

gi | 74007005 | ref | XP_538052.2 | MKVDRTKLLKKTPT--EAPADCRALIDKLVKVCND-EOLLLELOQIK--TWNIGKCELYHWVVDLLDRFDGILADAGQTVENMSWMLVCDRPEREQLKMLLLAVLNFTALLIEYFSRRLHLYSSIEHLLTLLASSDMQVVLAVLNLVYVFSKRS 145
gi | 158508566 | ref | NP_001103474.1 | MKVDRTKLLKKTPT--EAPADCRALIDKLVKVCND-EOLLLELOQIK--TWNIGKCELYHWVVDLLDRFDGILADAGQTVENMSWMLVCDRPEREQLKMLLLAVLNFTALLIEYFSRRLHLYSSIEHLLTLLASSDMQVVLAVLNLVYVFSKRS 145
gi | 61676188 | ref | NP_113584.3 | MKVDRTKLLKKTPT--EAPADCRALIDKLVKVCND-EOLLLELOQIK--TWNIGKCELYHWVVDLLDRFDGILADAGQTVENMSWMLVCDRPEREQLKMLLLAVLNFTALLIEYFSRRLHLYSSIEHLLTLLASSDMQVVLAVLNLVYVFSKRS 145
gi | 61676190 | ref | NP_067498.3 | MKVDRTKLLKKTPT--EAPADCRALIDKLVKVCND-EOLLLELOQIK--TWNIGKCELYHWVVDLLDRFDGILADAGQTVENMSWMLVCDRPEREQLKMLLLAVLNFTALLIEYFSRRLHLYSSIEHLLTLLASSDMQVVLAVLNLVYVFSKRS 145
gi | 189536055 | ref | XP_001923899.1 | MKVDRTKLLKKTPT--EAPADCRALIDKLVKVCND-EOLLLELOQIK--TWNIGKCELYHWVVDLLDRFDGILADAGQTVENMSWMLVCDRPEREQLKMLLLAVLNFTALLIEYFSRRLHLYSSIEHLLTLLASSDMQVVLAVLNLVYVFSKRS 145
gi | 24642256 | ref | NP_573059.1 | MKVDRTKLLKKTPT--EAPADCRALIDKLVKVCND-EOLLLELOQIK--TWNIGKCELYHWVVDLLDRFDGILADAGQTVENMSWMLVCDRPEREQLKMLLLAVLNFTALLIEYFSRRLHLYSSIEHLLTLLASSDMQVVLAVLNLVYVFSKRS 146
gi | 25148695 | ref | NP_500284.2 | MKIDDAEPSSSSGSDMPPASATLLRNIVAKNDNDFLAAINKGREVHVMGKTELYKNTVLRNCRDILEKAVHKNBFNQLQCDHDTVTKN---HAVAIVRFVLLFFECTSRRRYKSVDRILALLESSDMDLLAEVLRLLQVMGKRS 146



gi | 74007005 | ref | XP_538052.2 | NYIIT-RLGSDKRTPLLRLQHLAESWGGKENGFLAECCRDLHMMKYPPSATLHLEFVADPGAEVKIEKRTTSNTLHYIHIEQLDKISESPSEIMESLTKMYIIP-KDKQMLLFTHIRLAHGFNSHRKRLQAVQARLHAISILVYS--- 290
gi | 158508566 | ref | NP_001103474.1 | NYIIT-RLGSDKRTPLLRLQHLAESWGGKENGFLAECCRDLHMMKYPPSATLHLEFVADPGAEVKIEKRTTSNTLHYIHIEQLDKISESPSEIMESLTKMYIIP-KDKQMLLFTHIRLAHGFNSHRKRLQAVQARLHAISILVYS--- 290
gi | 61676188 | ref | NP_113584.3 | NYIIT-RLGSDKRTPLLRLQHLAESWGGKENGFLAECCRDLHMMKYPPSATLHLEFVADPGAEVKIEKRTTSNTLHYIHIEQLDKISESPSEIMESLTKMYIIP-KDKQMLLFTHIRLAHGFNSHRKRLQAVQARLHAISILVYS--- 290
gi | 61676190 | ref | NP_067498.3 | NYIIT-RLGSDKRTPLLRLQHLAESWGGKENGFLAECCRDLHMMKYPPSATLHLEFVADPGAEVKIEKRTTSNTLHYIHIEQLDKISESPSEIMESLTKMYIIP-KDKQMLLFTHIRLAHGFNSHRKRLQAVQARLHAISILVYS--- 290
gi | 189536055 | ref | XP_001923899.1 | NYIIT-RLGSDKRTPLLRLQHLAESWGGKENGFLAECCRDLHMMKYPPSATLHLEFVADPGAEVKIEKRTTSNTLHYIHIEQLDKISESPSEIMESLTKMYIIP-KDKQMLLFTHIRLAHGFNSHRKRLQAVQARLHAISILVYS--- 290
gi | 24642256 | ref | NP_573059.1 | NYIIT-RLGSDKRTPLLRLQHLAESWGGKENGFLAECCRDLHMMKYPPSATLHLEFVADPGAEVKIEKRTTSNTLHYIHIEQLDKISESPSEIMESLTKMYIIP-KDKQMLLFTHIRLAHGFNSHRKRLQAVQARLHAISILVYS--- 279
gi | 25148695 | ref | NP_500284.2 | KFLSTRIPQKECHALAQRLTAIAQCWGGKLRIVKMAEKLKREPKLPLMFP---FTYDAKQRTIIVEQPKKDESVG---ELITRVAQISPPVSDVPSQQFSEKEDLYCLLGRVRLMVTFFEDWHRKFKLIVRLLSVSLVYVCRIG 287



gi | 74007005 | ref | XP_538052.2 | NALQESANSILYNGLIEELVDVLD---ITDKQLMEIKAASLRTLTSIVHLERTP---KLSSIIDCTGTAHYHGFPLVLRNCIQAMIDP-SMDPPYF-HQFATALFSLFLYHLASVDAGGEALVSCGMMEALLKVIKFLGD 421
gi | 158508566 | ref | NP_001103474.1 | NALQESANSILYNGLIEELVDVLD---ITDKQLMEIKAASLRTLTSIVHLERTP---KLSSIIDCTGTAHYHGFPLVLRNCIQAMIDP-SMDPPYF-HQFATALFSLFLYHLASVDAGGEALVSCGMMEALLKVIKFLGD 421
gi | 61676188 | ref | NP_113584.3 | NALQESANSILYNGLIEELVDVLD---ITDKQLMEIKAASLRTLTSIVHLERTP---KLSSIIDCTGTAHYHGFPLVLRNCIQAMIDP-SMDPPYF-HQFATALFSLFLYHLASVDAGGEALVSCGMMEALLKVIKFLGD 421
gi | 61676190 | ref | NP_067498.3 | NALQESANSILYNGLIEELVDVLD---ITDKQLMEIKAASLRTLTSIVHLERTP---KLSSIIDCTGTAHYHGFPLVLRNCIQAMIDP-SMDPPYF-HQFATALFSLFLYHLASVDAGGEALVSCGMMEALLKVIKFLGD 421
gi | 189536055 | ref | XP_001923899.1 | NALQESANSILYNGLIEELVDVLD---ITDKQLMEIKAASLRTLTSIVHLERTP---KLSSIIDCTGTAHYHGFPLVLRNCIQAMIDP-SMDPPYF-HQFATALFSLFLYHLASVDAGGEALVSCGMMEALLKVIKFLGD 421
gi | 24642256 | ref | NP_573059.1 | NALQDNITDKVLYAGFGEELCELID---KEPVHLVETRAAVLRTLSTMLHFDNRNVPSPRAGSRMLKIVHYTGAERQGTLPPLLVRCIDNLTTHGLTFRYP---LILASLFLSLLYHLASVEMGGTALVKSGMCSLLCVSWPVG 419
gi | 25148695 | ref | NP_500284.2 | GTDETLLSLLYSGFIEEIVEMLKSDREADTQODNHLNDAIQTEALSILCSIVTYEKEP---KITQILEALSAGSYHGFPLVMTQVDELKSNLTKGPKPVSLSALALFSLFLYHLASVEMGGTALVKSGMCSLLCVSWPVG 429



gi | 74007005 | ref | XP_538052.2 | EQDQITFVTRAVRVVDLITNLDMAAFQSHSGLSIFIYRLEHEVDLCKRKECP---FVIKPKIQRPNSTTEG---EEMETDMDG 497
gi | 158508566 | ref | NP_001103474.1 | EQDQITFVTRAVRVVDLITNLDMAAFQSHSGLSIFIYRLEHEVDLCKRKECP---FVIKPKIQRPNSTTEG---EEMETDMDG 497
gi | 61676188 | ref | NP_113584.3 | EQDQITFVTRAVRVVDLITNLDMAAFQSHSGLSIFIYRLEHEVDLCKRKECP---FVIKPKIQRPNSTTEG---EEMETDMDG 497
gi | 61676190 | ref | NP_067498.3 | EQDQITFVTRAVRVVDLITNLDMAAFQSHSGLSIFIYRLEHEVDLCKRKECP---FVIKPKIQRPNSTTEG---EEMETDMDG 497
gi | 189536055 | ref | XP_001923899.1 | EQDQITFVTRAVRVVDLITNLDMAAFQSHSGLSIFIYRLEHEVDLCKRKECP---FVIKPKIQRPNSTTEG---EEMETDMDG 497
gi | 24642256 | ref | NP_573059.1 | DLEHITFVTRAVRVVDLITNLDMAAFQSHSGLSIFIYRLEHEVDLCKRKECP---FVIKPKIQRPNSTTEG---EEMETDMDG 569
gi | 25148695 | ref | NP_500284.2 | PTECTIFGTRCARIDLFTITDVTSKFANNMEICVNRVVEHEINECRKEQPFMIDISYDMPFEPEPRDDGEAHEPEDESERNP 521



gi | 74007005 | ref | XP_538052.2 | VQCIPORAALLKSMNLFKKAIDPAPFSDGIRHVMDGSLPTSLKHIIISNAEYYPGSLFLLATEVTVFVFOEPSSLSSLODNGLTDVMLHALLIKDVPATREV 600
gi | 158508566 | ref | NP_001103474.1 | VQCIPORAALLKSMNLFKKAIDPAPFSDGIRHVMDGSLPTSLKHIIISNAEYYPGSLFLLATEVTVFVFOEPSSLSSLODNGLTDVMLHALLIKDVPATREV 600
gi | 61676188 | ref | NP_113584.3 | VQCIPORAALLKSMNLFKKAIDPAPFSDGIRHVMDGSLPTSLKHIIISNAEYYPGSLFLLATEVTVFVFOEPSSLSSLODNGLTDVMLHALLIKDVPATREV 600
gi | 61676190 | ref | NP_067498.3 | VQCIPORAALLKSMNLFKKAIDPAPFSDGIRHVMDGSLPTSLKHIIISNAEYYPGSLFLLATEVTVFVFOEPSSLSSLODNGLTDVMLHALLIKDVPATREV 600
gi | 189536055 | ref | XP_001923899.1 | VQCIPORAALLKSMNLFKKAIDPAPFSDGIRHVMDGSLPTSLKHIIISNAEYYPGSLFLLATEVTVFVFOEPSSLSSLODNGLTDVMLHALLIKDVPATREV 600
gi | 24642256 | ref | NP_573059.1 | AGSINRDGSAARPPAINYPPNSYARPLAERKAEISSQLPSSLPAPKPSCHVTRAAALLKSMNLFKKAIDPAPFSDGIRHVMDGSLPTSLKHIIISNAEYYPGSLFLLATEVTVFVFOEPSSLSSLODNGLTDVMLHALLIKDVPATREV 719
gi | 25148695 | ref | NP_500284.2 | FVPIEVDAPLPPASPAPVVAASATSSDKIKGGPWEVQMGATQDRSLGIKGLLTFIKRAGIDVQFDIMKHLMDGDLPEALMHILSNAEYYPGSLFLLATEVTVFVFOEPSSLSSLODNGLTDVMLHALLIKDVPATREV 671



gi | 74007005 | ref | XP_538052.2 | LGSLLPNVFSALCLNARGLOS... 715
gi | 158508566 | ref | NP_001103474.1 | LGSLLPNVFSALCLNARGLOS... 715
gi | 61676188 | ref | NP_113584.3 | LGSLLPNVFSALCLNARGLOS... 715
gi | 61676190 | ref | NP_067498.3 | LGSLLPNVFSALCLNARGLOS... 715
gi | 189536055 | ref | XP_001923899.1 | LGSLLPNVFSALCLNARGLH... 715
gi | 24642256 | ref | NP_573059.1 | LGSLLPNVFSALCLNERGLF... 853
gi | 25148695 | ref | NP_500284.2 | ITTLGNVFTAMCLNERGLR... 820



gi | 74007005 | ref | XP_538052.2 | PRSNHAAEEASS... 827
gi | 158508566 | ref | NP_001103474.1 | PRSNHAAEEASS... 827
gi | 61676188 | ref | NP_113584.3 | PRSNHAAEEASS... 827
gi | 61676190 | ref | NP_067498.3 | PRSNHAAEEASS... 827
gi | 189536055 | ref | XP_001923899.1 | ARSNHAAEEASS... 824
gi | 24642256 | ref | NP_573059.1 | TGSASV... 1003
gi | 25148695 | ref | NP_500284.2 | GGDVEE... 950



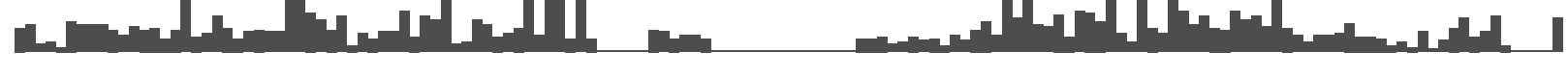
gi | 74007005 | ref | XP_538052.2 | CKSILTL... 967
gi | 158508566 | ref | NP_001103474.1 | CKSILTL... 967
gi | 61676188 | ref | NP_113584.3 | CKSILTL... 967
gi | 61676190 | ref | NP_067498.3 | CKSILTL... 967
gi | 189536055 | ref | XP_001923899.1 | CKSILTL... 964
gi | 24642256 | ref | NP_573059.1 | CKAILL... 1134
gi | 25148695 | ref | NP_500284.2 | IKHIVK... 1087



gi | 74007005 | ref | XP_538052.2 | QVDMQK... 1114
gi | 158508566 | ref | NP_001103474.1 | QADMQK... 1114
gi | 61676188 | ref | NP_113584.3 | QADMQK... 1114
gi | 61676190 | ref | NP_067498.3 | QADMQK... 1114
gi | 189536055 | ref | XP_001923899.1 | QADMQK... 1112
gi | 24642256 | ref | NP_573059.1 | DEPTQHP... 1257
gi | 25148695 | ref | NP_500284.2 | TIRTA... 1215



gi | 74007005 | ref | XP_538052.2 | WOPPPY... 1241
gi | 158508566 | ref | NP_001103474.1 | WOPPPY... 1241
gi | 61676188 | ref | NP_113584.3 | WOPPPY... 1241
gi | 61676190 | ref | NP_067498.3 | WOPPPY... 1241
gi | 189536055 | ref | XP_001923899.1 | WOPPPY... 1239
gi | 24642256 | ref | NP_573059.1 | HESIL... 1397
gi | 25148695 | ref | NP_500284.2 | EPPVQ... 1337



gi | 74007005 | ref | XP_538052.2 | LVVVTKAAAF C I K N L W N R K P L K V Y G G R M A E S M L A I L C H I L R G E P V I R E R L S K E K E G - S R G E E D T G O E E G G - - - - - F R R E P O V N Q O O L Q O L M D M G F T R E H A M E A L L N T S T M E Q A T E Y L L T H P P P I M G G V V R D L S M 1369
gi | 158508566 | ref | NP_001103474.1 | LVVVTKAAAF C I K N L W N R K P L K V Y G G R M A E S M L A I L C H I L R G E P V I R E R L S K E K E G - S R G E E D T G O E E G G - - - - - F R R E P O V N Q O O L Q O L M D M G F T R E H A M E A L L N T S T M E Q A T E Y L L T H P P P I M G G V V R D L S M 1369
gi | 61676188 | ref | NP_113584.3 | LVVVTKAAAF C I K N L W N R K P L K V Y G G R M A E S M L A I L C H I L R G E P V I R E R L S K E K E G - S R G E E D T G O E E G G - - - - - F R R E P O V N Q O O L Q O L M D M G F T R E H A M E A L L N T S T M E Q A T E Y L L T H P P P I M G G V V R D L S M 1369
gi | 61676190 | ref | NP_067498.3 | LVVVTKAAAF C I K N L W N R K P L K V Y G G R M A E S M L A I L C H I L R G E P V I R E R L S K E K E G - S R G E E E A G O E E G G - - - - - F R R E P O V N Q O O L Q O L M D M G F T R E H A M E A L L N T S T M E Q A T E Y L L T H P P P I I G G V V R D L S M 1369
gi | 189536055 | ref | XP_001923899.1 | L I V T Q K A A F S C I R N L W N R K P L K V Y G G R M A E S M L A I L C H I L R G E P I I Q E R L S K E R E G T A R P E E E S T E A S N - - - - - S T A R R E P O V N Q A Q L T O L M D M G F S R E H A M E A L L N T S T M E Q A T E Y L L T H P P P L L S A A V R E F T M 1372
gi | 24642256 | ref | NP_573059.1 | L T H I H C L A M Q A L R R I W A R R P I P N Y G P S M F E T M I L I L K H L I K S H Q L L L D R Y H T R M K E I K F E N L Y I R S T D D G - - - - - L N A D H I K T L T D M G F M H Y H V I E A L R N T A L E A T D V L L N N P E A S S L S T G G Q S S 1520
gi | 25148695 | ref | NP_500284.2 | N A Y K Q F F E K M A Q M P D W E L K S L K K V C E N A F S V F K E V A K N L V E E T E A T A A E A V N A A A A P A P A D A P A A E W G P A L R I P P V A V E P A P A V A V N A A A A D P H E D T T V M L M D L G F S R D I V L Y A L E S T R N A D R A A N V L L A H G N E I P - - - L Q D A N 1484
.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....1640.....1650



gi | 74007005 | ref | XP_538052.2 | S E E D Q M M R A I A M S L G D I P M D Q R A E S P E E V A C R K E E E E R K A R E K Q E E E E A K C L E K F O D A D P L E O D E L H T F D T M L P G - C F H L L D E L P D I V Y R V C D L I M T A I K R N G A D Y R D M I L K Q V V N Q V W E A A D V L I K A A L P L T S D T K I - - V S E W I S G 1516
gi | 158508566 | ref | NP_001103474.1 | S E E D Q M M R A I A M S L G D I P M D Q R A E S P E E V A C R K E E E E R K A R E K Q E E E E A K C L E K F O D A D P L E O D E L H T F D T M L P G - C F H L L D E L P D I V Y R V C D L I M T A I K R N G A D Y R D M I L K Q V V N Q V W E A A D V L I K A A L P L T S D T K I - - V S E W I S G 1516
gi | 61676188 | ref | NP_113584.3 | S E E D Q M M R A I A M S L G D I P M D Q R A E S P E E V A C R K E E E E R K A R E K Q E E E E A K C L E K F O D A D P L E O D E L H T F D T M L P G - C F H L L D E L P D I V Y R V C D L I M T A I K R N G A D Y R D M I L K Q V V N Q V W E A A D V L I K A A L P L T S D T K I - - V S E W I S G 1516
gi | 61676190 | ref | NP_067498.3 | S E E D Q M M R A I A M S L G D I P M D Q R A E S P E E V A C R K E E E E R K A R E K Q E E E E A K C L E K F O D A D P L E O D E L H T F D T M L P G - C F H L L D E L P D I V Y R V C D L I M T A I K R N G A D Y R D M I L K Q V V N Q V W E A A D V L I K A A L P L T S D T K I - - V S E W I S G 1516
gi | 189536055 | ref | XP_001923899.1 | S E E D Q M M R A I A M S L G Q E V S M E Q R S D P E E A A R R E E E E R A R E V E E E E A R C L E R L E A P L D T T E L H A F D S M L P G - C F H L L D E L P D I V Y R V C D L I M T A I K R N G P E Y R D L I L R O V V N Q V W E A A D V L I K A A V P L T S D T K I - - V S E W T R S 1519
gi | 24642256 | ref | NP_573059.1 | S S A P P P P P P S A S T - M D I D V D V P A D G - - - - - E S T S K S S T S P N S Y D Y K H L K L M P S L I F D R F C D E A I S R - A F E F M E A T P D V N S A A D L I A V L Y R R H N H L N K Q V F V T N F V R N I I Q W D F T L Q L F E P A K T I G S K A S R L E B C L I G 1655
gi | 25148695 | ref | NP_500284.2 | P F R D D L L N Q V L R E A G A E M I A G A N I P N A D E I E L Q L N A G F A E H C G Y E L V R I A C R V L R D A G A E Q I G L Q I M E A Y P D E S V D V A E Q L I N D V M D V R V R N P R S S Y E E N I A Q P L I P P L S Q L K I E Q D V S L N S A C K Q L F P L V K R L L L V S N D I T H P C A E L I V 1634
.....1660.....1670.....1680.....1690.....1700.....1710.....1720.....1730.....1740.....1750.....1760.....1770.....1780.....1790.....1800



gi | 74007005 | ref | XP_538052.2 | M A T L P Q A S N L A T R I L L L T L L F E E L K L P C A W V V E S S G I L N V L I K L L E V V Q P C L Q A A K - - - - - E Q K E V Q T P K W I T P V L L L I D F Y E K T A I S S K R R A Q M K Y L Q S N N N W R W F D D R S G R W C S Y S A S N N S T I D S A W K S G E T S V R F T A G R R R Y T V G 1661
gi | 158508566 | ref | NP_001103474.1 | M A T L P Q A S N L A T R I L L L T L L F E E L K L P C A W V V E S S G I L N V L I K L L E V V Q P C L Q A A K - - - - - E Q K E V Q T P K W I T P V L L L I D F Y E K T A I S S K R R A Q M K Y L Q S N N N W R W F D D R S G R W C S Y S A S N N S T I D S A W K S G E T S V R F T A G R R R Y T V G 1661
gi | 61676188 | ref | NP_113584.3 | M A T L P Q A S N L A T R I L L L T L L F E E L K L P C A W V V E S S G I L N V L I K L L E V V Q P C L Q A A K - - - - - E Q K E V Q T P K W I T P V L L L I D F Y E K T A I S S K R R A Q M K Y L Q S N N N W R W F D D R S G R W C S Y S A S N N S T I D S A W K S G E T S V R F T A G R R R Y T V G 1661
gi | 61676190 | ref | NP_067498.3 | M A T L P Q A S N L A T R I L L L T L L F E E L K L P C A W V V E S S G I L N V L I K L L E V V Q P C L Q A A K - - - - - E Q K E V Q T P K W I T P V L L L I D F Y E K T A I S S K R R A Q M K Y L Q S N N N W R W F D D R S G R W C S Y S A S N N S T I D S A W K S G E T S V R F T A G R R R Y T V G 1661
gi | 189536055 | ref | XP_001923899.1 | M A T L P Q A S N L A T R I L L L T L L F E E L K L S C A R V V E S S G V L T V L I K L L E V V Q P C L Q A A K - - - - - E Q K D I Q T P K W I T P V L L L I D F Y E K M A V S S K R R A Q M K Y L Q S N N W R W F D D R S G R W C S Y S A S N N S T I D S A W R A G E T S V R F T A G R R R Y T V G 1664
gi | 24642256 | ref | NP_573059.1 | M T A T R L F V R L K H S I L L L E E N Y S D L H R P L V E A I T A Q D M A V S L V K L L D C M S Q W M L E Q S F E T N T G O R A T V P R W Q N L V D L I D A I D S I S H I L Q R K A N M R - - - - - A V S S V W R W Y D A S T G K W N A Y S E A N N E L I R N A Y A G E R W L Y I N I G R C T V S 1802
gi | 25148695 | ref | NP_500284.2 | S I F P A M T E E W R K E H L I A E I C G E D L N K M A K S L V E Q E V D E N G R P K Q H D V A R T M T N R L H - - - - - F A V L I F D K I S E E Y V Q W I D A N G M T E V M L T S L E Y I V E R F K V D Y Y Q S L I T R I C W N D F A K T H R L I V R R A N L K S L S P L W S Y Y S Y E E D A 1778
.....1810.....1820.....1830.....1840.....1850.....1860.....1870.....1880.....1890.....1900.....1910.....1920.....1930.....1940.....1950



gi | 74007005 | ref | XP_538052.2 | F T T M V Q V N E E T G N R R P V M L I L L R V P R L N K N S K N S N G O E L E K T L - - - - - E S K E M D I K R K E N K A N D T P L A L E N - - - - - I N T E K E T S L E E T K I G E I L I Q G - - - - - L T E D M 1754
gi | 158508566 | ref | NP_001103474.1 | F T T M V Q V N E E T G N R R P V M L I L L R V P R L N K N S K N S N G O E L E K T L - - - - - E S K E M D I K R K E N K T S D T P L A L D S - - - - - I N T E K E T S L E E T K I G E I L I Q G - - - - - L T E D M 1754
gi | 61676188 | ref | NP_113584.3 | F T T M V Q V N E E T G N R R P V M L I L L R V P R L N K N S K N S N G O E L E K T L - - - - - E S K E M D I K R K E N K T P L A L E S - - - - - I N T E K E T S L E E T K I G E I L I Q G - - - - - L T E D M 1754
gi | 61676190 | ref | NP_067498.3 | F T T M V Q V N E E T G N R R P V M L I L L R V P R L N K N S K N S N G O E L E K T L - - - - - E S K E T D I K H K E N K G N D I P L A L E I - - - - - I N T E K E A S L D E T K I G E I L I Q G - - - - - L T E D M 1754
gi | 189536055 | ref | XP_001923899.1 | F N I M V Q V N E E T G N R R P V M L I V Q R V P R I P K A T R S G S V T D T E R - - - - - E S E Q R A K T E T Q T D T E S E L K D S - - - - - T P A A S V L Q D F S G S S G I V V Q G - - - - - L T E D M 1754
gi | 24642256 | ref | NP_573059.1 | L N C M T Q V S E A G T H R P V C P A L K L S E A I T S L N N P V A L H K V E H I L N R V R V T A P D G S G V H S D E L I S L R Q L V N F I D G Q P Q O S E N S A N P S E A T S E D G P A A A N G S P P A I M T R S K R R K S A A A A A A K N K S O S G G S P P I P K R T O K I I L N E Q 1952
gi | 25148695 | ref | NP_500284.2 | L R R R A D Y S S G E K K W P V D A A S Q K L L N D A F F A G V R R V K C I L R G - - - - - V R P N K V D V F A S M K Q G D S T S R E N K A E L P P T V V S I T P D L M D A E A K L S W S E - - - - - D Q N 1875
.....1960.....1970.....1980.....1990.....2000.....2010.....2020.....2030.....2040.....2050.....2060.....2070.....2080.....2090.....2100



gi | 74007005 | ref | XP_538052.2 | V V L I R A C V S M L G V P V D P - - - - - D I L H A T L R L C L R L R D H K Y A M M F A E L K S T R M I L N L T Q S S G F N G F T P L V T L L L R H I I E D P C T L R H M E K V V R S A A T S G A G S T T S G V V S G S L G S R E I N Y I L R V L G P A A C R N P D I F T E V A N C C I R I 1895
gi | 158508566 | ref | NP_001103474.1 | V V L I R A C V S M L G V P V D P - - - - - D I L H A T L R L C L R L R D H K Y A M M F A E L K S T R M I L N L T Q S S G F N G F T P L V T L L L R H I I E D P C T L R H M E K V V R S A A T S G A G S T T S G V V S G S L G S R E I N Y I L R V L G P A A C R N P D I F T E V A N C C I R I 1895
gi | 61676188 | ref | NP_113584.3 | V V L I R A C V S M L G V P V D P - - - - - D I L H A T L R L C L R L R D H K Y A M M F A E L K S T R M I L N L T Q S S G F N G F T P L V T L L L R H I I E D P C T L R H M E K V V R S A A T S G A G S T T S G V V S G S L G S R E I N Y I L R V L G P A A C R N P D I F T E V A N C C I R I 1895
gi | 61676190 | ref | NP_067498.3 | V V L I R A C V S M L G V P V D P - - - - - D I L H A T L R L C L R L R D H K Y A M M F A E L K S T R M I L N L T Q S S G F N G F T P L V T L L L R H I I E D P C T L R H M E K V V R S A A T S G A G S T T S G V V S G S L G S R E I N Y I L R V L G P A A C R N P D I F T E V A N C C I R I 1895
gi | 189536055 | ref | XP_001923899.1 | I I L I R A C V S M I S V P D P - - - - - D I L H A T L R L C L R L R D H H Y A M M F A E L K S T R M I L N L T Q S S G F N G F T P L V T L L R H I I E D P A T L R H M E K V V R S A V T S G A G S T T S G V V S G S L G S R E I N Y I L R V L G P A A C R N P E C F T E T A K S C I R I 1895
gi | 24642256 | ref | NP_573059.1 | V G L S K F D C G R I I G S I V D L L Q P S H O M L N E K L S I L L R C A R L R N V D N A Q V F I R R G V P L M L L H Q A C S F M G P T A N I I L R H V L E A P P V L Q E A M E R V L - - - - - G M R A A G I V - - - - - V G H R D L I Y V L T Q V S S A V S R N P Q I F V A A K E M L K G 2092
gi | 25148695 | ref | NP_500284.2 | D R F L D L S T Q I I L R T G A L D P - - - - - K C S H S M L S F I A R L R S H R N A V F R M E K D G V E A I L L R A R C A I T - N P F L V S I I I R N C I D D A L G H I E K T I R G Y I A V P Q P F A M S E Y A A G K K D F A D L I N F M A P L S T R N L P V T E A M N K L A M 2015
.....2110.....2120.....2130.....2140.....2150.....2160.....2170.....2180.....2190.....2200.....2210.....2220.....2230.....2240.....2250



gi | 74007005 | ref | XP_538052.2 | ALPAPRGSCTASDDEFENLRKIGPNNAVQLVKTPLPKPPLPVPIDTIKEVIYDMLNAAAYHAPPEEAKSDPKPGGTMQEVGQLLDMGDDVYQOYRSLTRQSSDFDFTQSGFINSQVFAADGASTETSFGTSCQE-ASTPEESRDGKK 2044
 gi | 158508566 | ref | NP_001103474.1 | ALPAPRGSCTASDDEFENLRKIGPNNAVQLVKTPLPKPPLPVPIDTIKEVIYDMLNAAAYHAPPEEAKSDPKPGGTMQEVGQLLDMGDDVYQOYRSLTRQSSDFDFTQSGFINSQVFAADGASTETSASGVVSGQE-VSTPEESRDGKK 2044
 gi | 61676188 | ref | NP_113584.3 | ALPAPRGSCTASDDEFENLRKIGPNNAVQLVKTPLPKPPLPVPIDTIKEVIYDMLNAAAYHAPPEEAKSDPKPGGTMQEVGQLLDMGDDVYQOYRSLTRQSSDFDFTQSGFINSQVFAADGASTETSASGVVSGQE-ASTPEESRDGKK 2044
 gi | 61676190 | ref | NP_067498.3 | ALPAPRGSCTASDDEFENLRKIGPNNAVQLVKTPLPKPPLPVPIDTIKEVIYDMLNAAAYHAPPEEAKSDPKPGGTMQEVGQLLDMGDDVYQOYRSLTRQSSDFDFTQSGFINSQVFAADGAPAEATSTTGTSGQGGASTPETREGKK 2045
 gi | 189536055 | ref | XP_001923899.1 | ALPAPRGSCTASDDEFENLRKIGPNNAVQLVKTPLPKPPLPVPIDTIKEVIYDMLNAAAYHAPPEEERANAVPG--NLDLCLLDVDDVYQOYRSLTRQSSDFDFTQSGAFPIINTQVFAADGAVAESSQGGTPTQGE-ASTPEEMREKK 2041
 gi | 24642256 | ref | NP_573059.1 | EYLINTNITLADRARVMVKSFKGQPTAAAGGATPHNQTPTPPAAKDELKDDPOVQSSVAVLKELLHGLVQPCWLYGGTGLSDRQGAELLQPDQPPGTAQGHDD-----EHTPAFVSSKKQSSGGGAAAAGTQATE 2231
 gi | 25148695 | ref | NP_500284.2 | NGSLILPMIKKKPTLVSSTAGGASISSSSAPPPLPSSSHHTVVENNSRAEKIVSMMLG-----EVLNGEFTTVQGRMLSQEKILQILAEIV 2107
2260.....2270.....2280.....2290.....2300.....2310.....2320.....2330.....2340.....2350.....2360.....2370.....2380.....2390.....2400



gi | 74007005 | ref | XP_538052.2 | DKEGDR---TSEEGKQKSKGSKPLMPTSTILRLLAELVRSVVGIAI-LIANYSYTVGQSELIKEDCS-VLAFVLDHLLPHTQNAEDKDTPALARLFLASLAAAGSGTDAQVALVNEVKAALGRALAMAESTEKHARLQAVMCIISTIME 2189
 gi | 158508566 | ref | NP_001103474.1 | DKEGDR---AEEGKQKSKGSKPLMPTSTILRLLAELVRSVVGIAI-LIANYSYTVGQSELIKEDCS-VLAFVLDHLLPHTQNAEDKDTPALARLFLASLAAAGSGTDAQVALVNEVKAALGRALAMAESTEKHARLQAVMCIISTIME 2189
 gi | 61676188 | ref | NP_113584.3 | DKEGDR---AEEGKQKSKGSKPLMPTSTILRLLAELVRSVVGIAI-LIANYSYTVGQSELIKEDCS-VLAFVLDHLLPHTQNAEDKDTPALARLFLASLAAAGSGTDAQVALVNEVKAALGRALAMAESTEKHARLQAVMCIISTIME 2189
 gi | 61676190 | ref | NP_067498.3 | DKEGDR---TSEEGKQKSKGSKPLMPTSTILRLLAELVRSVVGIAI-LIANYSYTVGQSELIKEDCS-VLAFVLDHLLPHTQNAEDKDTPALARLFLASLAAAGSGTDAQVALVNEVKAALGRALAMAESTEKHARLQAVMCIISTIME 2190
 gi | 189536055 | ref | XP_001923899.1 | EQEGDKGASSEESRAAKAKASKPLMPTSTILRLLAELVRSVVGIAI-LIANSYNTAGQSELIKEDCS-VLAFVLDHLLPHTQNAEDKDTPALARLFLASLAAAGTGTDAQVALVNEVKAALGRALAMAESTEKHARLQAVMCIISTIME 2189
 gi | 24642256 | ref | NP_573059.1 | KFEPCC--CWHIPTSQHTHAKPTISRALLKLLADSIRAMQSLVPRVLLSHVYTPADSPPLISAPQQFLGVLLDRFLPTQRHHVPEVSTMTRVLICSLSDCYQPGVQVHVAELHAARALAQDPSAEKHTRLQVLMSLFPNLIE 2379
 gi | 25148695 | ref | NP_500284.2 | KSYPSLAIIIAETQAEGRSALHSLIDVYIAPIEKIEITNALKILIAVISASQNSLKAQELLVLDVKNALASVSEKASELRVLAQLQDKESEREERATSLKKQTEVLSKISLCSIIIMCQSCFAHHHHHSSIDR----- 2248
2410.....2420.....2430.....2440.....2450.....2460.....2470.....2480.....2490.....2500.....2510.....2520.....2530.....2540.....2550



gi | 74007005 | ref | XP_538052.2 | CPSTSSFYSSATAKIQHNGMNNIIRLFLKKGVLNDLARVPHSLDLSPPNMANTVNAALKPLETLSRIVNQPSSL-----FGSKSASSKSKS-----EODAGG----- 2281
 gi | 158508566 | ref | NP_001103474.1 | CPSTSSFYSSATAKIQHNGMNNIIRLFLKKGVLNDLARVPHSLDLSPPNMANTVNAALKPLETLSRIVNQPSSL-----FGSKSASSKSKS-----EODAGG----- 2281
 gi | 61676188 | ref | NP_113584.3 | CPSTSSFYSSATAKIQHNGMNNIIRLFLKKGVLNDLARVPHSLDLSPPNMANTVNAALKPLETLSRIVNQPSSL-----FGSKSASSKSKS-----EODAGG----- 2281
 gi | 61676190 | ref | NP_067498.3 | CPSTSSFYSSATAKIQHNGMNNIIRLFLKKGVLNDLARVPHSLDLSPPNMANTVNAALKPLETLSRIVNQPSSL-----FGSKSASSKSKS-----EODAGG----- 2282
 gi | 189536055 | ref | XP_001923899.1 | CPSTSSFYSSATAKIQHNGMNNIIRLFLKKGVLNDLARVPHSLDLSPPNMANTVNAALKPLETLSRIVNQPSSL-----FGGKGGSSKNT-----EHDIVG----- 2281
 gi | 24642256 | ref | NP_573059.1 | P-----MLYDKVHMHRNMYRVLLRQGMVYTLTKVAQYKDLNHNHLSLAAAILRPMELLRFVSTLTGSKRILFGSGGGPGGPNAGNGNNTAGGSSGNPGPSGNTYGTIINRRLYRPLAARTGFGSAMERSNMGGEHVLRT 2520
 gi | 25148695 | ref | NP_500284.2 | -----NNRERSSQATMKMFHKRMCAPLVRTIICQLSLTKVSLDVTNQLTLTLLEGSTTTTSAI-----ITGPRSLMDIVAG----- 2324
2560.....2570.....2580.....2590.....2600.....2610.....2620.....2630.....2640.....2650.....2660.....2670.....2680.....2690.....2700



gi | 74007005 | ref | XP_538052.2 | -----AAODSNNOODPGEPE-----AEVQEEHDVTQTEVADGDMGAEATDSVVIAGQPEVLSSQEMQVENELDLIDELLERD-----GGSGNSTIIVSRSGEDE----- 2376
 gi | 158508566 | ref | NP_001103474.1 | -----AAODSNNOODPGEPE-----TEVQEEHDVTQTEVADGDMGAEATDSVVIAGQPEVLSSQEMQVENELDLIDELLERD-----GGSGNSTIIVSRSGEDE----- 2376
 gi | 61676188 | ref | NP_113584.3 | -----ASODSSNQODPGEPE-----AEVQEEHDVTQTEVADGDMGAEATDSVVIAGQPEVLSSQEMQVENELDLIDELLERD-----GGSGNSTIIVSRSGEDE----- 2376
 gi | 61676190 | ref | NP_067498.3 | -----ASODSSNQODPGEPE-----AEVQEEHDVTQTEVADGDMGAEATDSVVIAGQPEVLSSQEMQVENELDLIDELLERD-----GGSGNSTIIVSRSGEDE----- 2377
 gi | 189536055 | ref | XP_001923899.1 | -----NVRDSENNTDQGEVGE-----AEPVE---NRDRGATDSLDLMDGAEAGDQVVIAGQPEVLSTQAMQVENELDLIDELLERD-----AQIVNSTIIVSRSGEDE----- 2373
 gi | 24642256 | ref | NP_573059.1 | IIRNVLSDRRHAFEFIFNDDMAVDSDDAAPSGVGGGGGAGSVGGGVGSGVGNSSAAVLDVVEERNGGDNDPPANVVSASSGAGQSSSGGPFVRFVVDNQDWDFFLQSEGRLRLASRGGGAGSGSGVAGSSGQNGSNTIA 2670
 gi | 25148695 | ref | NP_500284.2 | -----RREQRREAAGG-----TMNREIDTIFQRDGLAFGEMENLLRRLQDHWGRGNSVQRGAGVAEEEGSETVEERERSD-----SFSSESEHAGDE----- 2412
2710.....2720.....2730.....2740.....2750.....2760.....2770.....2780.....2790.....2800.....2810.....2820.....2830.....2840.....2850



gi | 74007005 | ref | XP_538052.2 | -----SQEDVLMDEAPS-----NLSQASTLQANREDSMNIIDPEDEEEHTQEDSSGNEDEDDSSQDEEEEEE-----EDEEDD----- 2445
 gi | 158508566 | ref | NP_001103474.1 | -----SQEDVLMDEAPS-----NLSQASTLQANREDSMNIIDPEDEEEHTQEDSSGNEDEDDSSQDEEEEEE-----EDEEDD----- 2445
 gi | 61676188 | ref | NP_113584.3 | -----SQEDVLMDEAPS-----NLSQASTLQANREDSMNIIDPEDEEEHTQEDSSGNEDEDDSSQDEEEEEE-----EDEEDD----- 2445
 gi | 61676190 | ref | NP_067498.3 | -----SQEDVLMDEAPS-----NLSQASTLQANREDSMNIIDPEDEEEHTQEDSSGNEDEDDSSQDEEEEEE-----EDEEDD----- 2446
 gi | 189536055 | ref | XP_001923899.1 | -----SQEDVLMDEAPS-----NMSQASTLQANREDSMNIIDPEDEE-----SQDEEEEEE-----EDEEDD----- 2440
 gi | 24642256 | ref | NP_573059.1 | SINSGNNSGIGNLRIRINPVDVVGSGNGSGSGSNAGVVDNNGISGGGSDGASISSDTGAPGARDLNASLIGDVSISESDPSITNDRNEDEDDDDAPDEVDHSETVDVEERSQFIEVFDHLYEPESEETASNDADVDND 2820
 gi | 25148695 | ref | NP_500284.2 | -----VRDVAVTGDGE-----VDMADAQDAPLAAPDPGGINLVDIMQVQRVDEDEDEDDGDNHEHARE-----DDHRE----- 2482
2860.....2870.....2880.....2890.....2900.....2910.....2920.....2930.....2940.....2950.....2960.....2970.....2980.....2990.....3000



gi | 74007005 | ref | XP_538052.2 | QEDDEGEGEDDDDDGSEMELDEDYF --- DMNASPLVRFERFDREDDLLIEFDNMFSS --- AIDIPPSPG-NIPTHPLMVRHADHSSLLTGGSSSTTRLTQIGIR --- SQR 2549
 gi | 158508566 | ref | NP_001103474.1 | QEDDEGEGEDDDDDGSEMELDEDYF --- DMNASPLVRFERFDREDDLLIEFDNMFSS --- AIDIPPSPG-NIPTHPLMVRHADHSSLLTGGSSSTTRLTQIGIR --- SQR 2549
 gi | 61676188 | ref | NP_113584.3 | QEDDEGEGEDDDDDGSEMELDEDYF --- DMNASPLVRFERFDREDDLLIEFDNMFSS --- AIDIPPSPG-NIPTHPLMVRHADHSSLLTGGSSSTTRLTQIGIR --- SQR 2549
 gi | 61676190 | ref | NP_067498.3 | QEDDEGEGEDDDDDGSEMELDEDYF --- DMNASPLVRFERFDREDDLLIEFDNMFSS --- AIDIPPSPG-NIPTHPLMVRHADHSSLLTGGSSSTTRLTQIGIR --- SQR 2550
 gi | 189536055 | ref | XP_001923899.1 | QDD --- EGDDEDDDDGSEMELDEDYF --- DINAAPHIRFERFDREDDLLIEFDNMFST --- SADIPPSPG-NIPSSHPLMVRHADHSSLLTGGSSSTTRLTQIGIR --- SQR 2541
 gi | 24642256 | ref | NP_573059.1 | DDDDDDDDDDDDDDDDDDDVREEVQSVMDAIEINRIDIALALVSSNNRPRRSAAVNASGDGSANRFPDDEVDDEDDDDVDADPD --- GDPDVPDISGSAQAQAEAYLVERLGSGLMPFPBVFVRVMSSSIAQLLDIVVNGGNAGSSG 2967
 gi | 25148695 | ref | NP_500284.2 | DDDDDDDDDDEDEEEEAEDDDQEDDVR --- HVEQNPEPLARRLFEEDDDDEDDGDEGD --- SMDDVQRDLDDVYFDMGPFDAQRMDMIFPPSFRPAVTAFADLFR --- DDFDPLPYRA 2601



gi | 74007005 | ref | XP_538052.2 | LROLTANTGHTIHVHYPGNRQPNPPLILQRLGPF --- AAADILQLSSSLPQSRGRARLLVGN --- DVHIIAR --- SDELLDDFFHDQSTAFSAG --- TLSS --- 2643
 gi | 158508566 | ref | NP_001103474.1 | LROLTANTGHTIHVHYPGNRQPNPPLILQRLGPF --- AAADILQLSSSLPQSRGRARLLVGN --- DVHIIAR --- SDELLDDFFHDQSTAFSAG --- TLSS --- 2643
 gi | 61676188 | ref | NP_113584.3 | LROLTANTGHTIHVHYPGNRQPNPPLILQRLGPF --- AAADILQLSSSLPQSRGRARLLVGN --- DVHIIAR --- SDELLDDFFHDQSTAFSAG --- TLSS --- 2643
 gi | 61676190 | ref | NP_067498.3 | LROLTANTGHTIHVHYPGNRQPNPPLILQRLGPF --- AAADILQLSSSLPQSRGRARLLVGN --- DVHIIAR --- SDELLDDFFHDQSTAFSAG --- TLSS --- 2644
 gi | 189536055 | ref | XP_001923899.1 | LROLTANTGHTIHVHYPGNRQPNPPLILQRLGPF --- AAADILQLSSSLPQSRGRARLLVGN --- DVHIIAR --- SDELLDDFFHDQSTAFSAG --- TLSS --- 2635
 gi | 24642256 | ref | NP_573059.1 | NAGATGSSGGSGQRSTGGTTASIGAIASAALRPSGSSWMAPDFNFIRISGGDSSMGSGPATGGANAGGDMNVFITPSMELERAGGAPGSGG --- TMSSELLNEQPTGAGGGGGGGGASGVGGVANGGGTTGQHPNATLCTNGVRRRLVLDQ 3117
 gi | 25148695 | ref | NP_500284.2 | ERRLARGSHLGGVISEHPLMTRPPAENDVSRPPNIN --- IRAEILQMHTRSSLHRNAIRRTTEAR --- ELEAISR --- IRMGELPAGRMLVGRITTHGDG --- 2696



gi | 74007005 | ref | XP_538052.2 | --- IPALTRWTEECKVLDAESMHD --- CVS VVKVPIVNHLEFLRDEELEERREKRRKQLAEEET --- KIIDKKGEDKENRDSQAACNAKINDSAEONLSDG --- TPMPDSYPT 2746
 gi | 158508566 | ref | NP_001103474.1 | --- IPALTRWTEECKVLDAESMHD --- CVS VVKVPIVNHLEFLRDEELEERREKRRKQLAEEET --- KIIDKKGEDKENRDSQAACNAKINDSAEONLSDG --- TPMPDSYPT 2746
 gi | 61676188 | ref | NP_113584.3 | --- IPALTRWTEECKVLDAESMHD --- CVS VVKVPIVNHLEFLRDEELEERREKRRKQLAEEET --- KIIDKKGEDKENRDSQAACNAKINDSAEONLSDG --- TPMPDSYPT 2746
 gi | 61676190 | ref | NP_067498.3 | --- IPALTRWTEECKVLDAESMHD --- CVS VVKVPIVNHLEFLRDEELEERREKRRKQLAEEET --- KIIDKKGEDKENRDSQAACNAKINDSAEONLSDG --- TPMPDSYPT 2747
 gi | 189536055 | ref | XP_001923899.1 | --- IPALTRWTEECKVLDAESMHD --- CVAVVKVPILOHLESRLDEELEERREKRRRQLAEEETAKQNESSAAGEETREOSLOGSGIGIVNGAENAAEGE --- QAQGVSSCLDF 2744
 gi | 24642256 | ref | NP_573059.1 | YCVCMPTHONPTBETQMETPTQDALHWLEBATLLDMESQTDACLVAHFLLPHLIKELKAAHQKQEEAAROSTTPAEGSNASATSSSTTVVGTAAPIATSIASGLLANAVSAGSGSSSLVPPVAASATGGRSSIPVLISSTL 3267
 gi | 25148695 | ref | NP_500284.2 | --- GVHTSFFDHIFDIRPNSVAFSRSGARSNTDRDRERRDIRASVPTCLERLESYLSLMEPVSSRFVIVVNSHLNKIHAAREAQIK --- KEAEIKAKA 2792



gi | 74007005 | ref | XP_538052.2 | TPSSIDAATSES --- KDLVLVLQPSQQOQTLF --- PPPALGEIPOELQSPAGEGSSSTOLLMPVEPEELGP --- TRPSGEAETTOMELS --- 2826
 gi | 158508566 | ref | NP_001103474.1 | TPSSIDVATSEP --- RETLVLVLQPSQQOQTLF --- TPPALGEIPOELQSPAGEGSSSTOLLMPVEPEELGP --- TRPSGEAETTOMELS --- 2826
 gi | 61676188 | ref | NP_113584.3 | TPSSIDAATSES --- KETLGLTQSSQQOQTLF --- TPPALGEIPOELQSPAGEGSSSTOLLMPVEPEELGP --- TRPSGEAETTOMELS --- 2826
 gi | 61676190 | ref | NP_067498.3 | TPSSIDAPTSES --- KETLGLTQSSQQOQALP --- PPPALGEIPOELQSPAGEEVANSTOLLMPVLEELGP --- TRPSGEAETTOMELS --- 2827
 gi | 189536055 | ref | XP_001923899.1 | PRTEGFLTAPP --- SGEVPTPTPAPHEQALVSL --- ETATSQQVHPITTELLLADSNDDSHGALAGALPOLGAP --- DRPNCEBASQMEMS --- 2829
 gi | 24642256 | ref | NP_573059.1 | GPPSASATATGNATSDATTTGGPTRNFSSVDNVSSETQTTRPPRRGGLRQSQLPFNIIAYEIDLNEQDSEGRDRTSTTCTAADGAEQSQHNSSTAAQVAVPQHRHPVPLLPSSGRFSPRHTRLDTELLLLQLLDRG 3417
 gi | 25148695 | ref | NP_500284.2 | KKDAEAKKAAE --- DKKKAAEAPAPAPAEQSDSPASPDAPAPAEIIGL --- ATFAATNTNTVNSE --- 2855



gi | 74007005 | ref | XP_538052.2 | --- PAPTITSLSP --- ERAEDSDALTAVSSOLEGSPMDTSSLASCTLEAVGDTISAA --- 2877
 gi | 158508566 | ref | NP_001103474.1 | --- PAPTITSLSP --- ERAEDSDALTAVSSOLEGSPMDTSSLASCTLEAVGDTISAA --- 2877
 gi | 61676188 | ref | NP_113584.3 | --- PAPTITSLSP --- ERAEDSDALTAVSSOLEGSPMDTSSLASCTLEAVGDTISAA --- 2877
 gi | 61676190 | ref | NP_067498.3 | --- PAPTITSLSP --- ERAEDSDALTAVSSOLEGSPMDTSSLASCTLEAVGDTISAA --- 2878
 gi | 189536055 | ref | XP_001923899.1 | --- PAPTITSLSP --- DIAESSEFPVGVVQLEGSPMDTSSPASGTOEPEASSEVPS --- 2880
 gi | 24642256 | ref | NP_573059.1 | IRRRLCGSSGNTSSRSRSGSALINARPNRDLPACLQREHDPAGSIFPRPNAIRTPAPTLVSMPTPMSNAALEQLNVLAPDVVTRDRNFALPSSLEVDVLDVLPGLVLDLQEQEAQPEDDQLLPPPPPPPSDITPLVHAEDDLWPGTVVSA 3567
 gi | 25148695 | ref | NP_500284.2 | --- VAPNASTRGD --- DTLTLPAAAVQEDQASDQHLEEFPEMVEGDDQAAE --- 2901



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gi | 74007005 | ref | XP_538052.2 | GSEEDPLAGISLPEGVDPFLAALPDDIRREVLONQLGIRPPTR 2996
gi | 158508566 | ref | NP_001103474.1 | GSEEDPLAGISLPEGVDPFLAALPDDIRREVLONQLGIRPPTR 2996
gi | 61676188 | ref | NP_113584.3 | GSEEDPLAGISLPEGVDPFLAALPDDIRREVLONQLGIRPPTR 2996
gi | 61676190 | ref | NP_067498.3 | GSEEDPLAGISLPEGVDPFLAALPDDIRREVLONQLGIRPPTR 2997
gi | 189536055 | ref | XP_001923899.1 | NHMSDELSSGDSG---LTDROTDAETGTSVSSPGETMPSRDSAD---QSQAIEEPLPST 2984
gi | 24642256 | ref | NP_573059.1 | GPRESSAPAVATESLEAVNESNOPEPTESSESTSPNPQAPSAPTLEPFGAADVAVGVAQTPATEEAASAGAGTATITDMSPEVRAALGDLEVPDGVDPFLAALPEMREAVIRYQRCQRAERASRFPVAAQFVAVNPNAPA 3698
gi | 25148695 | ref | NP_500284.2 | APQSSAAIAASVAGTEIEDVERQAVDQVPEIENDDNLLPVEG-----AVEHAPQAQPEENVMP-----EFRAILGDITIPDGVDPFLAALPEMREAVIRYQRCQRAERASRFPVAAQFVAVNPNAPA 3025
.....3760.....3770.....3780.....3790.....3800.....3810.....3820.....3830.....3840.....3850.....3860.....3870.....3880.....3890.....3900

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gi | 74007005 | ref | XP_538052.2 | ---TAPSNSSAPAVVGN---PGVTEVSPFLAALPPAIQEEVLAQR---AEQORRELAQN---ASSDTPMDPVTFIOTLPDLRRSVLEDMEDSVLAVMPPDIAAEAQALRREQEARQRLMHERLFGHSST---SALSAILRSPAFTRSL 3135
gi | 158508566 | ref | NP_001103474.1 | ---TAPSNSSAPAVVGN---PGVTEVSPFLAALPPAIQEEVLAQR---AEQORRELAQN---ASSDTPMDPVTFIOTLPDLRRSVLEDMEDSVLAVMPPDIAAEAQALRREQEARQRLMHERLFGHSST---SALSAILRSPAFTRSL 3135
gi | 61676188 | ref | NP_113584.3 | ---TAPSNSSAPAVVGN---PGVTEVSPFLAALPPAIQEEVLAQR---AEQORRELAQN---ASSDTPMDPVTFIOTLPDLRRSVLEDMEDSVLAVMPPDIAAEAQALRREQEARQRLMHERLFGHSST---SALSAILRSPAFTRSL 3135
gi | 61676190 | ref | NP_067498.3 | ---TAPSNSSAPAVVGN---PGVTEVSPFLAALPPAIQEEVLAQR---AEQORRELAQN---ASSDTPMDPVTFIOTLPDLRRSVLEDMEDSVLAVMPPDIAAEAQALRREQEARQRLMHERLFGHSST---SALSAILRSPAFTRSL 3136
gi | 189536055 | ref | XP_001923899.1 | ---VASTLTITASAVLGGGPGVTEVSPFLAALPPAIQEEVLAQR---AEQORRELSQPTQGDQPLDVTIOTLPSELRRSVLEDMEDSVLAVMPPDIAAEAQALRREQEARQRLMHERLFGHSST---SALSAILRSPAFTRSL 3125
gi | 24642256 | ref | NP_573059.1 | ---RAQQNAIQIAHDSLVEVNPFLAALPLNIQSEVLMQOR---IEQORQ---AAQTANPEDPVDTAAFFQNLPENLRQAILLTDMESQIASLPELAAEAQFLRRDWESRNGARMDAHPFNSALSRFQITLQSLDDTRWHSSIW 3834
gi | 25148695 | ref | NP_500284.2 | GGEAAQEGQAEPAAAVPLVEPIIDVFLNALPELQEEVLAHERRLREAEQQORRQNAPEAVVEMDGAAVIATLPAANERQAQVLAEMDDAELAGLPADMQNEARRARAQHVEMNMLRYHRLFRGGVG----- 3156
.....3910.....3920.....3930.....3940.....3950.....3960.....3970.....3980.....3990.....4000.....4010.....4020.....4030.....4040.....4050

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gi | 74007005 | ref | XP_538052.2 | GNRGVQYTRLAVQRGGTFQMGSSSSNRPSSGNSVDTLRLRGRLLLDHEALSCLLVLLFVDEPKLNTSRLHRVLRNLCYHAQTRHWVIRSLLSILQRSSSEELCIEIPKLSSEEDK-----GKKSSKSCGSS 3262
gi | 158508566 | ref | NP_001103474.1 | GNRGVQYTRLAVQRGGTFQMGSSSSNRPSSGNSVDTLRLRGRLLLDHEALSCLLVLLFVDEPKLNTSRLHRVLRNLCYHAQTRHWVIRSLLSILQRSSSEELCIEIPKLSSEEDK-----GKKSSKSCGSS 3262
gi | 61676188 | ref | NP_113584.3 | GNRGVQYTRLAVQRGGTFQMGSSSSNRPSSGNSVDTLRLRGRLLLDHEALSCLLVLLFVDEPKLNTSRLHRVLRNLCYHAQTRHWVIRSLLSILQRSSSEELCIEIPKLSSEEDK-----GKKSSKSCGSS 3262
gi | 61676190 | ref | NP_067498.3 | GNRGVQYTRLAVQRGGTFQMGSSSSNRPSSGNSVDTLRLRGRLLLDHEALSCLLVLLFVDEPKLNTSRLHRVLRNLCYHAQTRHWVIRSLLSILQRSSSEELCIEIPKLSSEEDK-----GKKSSKSCGSS 3263
gi | 189536055 | ref | XP_001923899.1 | GNRGVQYTRLAVQRGGTFQMGSSANRSPSSGNSVDTLRLRGRLLLDHEALSCLLVLLFVDEPKLNTSRLHRVLRNLCYHSOTRGVWIRSLLSILQRSSSEELCIEIPKLSSEEDK-----GGSSTSSSS 3255
gi | 24642256 | ref | NP_573059.1 | YDASGNAQPQHHTTIVHQHHAHAPNMGGPLALLMDENLDPDSLALNLLVLLFVDEPKLNTSRLHRVLRNLCYHAEPTRDWIIISALTSIIQKNEEDANFAGQAGGKPEWLKLRVDAAPGYKSNIFLINRLYEGSARSISINPQ 3984
gi | 25148695 | ref | NP_500284.2 | ---GAPGAIGTVRARTNARAANAAGPSVQONAGNAIQAPPDQPHLLDRESILNCLLLYLVDDNRRVPHRLQKVLRSACVNTQCDFTVWCLLALLDKASEANTDDEE----- 3260
.....4060.....4070.....4080.....4090.....4100.....4110.....4120.....4130.....4140.....4150.....4160.....4170.....4180.....4190.....4200

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gi | 74007005 | ref | XP_538052.2 | SHENRP---LDLLHKMESKSSNQLSWLSVSMDAALGCRTNIFQIQR---SGGRKHTEKHAS-----SGSTVHIHPQAAPVVCRRHVDLTIOLAKVFPESHFTQORTKETNCESDRERGSKQACSPSSQSTSS---GICTDFWD 3391
gi | 158508566 | ref | NP_001103474.1 | SHENRP---LDLLHKMESKSSNQLSWLSVSMDAALGCRTNIFQIQR---SGGRKHTEKHAS-----SGSTVHIHPQAAPVVCRRHVDLTIOLAKVFPESHFTQORTKETNCESDRERGSK---ACSPSSQSTSS---GICTDFWD 3390
gi | 61676188 | ref | NP_113584.3 | SHENRP---LDLLHKMESKSSNQLSWLSVSMDAALGCRTNIFQIQR---SGGRKHTEKHAS-----GGSTVHIHPQAAPVVCRRHVDLTIOLAKVFPESHFTQORTKETNCESDRERGNK---ACSPSSQSTSS---GICTDFWD 3390
gi | 61676190 | ref | NP_067498.3 | SHENRP---LDLLHKMESKSSNQLSWLSVSMDAALGCRTNIFQIQR---SGGRKHTEKHAS-----GGSTVHIHPQAAPVVCRRHVDLTIOLAKVFPESHFTQORTKETNCESDRERGSKQACSPSSQSTSS---GICTDFWD 3392
gi | 189536055 | ref | XP_001923899.1 | SSSSSS---LLELLNRVESRSSLSWLSVSMDAALGCRTNIFQIQR---VSGRKHAEHRSAG-----GGSTVHIHPQAAPVVCRRHVDLTIOLAKVFPESHFTQORCKDPLSSSEELTLRCLASSFTMSAECR---SGISDFWD 3388
gi | 24642256 | ref | NP_573059.1 | AAGMIVRNCLDLLLEVLAKHYPSFVFNDRDVKARR-ILSAVFGMPSFAGSGGGAGSGSAAGGLTGVDDVPPGGTLDERSRRCRQVNVNRLRSIFDDHPAPKPSVPLDEAPS---SKAAAKAAATAKVTAGSNKHEVVPQTNAKNFW 4133
gi | 25148695 | ref | NP_500284.2 | ---LISVPAWLDLSIAVSGVGHNERAIRSEIN-----AOKTISHSMLATPCNKILDLLANITARAQVGNFLILLRHGAKPTDTPAQAP-----SFAQFVT 3348
.....4210.....4220.....4230.....4240.....4250.....4260.....4270.....4280.....4290.....4300.....4310.....4320.....4330.....4340.....4350

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gi | 74007005 | ref | XP_538052.2 | LLVKLDNMNVRKGG---KNSVKSVPVSAAGGEGETSPYSLASPLGOLMNMLSHPVIRRSLLTEKLLRLLSLISIALPENKVSQAQANSSSASSTTVAI---STTSTTTTAASTTTPPAATTPVTSAPALVAATAISTIAVAASTTV 3536
gi | 158508566 | ref | NP_001103474.1 | LLVKLDNMNVRKGG---KNSVKSVPVSAAGGEGETSPYSLASPLGOLMNMLSHPVIRRSLLTEKLLRLLSLISIALPENKVSQAQANSSSASSTTVAI---STTSTTTTAASTTTPPAATTPVTSAPALVAATAISTIAVAASTTV 3535
gi | 61676188 | ref | NP_113584.3 | LLVKLDNMNVRKGG---KNSVKSVPVSAAGGEGETSPYSLASPLGOLMNMLSHPVIRRSLLTEKLLRLLSLISIALPENKVSQAQANSSSASSTTVAI---STTSTTTTAASTTTPPTTAPTPVTSAPALVAATAISTIVVAASTTV 3535
gi | 61676190 | ref | NP_067498.3 | LLVKLDNMNVRKGG---KNSVKSVPVSAAGGEGETSPHLSLEASPLGOLMNMLSHPVIRRSLLTEKLLRLLSLISIALPENKVSQAQANSSSASSTTVAI---STTSTTTTAASTTTPPTTAPTPVTSAPALVAATAISTIVVAASTTV 3539
gi | 189536055 | ref | XP_001923899.1 | LLVKLDNMNVRKGG---KASMKVPLGGVGETEGALFLEASPLGOLMNMLSHPVIRRSLLTEKLLRLLSLISIALPENKVAEVPAS---HPVQNPATPSAPAPQTAGSGHISAVAATGTQGSVSGVGTTP 3518
gi | 24642256 | ref | NP_573059.1 | VVLNIDQQTQVRLANVACFLPTQPAAWEPQNTADFLSFSPPGOLMMLPKVVICRSPHLLTDMVLKLLASLTELPEBEELPLSDQMP-----PLVPTIGVQVQAGAAAAAHPPPPQPPAENIATATEIGDGLAANTEQA 4272
gi | 25148695 | ref | NP_500284.2 | MVQNTKVKPKSKDWI---ATPEQLKECPGLGOLMNSLRPKIMAKS---PLKKEVLRVAQIMVLTLPMTLKLKLDN----- 3418
.....4360.....4370.....4380.....4390.....4400.....4410.....4420.....4430.....4440.....4450.....4460.....4470.....4480.....4490.....4500

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gi |74007005|ref|XP_538052.2| QLAAFLEGFVEIIPKRLISIFTEQEELELLISGLPVIDIDDLKSNTEYHKYQSNISIQIOWFWRALRSFDQADRAKFLQFVTGTSKVPLOGFAALEGMNGIQKFOIHRDDRSTDRLPSAHTCFNQLDLPAYESFEKLRHMLLLAIQECSEGF 4372
gi |158508566|ref|NP_001103474.1| QLAAFLEGFVEIIPKRLISIFTEQEELELLISGLPVIDIDDLKSNTEYHKYQSNISIQIOWFWRALRSFDQADRAKFLQFVTGTSKVPLOGFAALEGMNGIQKFOIHRDDRSTDRLPSAHTCFNQLDLPAYESFEKLRHMLLLAIQECSEGF 4372
gi |61676188|ref|NP_113584.3| QLAAFLEGFVEIIPKRLISIFTEQEELELLISGLPVIDIDDLKSNTEYHKYQSNISIQIOWFWRALRSFDQADRAKFLQFVTGTSKVPLOGFAALEGMNGIQKFOIHRDDRSTDRLPSAHTCFNQLDLPAYESFEKLRHMLLLAIQECSEGF 4371
gi |61676190|ref|NP_067498.3| QLAAFLEGFVEIIPKRLISIFTEQEELELLISGLPVIDIDDLKSNTEYHKYQSNISIQIOWFWRALRSFDQADRAKFLQFVTGTSKVPLOGFAALEGMNGIQKFOIHRDDRSTDRLPSAHTCFNQLDLPAYESFEKLRHMLLLAIQECSEGF 4375
gi |189536055|ref|XP_001923899.1| QLAAFLEGFVEIIPKRLISIFTEQEELELLISGLPVIDIDDLKANTYHKYQSSISIQIOWFWRALRSFDQADRAKFLQFVTGTSKVPLOGFAALEGMNGIQKFOIHRDDRSTDRLPSAHTCFNQLDLPAYESFEKLRHMLLLAIQECSEGF 4357
gi |24642256|ref|NP_573059.1| QLDFALEGFVDIIPKHLISIFNEQEELELLISGLPDIDIEDLKANTYHKYTSKSAIQIOWFWRALRSFDQADRAKFLQFVTGTSKVPLOGFGLSEGMNGIQKFOIHRDDRSTDRLPSAHTCFNQLDLPAYESFEKLRHMLLLAIQECSEGF 5143
gi |25148695|ref|NP_500284.2| QLDFALEGFVEIIPKDLISMFNEQEELELLISGLPVIDIDDMAANTDYKGFQKTSIHIQWFWRALRSFEKEDKAKFLQFVTGTSKVPLOGFAALEGMNGVQKFSIHMDSRGGDRLPAAHTCFNQLDLPAYESFEKLRHMLLLAIQECSEGF 4174
.....5260.....5270.....5280.....5290.....5300.....5310.....5320.....5330.....5340.....5350.....5360.....5370.....5380.....5390.....5400

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gi |74007005|ref|XP_538052.2| GLA 4375
gi |158508566|ref|NP_001103474.1| GLA 4375
gi |61676188|ref|NP_113584.3| GLA 4374
gi |61676190|ref|NP_067498.3| GLA 4378
gi |189536055|ref|XP_001923899.1| GLA 4360
gi |24642256|ref|NP_573059.1| GFA 5146
gi |25148695|ref|NP_500284.2| GFA 4177
...

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