

gi | 28573181 | ref | NP_524282.4 | ---MFLSNSD VHVVEVCLRGN---DLRSNAIRNNVETALKAYFOARKLP RNVSF L P D-----LAEQTEHVHVSLLERDNGGV 150
gi | 158301936 | ref | XP_321602.4 | ---MNDISAPTRIEVACTRG---FNKSSQSCSEVYQHVDLIEERETLR-----MGTTFIPVLSVLOVEVCTDVD 150
gi | 11321607 | ref | NP_004228.1 | ---MDEAVGDLKQALPCVAESPT---VHVEVHQSGSTAKKEDINLSVRKLLNRHNIVFGD---YTWTEFDEPFLARNVQSVSIIDTELKVKDSG 150
gi | 114598830 | ref | XP_001141322.1 | ---MDEAVGDLKQALPCVAESPT---VHVEVHQSGSTAKKEDINLSVRKLLNRHNIVFGD---YTWTEFDEPFLARNVQSVSIIDTELKVKDSG 150
gi | 110625724 | ref | NP_081458.1 | ---MDEAVGDLKQALPCVAESPA---VHVEVLQSGSTAKKEDIKSSVYRLLNRHNIVFGD---YVWTEFDDPFLARNVQSVSIIDTELKAKDPQ 150
gi | 58865438 | ref | NP_001011930.1 | ---MDDAVGDLKQALPCVAESPT---VHVEVLQSGSTAKKEDIKQSVYRLLNRHNIVFGD---YVWTEFDDPFLARNVQSVSIIDTELKAKDPQ 150
gi | 74003129 | ref | XP_851775.1 | ---MDEAVGDLKQALPCVAEAPT---VHVEVHQSGSTAKKEDIKLSVRKLLNRHNIVFGD---YKWNTEFDDPFLARNVQSVSIIDTELKVKDPQ 150
gi | 118086321 | ref | XP_418892.2 | ---MDEAAGDLKQALPNTCDNVQ---LHVEVHQSGSTAKKEDIRMSVLLNRHNIVFGD---YKWTTEFDDGFLNRSVQSVSIIDTELKLRG 150
gi | 41053680 | ref | NP_956876.1 | ---MDISDHMTDVG---IIRPD---VHIEVHVKSQSTAKRSDVRTHVLSLLDRHSVLRSLRS---FKWMDFDNEFLKRVESVHIAD---VTGPK 150
gi | 79485764 | ref | NP_194202.3 | ---MEIABQKPMVEDPIPLPNASMEVSYQNP---IEAAIIPVQIAYA-EPVATPNPP---PCLHENKFLVSVVEVCLKPSSTARLEDVQRAVERMLENRSMSYADG---LVLIIPADDLFLVDNVRICICDTEWVKKND 150
gi | 115458982 | ref | NP_001053091.1 | ---NPKTLAEKSLPSPSRALLGRHHRPHGGLLLRAASSGCGICCRRGPIAGARVGGGGGDRHFLLAATDGVALVAVEVLLHATSTARAEEDVCAAVERMLEARSLSYVDG---FVPIPNDDPFLANVRRQICDTEWVENKH 150
gi | 17533043 | ref | NP_495711.1 | ---MHEPMKTLNRIHAEIRICQK---FPKSVVQKRFSEFEELIKAAEKARNWKPISVVEL---FOGDSSLNELFEKLVIGICELRDGELFENVN 150
gi | 9755327 | ref | NP_009745.2 | ---MSYIVDLQVRGSSLRVVIKCMFREDEQISSLHSGDSEKQNSNKKLGEFLNLLKAVVKKLSEFPKDRLKTSIIIGQELMREGQGSIEIKDPPTEAQHILRSLSAKVLLHQFSSINGKVNIVNEGDNDFLFWKKSIEQOSTSHVSIK 150
gi | 45190349 | ref | NP_984603.1 | ---MVRYIVDCCLKEDVLALIIPLMHEIGDEGNMDDP---TATFQELLVTRVRRRLKLEEDLDRHCAYDFLLNGOGAVSLASTPKAQESFIRSLVKVMHDFD---LGGNNQVIDYQGNLLIFCIEKLYIEK-ATGAFSPG 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 28573181 | ref | NP_524282.4 | P L K V A E I K F R F H F V A R P E G Q L ---G L F S G E E G S D G I D S I V A A S H A L L P A A F V G L W E N L I V E T G L K E K L L K F A L S A L M F S ---E H R V 300
gi | 158301936 | ref | XP_321602.4 | -OYTSRSALQNFVVLQEQDQ---VHETITTHCAEMETIHHMLLPARELHGLWESLIYREGIKDSVLAFAETMLFA---RKGV 300
gi | 11321607 | ref | NP_004228.1 | P I D L S A C T V A L H I F O L N E D G P ---S E N L E E E T E N I I A A N H W V L P A A E F H G L W D S L V Y D V E V K S H L L D Y V M T L L F S ---D K N V 300
gi | 114598830 | ref | XP_001141322.1 | P I D L S A C T V A L H I F O L N E D G P ---S E N L E E E T E N I I A A N H W V L P A A E F H G L W D S L V Y D V E V K S H L L D Y V M T L L F S ---D K N V 300
gi | 110625724 | ref | NP_081458.1 | P I D L S A C T I A L H I F O L N E E G P ---S E N L D E E T E N I I A A S H W V L P A A E F H G L W D S L V Y D V E V K S H L L D Y V M T V L F S ---D K N V 300
gi | 58865438 | ref | NP_001011930.1 | P I D L S A C T I A L H I F O L N E E G P ---S E N L D E E T E N I I A A S H W V L P A A E F H G L W D S L V Y D V E V K S H L L D Y V M T L L F S ---D K N V 300
gi | 74003129 | ref | XP_851775.1 | P I D L G A C T I A L H I F O L N E G G P ---S E T L E E E T E N I I A A S H W V L P A A E F H G L W D S L V Y D V E V K S H L L D Y V M T L L F S ---D K N V 300
gi | 118086321 | ref | XP_418892.2 | P I D L S K S S L I T I H I F H L N E E G P ---I E N L E E E N E D I V A A N H W V L P A A E F H G L W E S L I V D T E V K S H L L D Y V T L L F S ---D R N V 300
gi | 41053680 | ref | NP_956876.1 | L V D L K V N L C I H I F T L N D D S P ---S T L N L E E E -E E L S A A N L W L L P A V E F H G V W E S L I Y E E G I K Q L L D Y V S T L I F F S ---D K N V 300
gi | 79485764 | ref | NP_194202.3 | V L L F W Q V K P V V H T F L I E E G P ---C E D L C A D G ---Q P A S F N E W L P A K E F D G L W E S L I Y E S G L Q R L L R Y A A S A L L F T ---C K G V 300
gi | 115458982 | ref | NP_001053091.1 | V L L F W Q V R P V V H V F O L S E D G P ---E E E P G E D D ---T L S F F N E W A L P A K E F D G L W E L L Y E V G L K Q R L L R Y A A S A L L F T ---E K G V 300
gi | 17533043 | ref | NP_495711.1 | D L T I N P S ---N I H V V K L H K D G P ---L S Q N I G D D D G D E S I T G S Q L W L P C V E F D S I W E N L I Y D S N L K N E V M S Y V A A L A R S ---E K H V 300
gi | 9755327 | ref | NP_009745.2 | L N F H E K I N L G Q H I D S I L D S E E T N E S D T Y H M G S V D E F I I Y P F C C L E E Q D E L K N G S I L S T E F D K I D L E L D E D D G F E G E T L N N C I N S V G N F D I P L S K Q T L N L V N I S Y L P G T F E G Q W E S L Y F G N N I K E R L Y S Y A T I E L K I A R F K Q L G D N G E D 300
gi | 45190349 | ref | NP_984603.1 | V ---E A D D L V M V M A D A L G K G Q K L Q M I D H A R G K -E F D I N -F Y A T P E R F S K S L A Y A I S D E F D R I N L K D D E S G ---H E R I L T P L D P S I S ---W L P F S P E A F Q L V R V H F L P S R E V E G A W E A L Y F E D D I K G Q L F K Y A I T A L K M S H F I P ---E E T 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 28573181 | ref | NP_524282.4 | D T N V I A C N R L L I L L H G P P G T G K T S L C K A L A O K L S I R ---H Q G S Y A V T H L V E I N S H S L F S K W F S E S G K L V A Q L F N K T A E L V S D ---P N N L V C V L I D E V E S L A Y A R -S A M S S N E P R D A M R V V N A V L T O L D S L K T C P N V L I L A T S N L A G 450
gi | 158301936 | ref | XP_321602.4 | D K N L I T C N R L A L F H G P P G T G K T S L C K A I A O K L S I R ---L N E Q Y R H A H L V E I N S H S L F S R W F S E S G K L V Q K V F S E T V A L L E D ---E R S L V C V L V D E I E S T A Y A R -D R I S S N E P S D S I R V V N A V L T O L D R L R R F P N V F I L A T S N L A D 450
gi | 11321607 | ref | NP_004228.1 | N S N L I T W N R V V L L H G P P G T G K T S L C K A L A O K L T I R ---L S S R Y R Y G O L I E I N S H S L F S K W F S E S G K L V T K M F O K I Q D L I D D ---K D A L V F V L I D E V E S L T A A R N A C R A G E T P S D A I R V V N A V L T O I D O I K R H S N V V I L T S N I T E 450
gi | 114598830 | ref | XP_001141322.1 | N S N L I T W N R V V L L H G P P G T G K T S L C K A L A O K L T I R ---L S S R Y R Y G O L I E I N S H S L F S K W F S E S G K L V T K M F O K I Q D L I D D ---K D A L V F V L I D E V E S L T A A R N A C R A G E T P S D A I R V V N A V L T O I D O I K R H S N V V I L T S N I T E 450
gi | 110625724 | ref | NP_081458.1 | D S N L I T W N R V V L L H G P P G T G K T S L C K A L A O K L T I R ---L S S R Y R Y G O L I E I N S H S L F S K W F S E S G K L V T K M F O K I Q D L I D D ---K E A L V F V L I D E V E S L T A A R N A C R A G A E P S D A I R V V N A V L T O I D O I K R H S N V V I L T S N I T E 450
gi | 58865438 | ref | NP_001011930.1 | D S N L I T W N R V V L L H G P P G T G K T S L C K A L A O K L T I R ---L S S R Y R Y G O L I E I N S H S L F S K W F S E S G K L V T K M F O K I Q D L I D D ---K E A L V F V L I D E V E S L T A A R N A C R A G A E P S D A I R V V N A V L T O I D O I K R H S N V V I L T S N I T E 450
gi | 74003129 | ref | XP_851775.1 | D S N L I T W N R V V L L H G P P G T G K T S L C K A L A O K L T I R ---L S S R Y Q Y G O L I E I N S H S L F S K W F S E S G K L V T K M F O K I Q D L I D D ---K D A L V F V L I D E V E S L T A A R N A C R A G E T P S D A I R V V N A V L T O I D O I K R H C N V V I L T S N I T E 450
gi | 118086321 | ref | XP_418892.2 | D S N L I S W N R V V L L H G P P G T G K T S L C K A L A O K L T I R ---L S Y R Y R Y G O L I E I N S H S L F S K W F S E S G K L V T K M F O K I Q E L I D D ---K D A L V F V L I D E V E S L T A A R S A F K A G E T P S D A I R V V N A V L M O I D O I K R Y P N V V I L T S N I T E 450
gi | 41053680 | ref | NP_956876.1 | D S N L I T W N R V V L L H G P P G T G K T S L C K G L A O K L S I R ---L S D R Y A H S O F V E I N S H S L F S K W F S E S G K L V T K M F O K I Q E L I D D ---K D A L V F V L I D E V E S L T A A R S A A Q A G E T P S D A I R V V N S V L T O I D O I K R H P N V V I L T S N V T E 450
gi | 79485764 | ref | NP_194202.3 | N P N L V S W N R I I L L H G P P G T G K T S L C K A L A O K L S I R ---C N S R Y P H C O L I E V N A H S L F S K W F S E S G K L V A K L F O K I Q E M V E E ---D G N L V F V L I D E V E S L A A A R K A A L S G S E P S D S I R V V N A L L T O M D K L K S A P N V I I L T S N I T 450
gi | 115458982 | ref | NP_001053091.1 | D P C L V S W N R I V L L H G P P G T G K T S L C K A L A O K L S I R ---F K S R Y S M C O L I E V N A H S L F S K W F S E S G K L V A K L F O K I Q E M V E E ---E S N L V F V L I D E V E S L A A A R K A A I S G S E P S D S I R V V N A L L T O M D K L K S W P N V I I L T S N I T 450
gi | 17533043 | ref | NP_495711.1 | N P K I I N V N R L I L L T G P P G T G K T S L C K G L A O H L S I R ---M N D K Y S K S V M L E I N S H S L F S K W F S E S G K L V Q K M F D I D E L A E D ---E K C M V F V L I D E V E S L G M C R E S S S R S E P S D A I R A V N A L L T O I D R I R R R D N V I L C T S N L E S 450
gi | 9755327 | ref | NP_009745.2 | I I T L I I N K K L L V H G P P G T G K T I L C K A L C K L S V R R E F S D G S D I D T N Y K G I I I E L S C A R I F S K W F G E S S K N I I V F K D I E E L L K V N E R G I F I C L L I D E V E A L A S S R T L N S R N E S T D G I R V V N T L L T O L D R L K K H N F L A L A T S N L L D 450
gi | 45190349 | ref | NP_984603.1 | L A V I T G G N R L L L V H G P P G T G K T I I C K A L C H K L A I R -L H G L L P R N K S V P S V I L V E L A C S K V F S R W F G E S S K N I D T I F K D L E K L I K D G I I D N Q F V C L L I D E V E T A F S R T S L I N K N E T T D A I R V V N L L T O L D N M K K Y F L T L A T S N L L D 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



```

      :* ::* : * : : : : : : * : *
gi | 28573181 | ref | NP_524282.4 | SIDLAFVDRADIRLFIGYPGISAIREIYKGMIAELMSAGVLQREVLESE--DAEEGLLTQ-----LAERSVGLSGRTLRRKLPFLAHAQYTSSTLFEILDQKISLSDFLDAMLEALEHLEGEORLLKLESMEQL 599
gi | 158301936 | ref | XP_321602.4 | SIDAAFVDRADFVQYIDHPTEPAIYDIYRSALYNLQTIIGIVEKEANSNRRLSTMLDILLQ-----VVKLSAGLSGRTLRRKIPFLAHALYVK-----KETESVLNFLTAMRQAIRKVRNDKRLLLAKD 599
gi | 11321607 | ref | NP_004228.1 | KIDVAFVDRADIKQYIGPPSAAAIYFKIYLSCLLEELMKCOIIPROQLLTLRELEMIGFIEN-----NVSKLSLLLNDSIRKSEGLSGRVLRRKLPFLAHALYVK-----APTIVTIEGFLOALS LAVDKQFEERKKLAAYI 599
gi | 114598830 | ref | XP_001141322.1 | KIDVAFVDRADIKQYIGPPSAAAIYFKIYLSCLLEELMKCOIIPROQLLTLRELEMIGFIEN-----NVSKLSLLLNDSIRKSEGLSGRVLRRKLPFLAHALYVK-----APTIVTIEGFLOALS LAVDKQFEERKKLAAYI 599
gi | 110625724 | ref | NP_081458.1 | KIDVAFVDRADIKQYIGPPSAAAIYFKIYLSCLLEELMKCOIIPROQLLTLRELEMIGFIEN-----NVSKLSLLLEISIRKSEGLSGRVLRRKLPFLAHALYVK-----APSVTIEGFLOALS LAVDKQFEERKKLSAVV 599
gi | 58865438 | ref | NP_001011930.1 | KIDVAFVDRADIKQYIGPPSAAAIYFKIYLSCLLEELMKCOIIPROQLLTLRELEMIGFIEN-----NVSKLSLLLEISIRKSEGLSGRVLRRKLPFLAHALYVK-----APSVTIEGFLOALS LAVDKQFEERKKLSAHV 599
gi | 74003129 | ref | XP_851775.1 | RIDVAFVDRADIRQYIGPPSAAAIYFKIYLSCLLEELMKCOIIPROQLLTLRELEMIGFIEN-----NVSKLSLLLEISIRKSEGLSGRVLRRKLPFLAHALYVK-----APTIVTIEGFLOALS LAVDKQFEERKKLSSCI 599
gi | 118086321 | ref | XP_418892.2 | KIDMAFVDRADIKQYIGPPSAAAIYFKIYLSCLLEELMKCOIIPROHLLSLRELEMIGFIEN-----NVSRLLSLVLEISIRRSSEGLSGRVLRRKLPFLAHALYVK-----SPSVTMTAFLOALS LAVDKQFEERKKLADCV 599
gi | 41053680 | ref | NP_956876.1 | KIDLAFVDRADIKQYIGPPSAAAIYFKIYLSLEELMKROIIPROQLVSLLELETMNFMES-----DVTRLLSLCLMNISSRVSGLSGRALRRKIPFLAHALYVK-----TSMITLKGFLTAMEHAVNKORQASLVNVCV 599
gi | 79485764 | ref | NP_194202.3 | AIDVAFVDRADIKAYVGPPLHVRVEILRSVVELISKGISSFOGCDGLSIPSPFSLKKEKLESEEVHDTNTPVPWFCKQLIEAARGCEGLSGRSRRLRKLPLAHAALAD-----PYSHDFSNFLCTMIEI AKREKSEQPE 599
gi | 115458982 | ref | NP_001053091.1 | AIDIAFVDRADIKAYVGPPLQARVEILRSCLQELLRVIGILHTTQ-----GNSLWPTP----- 599
gi | 17533043 | ref | NP_495711.1 | TLDKALVDRADIVKNVQPPSDFARVSMKSSIMELARIGVVIDNEVETDVPWQDIDCTKAP-----RNEFTIILFKTAGEARGLSGRAISMLPTLVVSKSPE-----ETITLPLNCMNLFLAVKERLSRNN 599
gi | 9755327 | ref | NP_009745.2 | SLDDAFVDRADGVFYVGNPTAEGILHILKVCIEEMITSGIILFHARSTGVKFFNKYQDILR-----KIAIKCSIVDISGRITIRKLPMLCLSEYFR-----TFPVDDDEFVLALAMSARKLSAARK 599
gi | 45190349 | ref | NP_984603.1 | SMDPAFIDRADGIFNVPTPTQGCQNILELNI SKLLTAGVI--HASKEHMLYSPPVQAALQ-----PIVIRCADLRLSGRTMGKLPKALSENFT-----NLEVDLKDFTIVALASVI----- 599

```

