLSVGQPDVHDPYEFLOSPEPAAAKN 597
gi |109457691| ref |XP_217740.4| ---VDPLGDSGPPVLDVSMKQYVDVSLDVSMLSLGK---VKKELDHDHSHLNLDLAKLLDOLHEAQAERGGSRPSSNLSLSTAS---EREHPGSPSRLSVGQPDVHDPYEFLOSPEPAAAKN 596
gi |57770383| ref |NP_076413.2| ---VDPLGDSGPPVLDVSMKQYVDVSLDVSMLSLGK---VKKELDHDHSHLNLDLAKLLDOLHEAQAERGGSRPSSNLSLSTAS---ERDQHLGSPSRLSVGQPDVHDPYEFLOSPEPAAAKN 501
gi |114692424| ref |XP_001139048.1| ---VDPLGDSGPPVLDVSMKQYVDVSLDVSMLSLGK---VKKELDHDHSHLNLDLAKLLDOLHEAQAERGGSRPSSNLSLSTAS---ERDQHLGSPSRLSVGQPDVHDPYEFLOSPEPAAAKN 501
gi |74003131| ref |XP_851785.1| ---AGDPLGDSGPPVLDVSMKQYVDVSLDVSMLSLGK---VKKELDHDHSHLNLDLAKLLDOLHEAQAERGGSRPSSNLSLSTAS---ERDQHLGSPSRLSVGQPDVHDPYEFLOSPEPAAAKN 611
gi |194676433| ref |XP_872879.3| ---AGDPLGDSGPPVLDVSMKQYVDVSLDVSMLSLGK---VKKELDHDHSHLNLDLAKLLDOLHEAQAERGGSRPSSNLSLSTAS---ERDQHLGSPSRLSVGQPDVHDPYEFLOSPEPAAAKN 588
gi |118086323| ref |XP_418893.2| SKQIMVGESAGDNTSELDVSMKQYVDVSLDVSMLSLGK---VKKELDHDHSHLNLDLAKLLDOLHEAQAERGGSRPSSNLSLSTAS---ERDQHLGSPSRLSVGQPDVHDPYEFLOSPEPAAAKN 675
gi |41053660| ref |NP_956569.1| ---GTDGGMEAGVLDVSMKQYVDVSLDVSMLSLGK---VKKELDHDHSHLNLDLAKLLDOLHEAQAERGGSRPSSNLSLSTAS---ERDQHLGSPSRLSVGQPDVHDPYEFLOSPEPAAAKN 631

