

gi|6680644|ref|NP\_031430.1| MGPRALSPLASLRRLRWLLACGLLGPVLEAGRPDLEQTVHLSSYEIIPWRLTRERREALRPSKQ--ISYVIAQAGKQHIHLERNIT-----DLLPNDFFVVTYDKEGSLSDHPNVSCHCHYRGVVEGVNSAVAVSACFGLRGLLE 150  
gi|62339281|ref|NP\_001014772.1| MGPRALSPLASLRRLRWLLACGLLGPVLEAGRDSQTVHLSSYEIVPWRLSRERREALRPSKQ--ISYVIAQAGKQHIHLERNIT-----DLLPNDFFVVTYDEEGSLSDHPNVSCHCHYRGVVEGVNSAVAVSACFGLRGLLE 150  
gi|4501915|ref|NP\_003807.1| MGSGARFPSSGLRVRWLLLLGLVGPVLAARPGFOOTSHLSSYEIIPWRLTRERREAPRPYSKQ--VSYVIAQAGKEHIHLERNK-----DLLPEDFVVTYTKNEGTLIDHPNIONCHYRGVVEGVNSIALSDCFGLRGLLE 150  
gi|114619853|ref|XP\_519719.2| MGSGARFPSSGLRVRWLLLLGLVGPVLAARPGFOOTSHLSSYEIIPWRLTRERREAPRPYSKQ--VSYVIRAEQKEHIHLERNK-----DLLPEDFVVTYTKNEGTLIDHPNIONCHYRGVVEGVNSIALSDCFGLRGLLE 150  
gi|73979290|ref|XP\_532798.2| MGSAGSFPFGVRLQWLLLFVGPVLAARPGFOOTSHLSSYEIIPWRLTRERREAPRPYSKQ--VSYVIAQAGKEHIHLERNKGVSPSPGFLPRDFVVTYTKNEGALISDHPVDQNHCHYRGVVEGISNSIALSDCFGLRGLLE 150  
gi|194679248|ref|XP\_614306.4| MGSAGSFPFGVRLQWLLLFVGPVLAARPGFOOTSHLSSYEIIPWRLTRERREAPRPYSKQ--VSYVIAQAGKEHIHLERNK-----DLLPEDFVVTYTKNEGALISDHPVDQNHCHYRGVVEGISNSIALSDCFGLRGLLE 150  
gi|71897213|ref|NP\_001026567.1| MARAARSCLCRLLLLLLAALPAGPAGFQEIQLSSYEVIIPQKLGRRERETSASITDKVSYAIEIEGKEYITHLEKKN-----DLLPKDFVVTYTKNEGKLOSEYVDQDCHYQVGVVILDSVAVATCSGLRGLVT 150  
gi|292617167|ref|XP\_002663261.1| MLLDCHYSYGIETDVEGSSAALSLCSLRGLVIT 150



gi|6680644|ref|NP\_031430.1| LENA SFGIEPLHNSHPEHIFVPMDDGIEQLRRCGVSNRDEKEGEGQDEEEHPSVTLRRLRRRAVLPOTRYVELFVVDKERYDMMGRNQAVREEMIRLANVLD SMYI MLNIRIVLVGLEIWDNPNINIGGAGDVLGNFVOWREKF 300  
gi|62339281|ref|NP\_001014772.1| LENA SFGIEPLHNSHPEHIFVPMDDVHQEPLRRCGVSNRDEKEAEGQDEEEHPSVTLRRLRRRAVLPOTRYVELFVVDKERYDMMGRNQAVREEMIRLANVLD SMYI MLNIRIVLVGLEIWDNPNINIGGAGDVLGNFVOWREKF 300  
gi|4501915|ref|NP\_003807.1| LENA SYGIEPLQNSHPEHIIYRMDDVYKEPLKCCGVSNKDIKEKTADEEEEPSPMTQLRRLRRRAVLPOTRYVELFVVDKERYDMMGRNQAVREEMIRLANVLD SMYI MLNIRIVLVGLEIWDNPNINIGGAGDVLGNFVOWREKF 300  
gi|114619853|ref|XP\_519719.2| LENA SYGIEPLQNSHPEHIIYRMDDVYKEPLKCCGVSNKDIKEKTADEEEEPSPMTQLRRLRRRAVLPOTRYVELFVVDKERYDMMGRNQAVREEMIRLANVLD SMYI MLNIRIVLVGLEIWDNPNINIGGAGDVLGNFVOWREKF 300  
gi|73979290|ref|XP\_532798.2| IENVSYGIEPLQNSHPEHIFRMDDVHKEPLKCCGVSNKMEKETINYEDEEPLSVTLRRLRRRAVLPOTRYVELFVVDKERYDMMGRNQAVREEMIRLANVLD SMYI MLNIRIVLVGLEIWDNPNINIGGAGDVLGNFVOWREKF 300  
gi|194679248|ref|XP\_614306.4| IENVSYGIEPLQNSHPEHIFRMDDVHKEPLKCCGVSNKMEKETINYEDEEHPSTIQLRRLRRRAVLPOTRYVELFVVDKERYDMMGRNQAVREEMIRLANVLD SMYI MLNIRIVLVGLEIWDNPNINIGGAGDVLGNFVOWREKF 300  
gi|71897213|ref|NP\_001026567.1| IENVSYGIEPMDSSSGSEHIVSLDNVKKEPSCMGVMTGEGE--EGEHTCRNHPHPSMTQLRRLRRRAVLPOTRYVELFVVDKERYDMMGRNQAVREEMIRLANVLD SMYI MLNIRIVLVGLEIWDNPNINIGGAGDVLGNFVOWREKN 300  
gi|292617167|ref|XP\_002663261.1| TEGTSFGIEPLGSSSDHELVYRLDVTQPLNCGTPE-----HSYNHDDGSPRLTRQVRRKRAVLRHQTIVVELLMVVDNERYNKRNHIAVREEVQIANVDSMYIPLNIRIVLVGLEIWDNPNINIGGAGDVLGNFVOWREKE 300



gi|6680644|ref|NP\_031430.1| LI T RRRHDSAQLVLKKGFGGTAGMAFVGVVCSRSRHAGGINVFGQITVETFASIVAHELGNLGMNHDDGRDCEFCGAKSCIMNSGASGRNFSSCSAEDFEKLTLNKGGSCLLNIPKPDEAYSAFCGNKLVDPGEECDCCGPKCELDPC 450  
gi|62339281|ref|NP\_001014772.1| LI T RRRHDSAQLVLKKGFGGTAGMAFVGVVCSRSRHAGGINVFGQITVETFASIVAHELGNLGMNHDDGRDCEFCGAKSCIMNSGASGRNFSSCSAEDFEKLTLNKGGSCLLNIPKPDEAYSAFCGNKLVDPGEECDCCGPKCELDPC 450  
gi|4501915|ref|NP\_003807.1| LI T RRRHDSAQLVLKKGFGGTAGMAFVGVVCSRSRHAGGINVFGQITVETFASIVAHELGNLGMNHDDGRDCEFCGAKSCIMNSGASGRNFSSCSAEDFEKLTLNKGGSCLLNIPKPDEAYSAFCGNKLVDPGEECDCCGPKCELDPC 450  
gi|114619853|ref|XP\_519719.2| LI T RRRHDSAQLVLKKGFGGTAGMAFVGVVCSRSRHAGGINVFGQITVETFASIVAHELGNLGMNHDDGRDCEFCGAKSCIMNSGASGRNFSSCSAEDFEKLTLNKGGSCLLNIPKPDEAYSAFCGNKLVDPGEECDCCGPKCELDPC 450  
gi|73979290|ref|XP\_532798.2| LI T RRRHDSAQLVLKKGFGGTAGMAFVGVVCSRSRHAGGINVFGQITVETFASIVAHELGNLGMNHDDGRDCEFCGAKSCIMNSGASGRNFSSCSAEDFEKLTLNKGGSCLLNIPKPDEAYSAFCGNKLVDPGEECDCCGPKCELDPC 450  
gi|194679248|ref|XP\_614306.4| LI T RRRHDSAQLLILKKGFGGTAGMAFVGVVCSRSRHAGGINVFGQITVETKPFASIVAHELGNLGMNHDDGRDCEFCGAKSCIMNSGASGRNFSSCSAEDFEKLTLNKGGSCLLNIPKPDEAYSAFCGNKLVDPGEECDCCGPKCELDPC 450  
gi|71897213|ref|NP\_001026567.1| LV L RRRHDSAQLVLKKGFGGTAGMAFVGVVCSRSRHAGGINVFGQITVETKPFASIMAHDELGNLGMNHDDERVCHCGASSCIMSAGASGRNFSSCSAEDFEKLTLNKGGSCLLNIPRPDDEYSAFCGNKLVDMGEECDCCGPKCELDPC 450  
gi|292617167|ref|XP\_002663261.1| LV H RRRHDSAQLLILKKGFGGTAGMAFVGVVCSRSRHAGGINVFGQITVETKPFASIVAHELGNLGMNHDDGRDCEFCGAKSCIMNSGATGCFSSCSADDFEKMLNLSGGRCLLNIPRPDDEYSAFCGNKLVDMGEECDCCGPKCELDPC 450



gi|6680644|ref|NP\_031430.1| CEGSTCKLKSFAECAYGDCCKDQFLPGGSMCRGKTS ECDVPEYCNSSGQFCPPDVFIONGYPQNNKAYCYNGMCOYDAQCQVIFGSKAKAAPKDCFI E VNSKGRDFNGCGFSGNEYKKAATGNALCGKLOCE NVQETP-VFGIVPAI 600  
gi|62339281|ref|NP\_001014772.1| CEGSTCKLKSFAECAYGDCCKDQFLPGGSMCRGKTS ECDVPEYCNSSGQFCPPDVFIONGYPQNNKAYCYNGMCOYDAQCQVIFGSKAKAAPKDCFI E VNSKGRDFNGCGFSGNEYKKAATGNALCGKLOCE NVQETP-VFGIVPAI 600  
gi|4501915|ref|NP\_003807.1| CEGSTCKLKSFAECAYGDCCKDQFLPGGTLCRGKTS ECDVPEYCNSSGQFCPPDVFIONGYPQNNKAYCYNGMCOYDAQCQVIFGSKAKAAPKDCFI E VNSKGRDFNGCGFSGNEYKKAATGNALCGKLOCE NVQETP-VFGIVPAI 600  
gi|114619853|ref|XP\_519719.2| CEGSTCKLKSFAECAYGDCCKDQFLPGGTLCRGKTS ECDVPEYCNSSGQFCPPDVFIONGYPQNNKAYCYNGMCOYDAQCQVIFGSKAKAAPKDCFI E VNSKGRDFNGCGFSGNEYKKAATGNALCGKLOCE NVQETP-VFGIVPAI 600  
gi|73979290|ref|XP\_532798.2| CEGSTCKLKSFAECAYGDCCKDQFLPGGTLCRGKTS ECDVPEYCNSSGQFCPPDVFIONGYPQNNKAYCYNGMCOYDAQCQVIFGSKAKAAPKDCFI E VNSKGRDFNGCGFSGNEYKKAATGNALCGKLOCE NVQETP-VFGIVPAI 600  
gi|194679248|ref|XP\_614306.4| CEGSTCKLKSFAECAYGDCCKDQFLPGGTLCRGKTS ECDVPEYCNSSGQFCPPDVFIONGYPQNNKAYCYNGMCOYDAQCQVIFGSKAKAAPKDCFI E VNSKGRDFNGCGFSGNEYKKAATGNALCGKLOCE NVQETP-VFGIVPAI 600  
gi|71897213|ref|NP\_001026567.1| CEGSTCKLKSFAECAYGDCCKDQFLPGGTLCRGKTS ECDVPEYCNSSGQFCPPDVFIONGYPQNNKAYCYNGMCOYDAQCQVIFGSKAKAAPKDCFI E VNSKGRDFNGCGFSGNEYKKAATGNALCGKLOCE NVQETP-VFGIVPAI 600  
gi|292617167|ref|XP\_002663261.1| CEAKTCKLRS GAO CAYGVCCKNCRFLPGGTVCRSSD ECDLA EYCNSSALCQNDVFKDGHPCQDTAYCYNGCQHYDTCCQNFIFGSKAKAAPKELCFKVDNSKGRDFNGCGYHSSGFKKCESRNAMCGKLOCE NVFSLVIFGKIPAR 600



gi|6680644|ref|NP\_031430.1| I Q T P S R G K K C W G V D F L G S D V P D P G M V N E G T K C D A G K I C R N F C V N A S V L N Y D C D I Q K K C H G H G V C N S N K N C H C E D G W A P P H C D T K G Y G G S V D S G P T Y N A K S T A L R D G L L V F F L I V L P V A A I F L I K R D E L R K T - F R K K R S Q --M S D G 750  
gi|62339281|ref|NP\_001014772.1| I Q T P S R G K K C W G V D F L G S D V P D P G M V N E G T K C D A G K I C R N F C V N A S V L N Y D C D I Q K K C H G H G V C N S N K N C H C E D G W A P P H C D T K G Y G G S V D S G P T Y N A K S T A L R D G L L V F F L I V L P V A A I F L I K R D E L R K T - F R K K R S Q --M S D G 750  
gi|4501915|ref|NP\_003807.1| I Q T P S R G K K C W G V D F L G S D V P D P G M V N E G T K C D A G K I C R N F C V D A S V L N Y D C D I Q K K C H G H G V C N S N K N C H C E N G W A P P N C E T K G Y G G S V D S G P T Y N E M T A L R D G L L V F F L I V L P V I V C A I F I K R D L W R S Y F R K K R S Q T Y E S D G 750  
gi|114619853|ref|XP\_519719.2| I Q T P S R G K K C W G V D F L G S D V P D P G M V N E G T K C D A G K I C R N F C V D A S V L N Y D C D I Q K K C H G H G V C N S N K N C H C E N G W A P P N C E T K G Y G G S V D S G P T Y N E M T A L R D G L L V F F L I V L P V I V C A I F I K R D L W R S Y F R K K R S Q T Y E S D G 750  
gi|73979290|ref|XP\_532798.2| I Q T P S R G K K C W G V D F L G S D V P D P G M V N E G T K C D N G K I C R N F C V N A S V L N Y D C D I Q K K C H G H G V C N S N K N C H C E N G W A P P N C E T K G Y G G S V D S G P T Y N E M T A L R D G L L V F F L I V L P V I V C A A F V F I K R D L W R S Y F R K K R S Q T Y E S D G 750  
gi|194679248|ref|XP\_614306.4| I Q T P G K G K K C W G V D F L G S D V P D P G M V N E G T S C D V G K I C R N F A C V N S V L N Y D C D I Q K K C H G H G V C N S N K N C H C D N G W A P P N C E T K G Y G G S V D S G P T Y N E M T A L R D G L L V F F L I P L P L I V L A V F V I K R D L R K S C R R K R S Q T Y E S G G 750  
gi|71897213|ref|NP\_001026567.1| I R P T P D G T C W G V D F L G S D V P D P G M V N E G T K C D N G K V C R F F C V S A S V L N Y D C D V E K Q C H G H G V C N N R N C H C E P G W A P P F C N T K G Y G G S I D S G P T Y N D K D N S L R D G L L V F F S W S Y H S L ----- 750  
gi|292617167|ref|XP\_002663261.1| I E T P I A G T T C W G V D F L G S D V P D P G M V N E G T K C D N K V C L F E C R S A D V L N Y D C D V E K R C H G H G V C N S N K N C H C E Y G W A P P F C E A S G Y G G S I D S G P T Y N D K D T S L R D G L L V F F L V L P L L A I G L V F F K R N E L K Q R F L R K R S Q A Y E --- 750



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gi|6680644|ref|NP_031430.1| RNCANVSRQPGDPISRPPGGPNVSRPPGGPGVSRPPGGPGVSRPPGGPGVSRPPPGHGNRFVPTIYAAKQPAQFPRPPPPQPKISSQGNLIPARPAPAPP--LYSSLT 860
gi|62339281|ref|NP_001014772.1| RNCANASRPPGDPVSRPPGGPNVSRPPGGPNVSRPPGGPNVSRPPGGPNVSRPPVHGGRFVPTIYAIKQPPQFPRPPPPQPKIPSQGNLVPARPAPAPP--LYSSLT 860
gi|4501915|ref|NP_003807.1| KNCANPSRQPG--SVPRHVS--PVTTP-----REVPIYANRFVAVPTIYAAKQPOQFPRPPPPQPKVSSQGNLIPARPAPAPP--LYSSLT 860
gi|114619853|ref|XP_519719.2| KNCANPSRQPG--SVPRHVS--PVTTP-----REVPIYANRFVAVPTIYAAKQPOQFPRPPPPQPKVSSQGNLIPARPAPAPP--LYSSLT 860
gi|73979290|ref|XP_532798.2| KNCAKASRQPV--SVPRHVS--SVTTP-----REAPIYANRFVAVPTIYAAKQPOQFPRPPPPQPKVSSQGNLIPARPAPAPP--LYSSLT 860
gi|194679248|ref|XP_614306.4| KNCAKDSRQPA--SVPRPVS--SVIIP-----RNVPVQTNRFVAVPTIYGARQPOQYPRPPPPQPKESFQGNLVPARPAPPPPPPLYSSLT 860
gi|71897213|ref|NP_001026567.1| ----- 860
gi|292617167|ref|XP_002663261.1| ----- 860
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